

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 26, 2004, 09:57:57 ; Search time 164 Seconds
(without alignment)
6811.684 Million cell updates/sec

Title: US-10-025-145A-64

Perfect score: 2013

Sequence: 1 ttttgacgtgccttcttctc.....aaaaaaaaaaaaaaaaaa 2013

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------------|
| 1 | 2013 | 100.0 | 2013 | 4 | US-09-360-545-64 |
| 2 | 1306.8 | 64.9 | 2018 | 4 | US-09-360-545-3 |
| 3 | 1306.8 | 64.9 | 2018 | 4 | US-09-398-395A-19 |
| 4 | 1306.8 | 64.9 | 2018 | 4 | US-09-887-586A-19 |
| 5 | 1306.8 | 64.9 | 2018 | 4 | US-09-895-752-19 |
| 6 | 1306.8 | 64.9 | 2018 | 4 | US-09-903-012B-19 |
| 7 | 1306.8 | 64.9 | 2018 | 4 | US-09-900-797-19 |
| 8 | 1092.4 | 54.3 | 1890 | 4 | US-09-360-545-77 |
| 9 | 1072.4 | 53.3 | 2186 | 4 | US-09-360-545-66 |
| 10 | 1071.6 | 53.2 | 2196 | 4 | US-09-360-545-1 |
| 11 | 1071.6 | 53.2 | 2196 | 4 | US-09-398-395A-29 |
| 12 | 1071.6 | 53.2 | 2196 | 4 | US-09-887-586A-29 |
| 13 | 1071.6 | 53.2 | 2196 | 4 | US-09-895-752-29 |
| 14 | 1071.6 | 53.2 | 2196 | 4 | US-09-903-012B-29 |
| 15 | 1071.6 | 53.2 | 2196 | 4 | US-09-900-797-29 |
| 16 | 1071.6 | 53.2 | 2205 | 4 | US-09-360-545-31 |
| 17 | 929.4 | 46.2 | 2429 | 4 | US-09-360-545-68 |
| 18 | 925.4 | 46.0 | 2089 | 4 | US-09-360-545-5 |
| 19 | 925.4 | 46.0 | 2089 | 4 | US-09-398-395A-57 |
| 20 | 925.4 | 46.0 | 2089 | 4 | US-09-887-586A-57 |
| 21 | 925.4 | 46.0 | 2089 | 4 | US-09-895-752-57 |
| 22 | 925.4 | 46.0 | 2089 | 4 | US-09-903-012B-57 |
| 23 | 925.4 | 46.0 | 2089 | 4 | US-09-900-797-57 |
| 24 | 471 | 23.4 | 696 | 4 | US-09-360-545-70 |
| 25 | 448.6 | 22.3 | 1885 | 3 | US-09-234-393-47 |
| 26 | 448.6 | 22.3 | 1885 | 4 | US-09-865-171-47 |
| 27 | 445.8 | 22.1 | 1865 | 4 | US-09-398-395A-47 |

| | | | | | | |
|----|-------|------|------|---|-------------------|-------------------|
| 28 | 445.8 | 22.1 | 1865 | 4 | US-09-887-586A-47 | Sequence 47, Appl |
| 29 | 445.8 | 22.1 | 1865 | 4 | US-09-895-752-47 | Sequence 47, Appl |
| 30 | 445.8 | 22.1 | 1865 | 4 | US-09-903-012B-47 | Sequence 47, Appl |
| 31 | 445.8 | 22.1 | 1865 | 4 | US-09-900-797-47 | Sequence 47, Appl |
| 32 | 445.8 | 22.1 | 1885 | 3 | US-09-234-393-45 | Sequence 45, Appl |
| 33 | 445.8 | 22.1 | 1885 | 4 | US-09-865-171-45 | Sequence 45, Appl |
| 34 | 445.8 | 22.1 | 1885 | 3 | US-09-234-393-19 | Sequence 19, Appl |
| 35 | 445.8 | 22.1 | 1885 | 4 | US-09-865-171-19 | Sequence 19, Appl |
| 36 | 444.2 | 22.1 | 1885 | 3 | US-09-234-393-43 | Sequence 43, Appl |
| 37 | 444.2 | 22.1 | 1885 | 4 | US-09-865-171-43 | Sequence 43, Appl |
| 38 | 429.6 | 21.3 | 1967 | 3 | US-09-234-393-14 | Sequence 14, Appl |
| 39 | 429.6 | 21.3 | 1967 | 4 | US-09-360-545-17 | Sequence 17, Appl |
| 40 | 429.6 | 21.3 | 1967 | 4 | US-09-865-171-14 | Sequence 14, Appl |
| 41 | 427 | 21.2 | 2700 | 3 | US-09-315-861-1 | Sequence 1, Appl |
| 42 | 427 | 21.2 | 2700 | 4 | US-09-398-395A-43 | Sequence 43, Appl |
| 43 | 427 | 21.2 | 2700 | 4 | US-09-887-586A-43 | Sequence 43, Appl |
| 44 | 427 | 21.2 | 2700 | 4 | US-09-895-752-43 | Sequence 43, Appl |
| 45 | 427 | 21.2 | 2700 | 4 | US-09-903-012B-43 | Sequence 43, Appl |

ALIGNMENTS

| | | | | | | | | | |
|--|-----|--|-----|--|--|--|--|--|--|
| RESULT 1 | | | | | | | | | |
| US-09-360-545-64 | | | | | | | | | |
| ; Sequence 64, Application US/09360545 | | | | | | | | | |
| ; Patent No. 6429014 | | | | | | | | | |
| ; GENERAL INFORMATION: | | | | | | | | | |
| ; APPLICANT: Croteau, Rodney B | | | | | | | | | |
| ; APPLICANT: Bohlmann, Joÿg | | | | | | | | | |
| ; APPLICANT: Steele, Christopher L | | | | | | | | | |
| ; APPLICANT: Phillips, Michael A | | | | | | | | | |
| ; TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS) | | | | | | | | | |
| ; FILE REFERENCE: wbur13835 | | | | | | | | | |
| ; CURRENT APPLICATION NUMBER: US/09/360, 545 | | | | | | | | | |
| ; CURRENT FILING DATE: 1999-07-26 | | | | | | | | | |
| ; EARLIER APPLICATION NUMBER: 60/052, 249 | | | | | | | | | |
| ; EARLIER FILING DATE: 1997-11-07 | | | | | | | | | |
| ; EARLIER APPLICATION NUMBER: PCT/US98/14528 | | | | | | | | | |
| ; EARLIER FILING DATE: 1998-07-10 | | | | | | | | | |
| ; NUMBER OF SEQ ID NOS: 107 | | | | | | | | | |
| ; SOFTWARE: PatentIn Ver. 2.0 | | | | | | | | | |
| ; SEQ ID NO 64 | | | | | | | | | |
| ; LENGTH: 2013 | | | | | | | | | |
| ; TYPE: DNA | | | | | | | | | |
| ; ORGANISM: Abies grandis | | | | | | | | | |
| ; FEATURE: | | | | | | | | | |
| ; NAME/KEY: CDS | | | | | | | | | |
| ; LOCATION: (36)..(1889) | | | | | | | | | |
| US-09-360-545-64 | | | | | | | | | |
| Query Match | | | | | | | | | |
| Best Local Similarity 100.0%; Pred. No. 0; | | | | | | | | | |
| Matches 2013; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | | | | | | | |
| Qy | 1 | TTTTGACGTGCTTCTTATCTGATGCAAGCTGAATGGCTCTTCTTCTATTACTCCGC | 60 | | | | | | |
| Db | 1 | TTTTGACGTGCTTCTTATCTGATGCAAGCTGAATGGCTCTTCTTCTATTACTCCGC | 60 | | | | | | |
| Qy | 61 | TGGTTCCAGCTGCTGCTCAGTCTTCTCATGAGATTAAAGGCTCCGTAGAACATCC | 120 | | | | | | |
| Db | 61 | TGGTTCCAGCTGCTGCTCAGTCTTCTCATGAGATTAAAGGCTCCGTAGAACATCC | 120 | | | | | | |
| Qy | 121 | CAACTCTGGAATCTGCAGCGCGGAATCCGCGCATTCATTAACATGTGTTGA | 180 | | | | | | |
| Db | 121 | CAACTCTGGAATCTGCAGCGCGGAATCCGCGCATTCATTAACATGTGTTGA | 180 | | | | | | |
| Qy | 181 | CAAGCTCGCACTACTGATTCTGTACAGACGCGTGCGCACTATCCAACTGT | 240 | | | | | | |
| Db | 181 | CAAGCTCGCACTACTGATTCTGTACAGACGCGTGCGCACTATCCAACTGT | 240 | | | | | | |
| Qy | 241 | GGACGATGATTCATACAGTCTCTGATCTCAACGCCTTATGAGACCTGATTACCGG | 300 | | | | | | |
| Db | 241 | GGACGATGATTCATACAGTCTCTGATCTCAACGCCTTATGAGACCTGATTACCGG | 300 | | | | | | |

Db 241 GGGACGATGATTTTCATACAGTCTCTGATCTCAACGCCCTTANGAGCACCTGATTACCGGG 300
Qy 301 AACGTCTGACAGACTTATTTGGGGAAGTAAAGATATATATGTTCAATTTCAAGTCGCTGG 360
Db 301 AACGTCTGACAGACTTATTTGGGGAAGTAAAGATATATATGTTCAATTTCAAGTCGCTGG 360
Qy 361 AAGATGGAGCAATGATCTCTTCAACGACTTTTGGTGTGATGACGTTGAACGTTTGG 420
Db 361 AAGATGGAGCAATGATCTCTTCAACGACTTTTGGTGTGATGACGTTGAACGTTTGG 420
Qy 421 GAATCGACGACATTTCAAAAAAGAGTAAACGGCACTCGATTATGTTAACAGTTATT 480
Db 421 GAATCGACGACATTTCAAAAAAGAGTAAACGGCACTCGATTATGTTAACAGTTATT 480
Qy 481 GGAACGAAAAAGGCATTGGATGTGGAGGGAGAGTGTGTGACTGACCTCAACTCAACCG 540
Db 481 GGAACGAAAAAGGCATTGGATGTGGAGGGAGAGTGTGTGACTGACCTCAACTCAACCG 540
Qy 541 CCTTGGGCTTCGAACCTCTCCGACTACAGGATACACTGTGTCTTCAGATGTTTGAACG 600
Db 541 CCTTGGGCTTCGAACCTCTCCGACTACAGGATACACTGTGTCTTCAGATGTTTGAACG 600
Qy 601 TTTTAAAGCAAAAAATGGCAATTTTCTCCACTGCAATATTCAGATAGAGGAGAGA 660
Db 601 TTTTAAAGCAAAAAATGGCAATTTTCTCCACTGCAATATTCAGATAGAGGAGAGA 660
Qy 661 TTAGAGCGCTTCTCAATTTATTCAGGCGCTCCCTCGCTTCCCGCGAGAAAGTTA 720
Db 661 TTAGAGCGCTTCTCAATTTATTCAGGCGCTCCCTCGCTTCCCGCGAGAAAGTTA 720
Qy 721 TGGATGAGCTGAAACATTCTCTACAAATATTTAAGAGAGCCCTGCAAAAAGATTCCGG 780
Db 721 TGGATGAGCTGAAACATTCTCTACAAATATTTAAGAGAGCCCTGCAAAAAGATTCCGG 780
Qy 781 CATCCAGTATCTTCTACAGAGATACGGGACGTTCTGGAATATGTTGGCACACCAATT 840
Db 781 CATCCAGTATCTTCTACAGAGATACGGGACGTTCTGGAATATGTTGGCACACCAATT 840
Qy 841 TGGCAGCGTTGGAAAGCAAGGAATTACATGAGCGTCTTGGACAGCACATAAAATAAGA 900
Db 841 TGGCAGCGTTGGAAAGCAAGGAATTACATGAGCGTCTTGGACAGCACATAAAATAAGA 900
Qy 901 ACGCCGCCGAGAACTTTTAGAAGCTTGCAAAATTGGAATTCAATATATTTCACTCCTTAC 960
Db 901 ACGCCGCCGAGAACTTTTAGAAGCTTGCAAAATTGGAATTCAATATATTTCACTCCTTAC 960
Qy 961 AAGAGAGAGGTAAACATGTTCCCGATGGTGAAGAGACTCGGCTTCTCTGAGATGA 1020
Db 961 AAGAGAGAGGTAAACATGTTCCCGATGGTGAAGAGACTCGGCTTCTCTGAGATGA 1020
Qy 1021 CCTTCTGTGACATCGTCAAGTGAATCTACGCTTTGGCTTCCGTGCAATTGCGTTGAGC 1080
Db 1021 CCTTCTGTGACATCGTCAAGTGAATCTACGCTTTGGCTTCCGTGCAATTGCGTTGAGC 1080
Qy 1081 CTCAACATTTCTGATTCAGACTCGGCTTTACCAAGATGTCTCATCTTATCAACGGTCTTG 1140
Db 1081 CTCAACATTTCTGATTCAGACTCGGCTTTACCAAGATGTCTCATCTTATCAACGGTCTTG 1140
Qy 1141 ACGACATGTACGACGTCTTCGGCACAGTACGAGCTGGAACCTTCAACGCAACATTA 1200
Db 1141 ACGACATGTACGACGTCTTCGGCACAGTACGAGCTGGAACCTTCAACGCAACATTA 1200
Qy 1201 AGAGATGGATCCGTCGCGATGGAATGCTTCCAGAATATATGAAGAGTGTACATGA 1260
Db 1201 AGAGATGGATCCGTCGCGATGGAATGCTTCCAGAATATATGAAGAGTGTACATGA 1260
Qy 1261 TGGTTTATCACACCGTAAATGAGTGGCTGAGTGGCAGAGAAAGCTCAAGCCGAGACA 1320
Db 1261 TGGTTTATCACACCGTAAATGAGTGGCTGAGTGGCAGAGAAAGCTCAAGCCGAGACA 1320
Qy 1321 CGCTCAACTATGCAAGACAGGCTTGGGAGCGCTTTTGATTCTGTATATGCAGGAAGCAA 1380
Db 1321 CGCTCAACTATGCAAGACAGGCTTGGGAGCGCTTTTGATTCTGTATATGCAGGAAGCAA 1380

Qy 1381 AGTGATCGCCACTGGTTATCTGCCACGTTTGAGAGTACTTGAGAACGGAAAGTTA 1440
Db 1381 AGTGATCGCCACTGGTTATCTGCCACGTTTGAGAGTACTTGAGAACGGAAAGTTA 1440
Qy 1441 GCTTCTCATCGCCCATGCGCACTGCAACCCATTCTGACGTTGGACATCCCTTCTCTG 1500
Db 1441 GCTTCTCATCGCCCATGCGCACTGCAACCCATTCTGACGTTGGACATCCCTTCTCTG 1500
Qy 1501 ATCAATCCTCAAGGAAGTTGACTTCCCATCGAAGCTCAATGACTTGATATGTATCATCC 1560
Db 1501 ATCAATCCTCAAGGAAGTTGACTTCCCATCGAAGCTCAATGACTTGATATGTATCATCC 1560
Qy 1561 TTGATTAAGAGGTGATACACGCTGCTACAAAGGCAGACAGGCCCCGTGAGAGAAGCTT 1620
Db 1561 TTGATTAAGAGGTGATACACGCTGCTACAAAGGCAGACAGGCCCCGTGAGAGAAGCTT 1620
Qy 1621 CGTCTATATCATGTTATATGAAGACAATCCTGATTTAACGGAAGAGTCTTGAATC 1680
Db 1621 CGTCTATATCATGTTATATGAAGACAATCCTGATTTAACGGAAGAGTCTTGAATC 1680
Qy 1681 ATATCACTTCATGATCAGGACGCAATCAGAGAATTAATTGGAGCTTCTAAAGCCAG 1740
Db 1681 ATATCACTTCATGATCAGGACGCAATCAGAGAATTAATTGGAGCTTCTAAAGCCAG 1740
Qy 1741 ACAACAGTGTTCCTCATCATCTTCCAAGAAACACGCAATTTGACATAAGCAGATTGGCATC 1800
Db 1741 ACAACAGTGTTCCTCATCATCTTCCAAGAAACACGCAATTTGACATAAGCAGATTGGCATC 1800
Qy 1801 ACGGTTACAGATACCGAGATGGCTACAGCTTTGCCAACGTTGAAACAAAGAGTTTGTGTA 1860
Db 1801 ACGGTTACAGATACCGAGATGGCTACAGCTTTGCCAACGTTGAAACAAAGAGTTTGTGTA 1860
Qy 1861 TGAGAACCGTCATTGGAACCTGTGCTTGTGAACAACACTTCAAACTTACAATATTAATCTG 1920
Db 1861 TGAGAACCGTCATTGGAACCTGTGCTTGTGAACAACACTTCAAACTTACAATATTAATCTG 1920
Qy 1921 AGGATGCCCTATGGGTGATATAGGGCACACAAAAATTAATATGTTGTGTAGTAAAGC 1980
Db 1921 AGGATGCCCTATGGGTGATATAGGGCACACAAAAATTAATATGTTGTGTAGTAAAGC 1980
Qy 1981 TGTATTTATGAAAAAATAAAAAAAAAAAAAA 2013
Db 1981 TGTATTTATGAAAAAATAAAAAAAAAAAAAA 2013

RESULT 2
US-09-360-545-3
; Sequence 3, Application US/09360545
; Patent No. 6429014
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B
; APPLICANT: Bohlmann, Jorg
; APPLICANT: Steele, Christopher L
; APPLICANT: Phillips, Michael A
; TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
; FILE REFERENCE: wsur13885
; CURRENT APPLICATION NUMBER: US/09/360,545
; EARLIER FILING DATE: 1999-07-26
; EARLIER APPLICATION NUMBER: 60/052,249
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: PCT/US98/14528
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2018
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)..(1892)
; OTHER INFORMATION: Clone AG3.18 encoding pinene synthase

US-09-360-545-3

```
Query Match      64.9%; Score 1306.8; DB 4; Length 2018;
Best Local Similarity 81.0%; Pred. No. 0;
Matches 1595; Conservative 0; Mismatches 342; Indels 33; Gaps 5;

Qy      68 CAGGTCGCTCAAGTCTTCTCATGAGATTAAAGGCTCTCCGTAGAACATCCCACTCT 127
Db      53 CAAATCGTTGATCAAGTTCTACCCCATGAGCTTAAAGGCTCTCTAGAACATTCAGCTCT 112

Qy     128 TGGAACTGCAAGCGCCGGGAAATCCGCGGCATTCATTAACATGTTGACAAGCGT 187
Db     113 AGGAATGAGTAGCGAGGAAATCTATCACTCTCCATCAGCATGAGCTCTAACACCGT 172

Qy     188 CGCATCTAAGTCTGTACAGAGACGCGGCAACTATCATTCCTCAACCTGTGGAGCA 247
Db     173 TGTAAACGATGATGGTGTACGAGACGCAATGGCGGATTCATTCCAACCTCTGGAGCA 232

Qy     248 TGATTTCAATACAGTCTCTGATCTCAACGCTTATGAGCACCTGATTAACGGGAACGTG 307
Db     233 TGATGTCATACAGTCT--TTACCAACGGCTTATGAGGAAATCGTACCTGGAACGTG 289

Qy     308 TGACAGACTTATTTGGGGAAGTAAAGGATTAATGTTCAATTTCAAGTCGCTGGAAGATGG 367
Db     290 TGAGAACTGATCGGGGAAGTAAAG--AACTGTTCAATTCGATGTCATTAAGAAATGG 346

Qy     368 AG-----GCAATGATCTCTCTCAACGACTTTTGTGCTGATGACGTTGA 412
Db     347 AGAGTTAATGAGTCCGCTCAATGATCTCATTCAAACGCTTGGATGTCGACAGCCTTGA 406

Qy     413 ACGTTTGGGAATCGACAGGCAATTTCAAAAAAGATAAAAAAGGCACTCGATTATGTTAA 472
Db     407 ACGTTTGGGATCCATAGACATTTCAAGATGAGATAAAATCGCGCTTGATTATGTTA 466

Qy     473 CAGTTATGGAACGAAAAAGCATTTGATGAGGAGGAGAGATGTTGACTGACCTCAA 532
Db     467 CAGTTATGGGGCGAAATGCGATCGGATGGGAGAGAGATGTTGTTAATGATCTGAA 526

Qy     533 CTCAACCGCTTGGGCTTGCAGACTCTCCGACTACACGATACACTGCTCTTCAGATGT 592
Db     527 CTCAACTGCTTGGGCTTCGAACCTTCAGCACTACACGATACCCGCTCTCTTCAGATGT 586

Qy     593 TTTGAACGTTTTTAAAGACAAAAATGGGCAATTTCTCCACTGCCAATATTCAGATAGA 652
Db     587 TTTCAAGCTTTCAAAAGGCCAAATGGGCAATTTCTGCTCTGAAAAATATTCAGACAGA 646

Qy     653 GGGAGAGATTAGAGCGCTTCTCAATTTATTCAGGCGCTCCCTCGTCGCTTCCCGGCGA 712
Db     647 TGAAGAGATCAGAGCGCTTCTGAATTTATTCGGGCGCTCCCTCATTTGCTTCCAGGGGA 706

Qy     713 GAAAGTTATGAGTGAAGCTGAACATTTCTCAAAATATTTAAGAGAACCCCTGCAAAA 772
Db     707 GAAATATATGATGAGGCTGAATCTTCTACCAATATTTAAAGAACCCCTGCAAAA 766

Qy     773 GATTCGCGATCCAGTATATCTTCACTAGAGATACGGGACGTTCTGAATATGTTGCA 832
Db     767 GATTCGCGTCTCCAGT--CTTTCGCGAGAGATCGGGGACGTTTGAATATGTTGCA 823

Qy     833 CACCAATTTGCCACGCTTGAAGCAAGAAATTAATGAGCGTCTTTGACAGACACTAA 892
Db     824 CACATATTTGCCCGCATTTGAAGCAAGAAATTAATCCAAAGTCTTTGACAGACACTGA 883

Qy     893 AAATAAGAAAGC-----CGCCGAGAACTTTTGAAGCTTGAACCTTGAATTCAA 943
Db     884 GAACACGAGTCAATATGTGAAAGAGCAAAAACTTTAGAACTCGCAAAATGGAAGTTCAA 943

Qy     944 TATATTTCACTCTTACAAAGAGAGAGATTAAACATGTTTCCCGATGCTGAAAGACTC 1003
Db     944 CATCTTCAATCCTTACAAAAAGAGGAGATTAGAAAAGTCTGTCAAGTGTGAAAAAGATC 1003

Qy     1004 GGGTTCCTGAGATGACCTTCTGTGACATCGTCAAGTGAATATAAGCTTTGGCTTC 1063
Db     1004 GGGTTTCTGAGATGACCTTCTGCGGACATCGTCAAGTGAATATACTTTGGCTTC 1063
```

```
Qy      1064 CTGCATTGCGCTTCAGCCTCAACATTTCTGATTCAGACTCGGCTTTAACCAAGATGTCTCA 1123
Db      1064 CTGCATTGCGCTTCAGCCTCAACATTTCTGATTCAGACTCGGCTTTGCAAGACGTGTCA 1123

Qy     1124 TCTTATCAGGTTCTTGACGACATGTAAGACGCTCTTCGGACAGTGAAGAGCTGAACT 1183
Db     1124 TCTTATCAGGTTCTTGACGATATGTAAGACACTTCGGACAGTGAAGAGCTGAACT 1183

Qy     1184 CTTACAGCGCAATTAAGAGATGGATCCGTCGCGATGGAATGCTTCCAGATATAT 1243
Db     1184 CTTACAGCGCAATGAAGATGGATCCGTCCTCGATAGATTGCTTCCAGATATAT 1243

Qy     1244 GAAAGAGTGTACATGATGTTTATCACACCGTAAATGAATGGCTCGAGTGGCAGAGAA 1303
Db     1244 GAAAGAGTGTACATAGCGGTTTACGACACCGTAAATGAATGGCTCGAGAGCAGAGAA 1303

Qy     1304 GGCTCAAGCGCGAGACACGCTCAACTATGCAAGACAGGCTTGGAGGCGTGTGATTC 1363
Db     1304 GGCTCAAGCGCGAGATACGCTCAATATGCTCGGGAAGCTTGGAGGCTTATATGATTC 1363

Qy     1364 GTATATGACAGAAACAAAGTGAATGCCACTGTTATCTGCCACGTTTGAGAGTACTT 1423
Db     1364 GTATATGACAGAAACAAAGTGAATGCCACTGTTACTGCTGCCCTCTTGATGAGTACTA 1423

Qy     1424 GGAGAACGGGAAGTTAGCTCTGCTCATCGCCCATGCGCACCTGCAACCATTTGACGTT 1483
Db     1424 CGAGATGGGAAGTTAGCTGTGTGTCATCGCATATCCGATGCAACCATTTGACAAAT 1483

Qy     1484 GGACATCCCTTCTCTGATCACATCTCTCAAGGAAGTTGACTTCCCATCGAAGCTCAATGA 1543
Db     1484 GGACATCCCTTCTCTGATCATATCTCTCAAGGAAGTTGACTTCCCATCAAGCTTAAAGCA 1543

Qy     1544 CTGTATATGATCATCTCTGATTAAGAGTGATACACGCTGCTTACAGGACAGAGGCG 1603
Db     1544 CTGGCATGCTCATCTCTGATTAAGAGTGATACGCGCTGCTTACAGGACAGAGGCG 1603

Qy     1604 CCGTGAGAGAAAGCTTCGCTTATATCATGTTATATGAAGACAACTCTGATTAACGGA 1663
Db     1604 TCGTGAGAGAAAGCTTCCTCTATATCATGTTATATGAAGACAACTCTGAGTATCAGA 1663

Qy     1664 AGAAGATGCTCTAATCATATCAACTTCATGATCAGGAGCGCAATGAGAAATTAATTG 1723
Db     1664 GGAAGATGCTCTGATCATATCAAGCCATGATCAGTACGTAATCAAGATTAATTTG 1723

Qy     1724 GGAGCTTCTAAGCCAGACAAAGTGTCCCATCACTTCCAGAAACAGCATTTGACAT 1783
Db     1724 GGAATGCTCTGATCATATCAAGCCATGATCAGTACGTAATCAAGATTAATTTG 1783

Qy     1784 AAGCAGATTGCGCATCAAGGTTACAGATACCGAGATGGCTACAGCTTTGCCAACGTTGA 1843
Db     1784 CGCCAGAGCTTTCATTACGCGCTACAAATACCGAGACGCGTACAGCGTTGCCAACGTTGA 1843

Qy     1844 AACAAAGATTGGTGATGAGAACCGCTCATTTGAACCTGTGCTTTGTTAAACAACACTTCAA 1903
Db     1844 AACAAAGATTGGTGATGAGAACCGCTCATTTGAATCTGTGCTTTGTTAAACAACACTTCAA 1903

Qy     1904 ATCTACAAATATTAACCTGAGGATGCCCTATGGGTATATATAGGGCACAAAAATTAATAT 1963
Db     1904 ATCTATGCCCTATGCTATGTGCGGTTAAATATATGTGAAGGTAGCGCTTGATGTAGA 1963

Qy     1964 GGTGTGTAGTAAAGCTGTAAATTTATGAAAAAATTTGAAAAAATTTGAAAAAATTTGAAAAA 2013
Db     1964 GGATAGTTGTATATATTAATTAAGTTGTAATTTTAAAAAATTTGAAAAAATTTGAAAAA 2013
```

RESULT 3
US-09-398-395A-19
; Sequence 19, Application US/09398395A
; Patent No. 6468772
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 6468772.1, Joseph P.

| | | | | | | | | | | | | | | | | |
|----|------|---------|---------|--------|--------|---------|--------|-------|--------|-------|--------|--------|--------|--------|------|------|
| QY | 1124 | TCTTATC | ACGGTTC | TGACG | CATGT | ACG | CGTCTT | CGG | CAC | AGT | AGAC | AGCTG | GA | 1183 | | |
| Db | 1124 | TCTTATC | ACGGTTC | TGACG | ATATGT | ACG | ACAC | CGTTC | GGC | AC | AGT | AGAC | AGCTG | GA | 1183 | |
| QY | 1184 | CTTCA | CGCGA | CAATTA | AGAGAT | GGGAT | CCGTC | CGG | CA | TGA | ATG | CCCTT | CCAG | ATATAT | 1243 | |
| Db | 1184 | CTTCA | CGCGA | CAATTA | AGAGAT | GGGAT | CCGTC | CGG | CA | TGA | ATG | CCCTT | CCAG | ATATAT | 1243 | |
| QY | 1244 | GAAAG | AGGTG | TACAT | GATGG | CTTTAT | CA | CAC | CGT | AAAT | GAAAT | GGCTC | GAG | GTG | 1303 | |
| Db | 1244 | GAAAG | AGGTG | TACAT | AGCGG | TTTAC | GAC | AC | CGT | AAAT | GAAAT | GGCTC | GAG | GTG | 1303 | |
| QY | 1304 | GGCTC | AAGG | CCGAG | ACGCT | CAACTAT | GCA | AGAC | AGG | CTTGG | GAGG | CGTGT | TTGAT | TC | 1363 | |
| Db | 1304 | GGCTC | AAGG | CCGAG | ATACG | CTCA | CATAT | AGCTC | CGG | AGAG | CGTTGG | GAGG | CGTTAT | TTGAT | TC | 1363 |
| QY | 1364 | GTA | TATG | CAGG | AGCA | AGTGS | ATCG | CCCA | CTGG | TATCT | GGCCA | CGTTG | AGG | AGTACT | 1423 | |
| Db | 1364 | GTA | TATG | CAGG | AGCA | AGTGS | ATCG | CCCA | CTGG | TATCT | GGCCA | CGTTG | AGG | AGTACT | 1423 | |
| QY | 1424 | GGAG | AACG | GGAAG | TAGCT | CTGCT | CA | TGCG | CCCAT | GCG | CACTG | CAACCC | CA | TTCTG | 1483 | |
| Db | 1424 | GGAG | AATG | GGAAG | TAGCT | GTG | CTC | ATCG | CA | TGCG | CCCAT | GCG | CA | TTCTG | 1483 | |
| QY | 1484 | GGAC | ATC | CCCC | TTCT | CTG | ATCA | TCCT | CA | AGGA | AGTTG | ACTTCC | CA | TGGA | 1543 | |
| Db | 1484 | GGAC | ATC | CCCC | TTCT | CTG | ATCA | TCCT | CA | AGGA | AGTTG | ACTTCC | CA | TGGA | 1543 | |
| QY | 1544 | CTTGA | TATG | TATCAT | CTCG | ATTA | AGAG | GTG | ATAC | ACG | GTGTA | CAAG | CG | CAG | 1603 | |
| Db | 1544 | CTTGA | TATG | TATCAT | CTCG | ATTA | AGAG | GTG | ATAC | ACG | GTGTA | CAAG | CG | CAG | 1603 | |
| QY | 1604 | CCGTG | AG | AGAG | AGCTT | CGTCTA | TAT | ATCAT | GT | TATAT | GAA | AGCAAT | CC | CTG | 1663 | |
| Db | 1604 | TCGTG | AG | AGAG | AGCTT | CGTCTA | TAT | ATCAT | GT | TATAT | GAA | AGCAAT | CC | CTG | 1663 | |
| QY | 1664 | AGA | AGATG | CTCT | GATCAT | ATCA | CTT | CATG | ATCA | GGG | AGCG | CAATC | AGA | ATTA | 1723 | |
| Db | 1664 | GGAA | GATG | CTCT | GATCAT | ATCA | CGCC | ATGAT | CA | GTG | ACGT | TAAT | CA | AAAG | 1723 | |
| QY | 1724 | GGAG | CTT | CTA | AAAG | CCAG | ACA | CA | GTG | TTCC | CA | CTT | CA | AGAA | 1783 | |
| Db | 1724 | GGA | ACTT | CTCA | AAAC | CGAC | ATCA | ATG | TTCC | CA | CTT | CGG | CA | AGAA | 1783 | |
| QY | 1784 | AAG | CAG | AGTTG | G | CA | TCA | CGG | TTA | CAG | ATAC | CG | AG | ATG | 1843 | |
| Db | 1784 | CGC | CAG | AGCTT | CCAT | TA | CGG | CTA | CA | AAAT | AC | GAG | AC | G | 1843 | |
| QY | 1844 | AACA | AAAG | ATTTG | G | TGA | AGAA | CCG | TCAT | TGA | AC | CTG | GC | TTG | 1903 | |
| Db | 1844 | AAC | GAAG | ATTTG | G | TGA | AGAA | CCG | TCAT | TGA | AC | CTG | GC | TTG | 1903 | |
| QY | 1904 | ATCTA | CA | TATTA | CTGA | CGAT | CGCC | TATG | GGT | GTAT | ATAG | GG | CA | CA | 1963 | |
| Db | 1904 | ATCTA | TG | CCCTAT | GCTAT | GT | CGG | GTTAA | AAATAT | ATAT | GTG | GA | AG | CGCTG | 1963 | |
| QY | 1964 | GGT | TG | TAGT | AAAG | CTG | TAA | TTTAT | G | AAAA | AAAA | AAAA | AAAA | AAAA | 2013 | |
| Db | 1964 | GGAT | AA | GTTTGT | TAT | TAAT | TAA | AGTTG | TAA | TTTAA | AAAA | AAAA | AAAA | AAAA | 2013 | |

```

RESULT 6
US-09-903-012B-19
; Sequence 19, Application US/09903012B
; Patent No. 6569656
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 65696561, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903, 012B

```

```

; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 2018
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)..(1889)
; OTHER INFORMATION: pinene synthase
US-09-903-012B-19

```

| | | | | |
|----------------------------|-------|-----------------|------------|--------------|
| Query Match | 64.9% | Score 1306.8; | DB 4; | Length 2018; |
| Best Local Similarity | 61.0% | Pred. No. 0; | | |
| Matches 1595; Conservative | 0; | Mismatches 342; | Indels 33; | Gaps 5 |

| | | | |
|----|-----|--|-----|
| QY | 68 | CAGGTCGTGCTCAGTTCCTTCATGAGATTAAAGCTCTCCGTAGAACAAATCCCAACTCT | 127 |
| Db | 53 | CAAAATCGTTGATGATTTCTAACCATGAGCTTAAAGCTCTCTCTAGAACAAATCCCACTCT | 112 |
| QY | 128 | TGGAATCTGCAGAGCCGGGAAATCCGTCGCCATTCATMAACATGTTGACAAAGCGT | 187 |
| Db | 113 | AGGAATGAGTAGAGCGAGGAAATCTATCACTCTTCATCAGCATGAGCTCTACCAACGT | 172 |
| QY | 188 | CGCATCTACTGATTCGTGTACAGACGCGTGGGCAACTATCATTCCAACCTGTGGACGA | 247 |
| Db | 173 | TGTAACCGATGATGGGTGTACAGACGCAATGGGCGATTCATTCCAACCTCTGGGACGA | 232 |
| QY | 248 | TGATTTCATACASTCTCTGATCTCAACGCCCTTATGAGCACCTGATTAACGGGAACGTGC | 307 |
| Db | 233 | TGATGTCATACAGTCT--TTACCAACGCGCTTATGAGGAAAAATCGTACTCGGAGCGTGC | 289 |
| QY | 308 | TGACAGACTTATTTGGGGAAGTAAAGGATATATATGTTCAATTTCAAGTCGCTGGAAGATGG | 367 |
| Db | 290 | TGAGAAACTGATCGGGGAAGTAAAG--AACATGTTCAATTCGATGTCTATTAGAAAGATGG | 346 |
| QY | 368 | AG-----GCAATGATCTCTCTCAACGACTTTTGTGCTGTGATGACGTTGA | 412 |
| Db | 347 | AGAGTTAATGAGTCCGCTCAATGATCTCATTCAAACGCTTGTGATGTGTGACAGCCTTGA | 406 |
| QY | 413 | ACGTTTGGGAATCGACAGGCAATTCAAAAAAGAGATMAAAACGGCACTGATTAATGTTAA | 472 |
| Db | 407 | ACGTTTGGGATCCATGACATTAATTCAAAGATGAGATAAATCGCGCTTGATTAATGTTAA | 466 |
| QY | 473 | CAGTTATTGAAACGAAAAAGCATTTGATGTGGAGGAGAGAGTGTGTGACTGACCTCAA | 532 |
| Db | 467 | CAGTTATTGGGCGGAAATGGCATCGGATCGGGAGGAGAGTGTGTACTGATCTGAA | 526 |
| QY | 533 | CTCAACCGCCTTGGGGCTTCGAACCTCTCCGACTACACGGATACACTGTCTTCAGATGT | 592 |
| Db | 527 | CTCAACTGCGTGGGGCTTCGAACCTTACGACTACACGGATACCCGGTGTCTTCAGATGT | 586 |
| QY | 593 | TTTGAACGTTTATAAGACAAAAATGGGCAATTTCTCTCCACTGCGCAATATTCAGATAGA | 652 |
| Db | 587 | TTTCAAAAGCTTTCAAAGGCCAAAAATGGGCAATTTCTCTGTCTGTGAAAAATTCAGACAGA | 646 |
| QY | 653 | GGGAGAGATTAGAGCGCTTCTCAATTTATTCAGGGCCTCCCTCGTCGCTTTCCCGGCGA | 712 |
| Db | 647 | TGAAGAGATCAGAGCGCTTCTGAATTTATTCGGGCTCCCTCATTTGCTTCCAGGGGA | 706 |
| QY | 713 | GAAAGTTATGATGAAGCTGAACATTTCTCTACAAATATTTAAGAAAGCCCTGCAAAA | 772 |
| Db | 707 | GAAATTTATGATGAGGCTGAACATTTCTCTACCAATATTTAAGAAAGCCCTGCAAAA | 766 |
| QY | 773 | GATTCGCGCATCCAGTATACTTTCCTAGAGATACGGACGTTCTGGAATATGTTGGCA | 832 |

```
Db 767 GATTCGGTCTCCAGT--CTTTCGGAGAGATCGGGGACGTTTGGAAATATGTTGGCA 823
Qy 833 CACCAATTGGCCAGCCTTGGAGCAAGAAATTACATGAGCGTCTTTGGACAGCACACTAA 892
Db 824 CACATATTTGCCGATTTGGAAGCAAGAAATTACATCCAAAGTCTTTGACAGAGACTGA 883
Qy 893 AAATAAGAACGC-----CGCCGAGAACTTTTAGAACTTGCAAAATTGGAATTCAA 943
Db 884 GAAACAGAGATCATATGTGAAGAGCAAAAACTTTAGAACTCGCAAAATTGGAGTTCAA 943
Qy 944 TATATTTCACTCCTTACAGAGAGAGAGTTAAACATGTTCCCGATGGTGAAGACTC 1003
Db 944 CATCTTTCAATCCTTACAAAGAGGAGTTAGAAAGTCTGTCAGATGGTGAAGAATC 1003
Qy 1004 GGGTTCCTCGAGATGACCTTCTGTCGACATCGTCACGTGGAATACTACGCTTTGGCTTC 1063
Db 1004 GGGTTTCTCGAGATGACCTTCTGCGCACATCGTCACTGGAATACTACACTTTGGCTTC 1063
Qy 1064 CTGCATTGCGTTGAGCCTCAACATTTGGAATTCAGACTCGGCTTTACCAAGATGCTCA 1123
Db 1064 CTGCATTGCGTTGAGCCTCAACATTTGGAATTCAGACTCGGCTTTGCAAGACGTGCTCA 1123
Qy 1124 TCTTATCAGCGTCTTGAAGATGAGATGCGTCCGCGATGGAATGCTTCCAGATATAT 1183
Db 1124 TCTTATCAGCGTCTTGAAGATGAGATGCGTCCGCGATGGAATGCTTCCAGATATAT 1183
Qy 1184 CTTACAGCGCAATTAAGAGATGGATCGCTCCGCGATGGAATGCTTCCAGATATAT 1243
Db 1184 CTTACAGCGCAATTAAGAGATGGATCGCTCCGCGATGGAATGCTTCCAGATATAT 1243
Qy 1244 GAAAGAGTATCATGATGTTTATCACACCGTAAATGAATGGCTGAGTGGCAGAGAA 1303
Db 1244 GAAAGAGTATCATGATGTTTATCACACCGTAAATGAATGGCTGAGTGGCAGAGAA 1303
Qy 1304 GGGTCAAGGCCGAGACACGCTCAACTATGCAAGACAGGCTTGGAGCGCTTTGATTTC 1363
Db 1304 GGGTCAAGGCCGAGATACGCTCAACTATGCTCGGGAAGCTTGGAGCGCTTATTTGATTTC 1363
Qy 1364 GTATATGCAAGAGCAAAAGTGGATCGGCACTGGTTATCTGCCACGTTTGAGGATCTT 1423
Db 1364 GTATATGCAAGAGCAAAAGTGGATCGGCACTGGTTATCTGCCACGTTTGAGTACTTA 1423
Qy 1424 GGAGAACGGGAAAGTTAGCTCTGCTCATCGCCCATGCGCACATGCAACCCATTTGACGTT 1483
Db 1424 CGAGATGGGAAAGTTAGCTGTGTCATGCGCATATCCGATTTGCAACCCATTTGACAAAT 1483
Qy 1484 GGACATCCCTTCTCTGATCACATCTCTCAAGAAAGTTGACTTCCCATCGAAAGCTCAATGA 1543
Db 1484 GGACATCCCTTCTCTGATCATATCTCTCAAGAAAGTTGACTTCCCATCGAAAGCTTAAAGA 1543
Qy 1544 CTTGATATGATCATCTCTGATTAAGAGTGTATACACGCTGTACAGAGGACAGACAGGC 1603
Db 1544 CTTGGCATGTGCCATCTCTGATTAAGAGTGTATACACGCTGTGTACAGAGGACAGAGGC 1603
Qy 1604 CCGTGAGAGAGAGCTTCTGTATATCATGTTATATGAAGACAAATCTGGATTTAACGGA 1663
Db 1604 TCGTGAGAGAGAGCTTCTGTATATCATGTTATATGAAGACAAATCTGGAGTATCAGA 1663
Qy 1664 AGAAGATGCTCTGAATCATATCATCACTTATGATCAGGAGCGCAATCAGAGAAATTAATTG 1723
Db 1664 GGAAGATGCTCTGATCATATCATCAAGCGCATGATCAGTACGTAATCAAGGAATTAATTG 1723
Qy 1724 GGAGCTTTAAAGCCAGACACAGTGTCCCATCACTTCCAGAGAAACGCAATTTGACAT 1783
Db 1724 GGAAGCTTTCAAAACAGACATCAATGTTCCCATCTCGGCAAGAAACATGCTTTGACAT 1783
Qy 1784 AAGCAGAGTTGGCATCAGGTTACAGATCCAGATGCTACAGCTTTGCCAAGCTTGA 1843
Db 1784 CGCCAGAGCTTTCCATTAACGCTACAAATACGAGACGCTACAGCGTTGCCAAGCTTGA 1843
Qy 1844 AACCAAGAGTTTGGTATGAGAACCGTCAATTTGAACCTGTGCTTTGTAACAACACTTCA 1903
Db 1844 AACGAAGAGTTTGGTACAGAGAACCTCTTGAATCTGTGCTTTGTAACAACAGCTCA 1903
```

```
Qy 1904 ATCTACAATATTAAGAGATGCCCTATGGGTATATAGGCAACAAAAATAAATAT 1963
Db 1904 ATCTATGCCCTATGCTATGCGGTTAAATATATATGTGAAGGTAAGCCGTTGATGTAGA 1963
Qy 1964 GGTGTGTAGTAAGCTGTATTTATGAAGAAAAAAGAAAAAAGAAAAA 2013
Db 1964 GGATAGTTTGTATATTTAATAAAGTTGTAATTTAAGAAAAAAGAAAAA 2013

RESULT 7
US-09-900-797-19
; Sequence 19, Application US/09900797
; Patent No. 6645762
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 66457621, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/900,797
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 2018
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)....(1889)
; OTHER INFORMATION: pinene synthase
US-09-900-797-19

Query Match 64.9%; Score 1306.8; DB 4; Length 2018;
Best Local Similarity 81.0%; Pred. No. 0;
Matches 1595; Conservative 0; Mismatches 342; Indels 33; Gaps 5;

Qy 68 CAGTCTGCTCCTCAGTCTTCTTCATGAGATTAAGGCTCCGTAAGAACATCCCACTCT 127
Db 53 CAATCGTTGATCAGTCTTACCATGAGCTTAAGGCTCTCTCTAGAACATTTCCAGCTCT 112
Qy 128 TGAATCTGACAGCGCGGGAATCCGTCGCGCATTTCCATTAACATGTGTTGACAAAGCT 187
Db 113 AGGAATGAGTAGGCGAGGGAATTTATCACTCTTCCATGAGATGAGCTCTAACACCTG 172
Qy 188 CGCATCTACTGATTTCTGTACAGAGACGCGTGGCAACTATCATTTCCAACCTGTGGAGCA 247
Db 173 TGTAACGATGATGTGTACAGAGACGATGGCGATTTCCATTTCAACCTGTGGAGCA 232
Qy 248 TGATTTATACAGTCTCTGATCTCAACGCTTATGAGACCTGATTAACCGGAACGTGC 307
Db 233 TGATGTATACAGTCT--TTACCAACGCGCTTATGAGGAAAAATCGTACCTGAGCGTGC 289
Qy 308 TGACAGACTTATTTGGGAAGTAAGATATATATGTTCAATTTCAAGTGGCTGGAAGATGG 367
Db 290 TGAGAACTGATCGGGGAGTAAG--AACATGTTCAATTCGATGTCAATGAGAGATGG 346
Qy 368 AG-----GCAATGATCTCTTCAACGACTTTTCTGTGTCGATGACGTTGA 412
Db 347 AGAGTTAATGAGTCCGCTCAATGATCTCATTTCAACGCTTTGATGTCGACAGCCTTGA 406
Qy 413 ACGTTGGGAATGACAGGCAATTTCAAAAAAGATAAAAAAGGCACTCGATTATGTTAA 472
Db 407 ACGTTGGGATCCATAGACATTTCAAAAGATGAGATAAATCGCGCTTGATTATGTTTA 466
```



```
OY 473 CAGTATTGGAAGAAAAGCATGTGAGGAGAGAGTGTGACTGACCTCAA 532
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 467 CAGTATTGGGCGAAAATGCGATCGGATGGGAGGAGAGTGTGTAAGTCTGAA 526
OY 533 CTCAACCGCTTGGGGCTTGAAGTCTCCACTACACGGATACATGCTCTTCAAGATGT 592
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 527 CTCAACTGCGTTGGGGCTTGAAGTCTCCACTACACGGATACCGGCTCTTCAAGATGT 586
OY 593 TTTGAACGTTTTTAAGACAAAATGGGCAATTTCTCCACTGCCAATATTCAGATAGA 652
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 587 TTTCAAGCTTTCAAAAGGCCAAAATGGGCAATTTCTCCACTGCCAATATTCAGACAGA 646
OY 653 GGGAGAGATTAGAGGCGTTCTCAATTTATTCAGGCGCTCCCTCGCTTCCCGCGGA 712
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 647 TGAAGAGATCAGAGCGCTTCTGAATTTATCCGGGCTCCCTCATGCTTTCCAGGGA 706
OY 713 GAAAGTTATGATGAAGCTGAACATTTCTCAAAAATATTTAAGAGAGCCCTGCAAAA 772
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 707 GAAATATTGATGAGGCTGAATCTTCTCAACCAATATTAAAGAGCCCTGCAAAA 766
OY 773 GATTCGGCATCCAGTATATCTTCACTAGAGATACGGGAGCTTCTGAATATGTTGCA 832
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 767 GATTCGGGTCTCCAGT---CTTCCGAGAGATCGGGGAGCTTTTGAATATGTTGCA 823
OY 833 CACCAATTGGCCACCGCTTGGAGAGAGAAATTAATGAGCGCTTTGACAGACACTAA 892
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 824 CACATATTGCGCGGATTTGAGAGCAAGAAATTAATCCAGTCTTTGACAGAGACACTGA 883
OY 893 AATTAAGACGC-----CGCCGAGAACTTTAGAACTTGCAAAATTTGAATTCAA 943
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 884 GAACACGAAATCATATGTGAGAGCAAAAACCTTTAGAACTCGCAAAATTTGAGTTCAA 943
OY 944 TATATTTCACTCTTCAAGAGAGAGATTAAACATGTTTCCCGATGCTGAAAGACTC 1003
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 944 CATCTTCAATCCTTACAAAAGAGGAGTTAAGAAAGTCTGTCAAGTGTGAAAGAAATC 1003
OY 1004 GGGTCTCTGAGATGACCTTCTGCAATCTGACGTAAGTGAATATACGCTTTGGCTTC 1063
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1004 GGGTCTCTGAGATGACCTTCTGCGGACATCGTCAAGTGAATATACGCTTTGGCTTC 1063
OY 1064 CTGCATTCGCTTGAAGCTCTCAACATTTCTGATTCAGACTCGGCTTTGCCAAGAGCTGCA 1123
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1064 CTGCATTCGCTTGAAGCTCTCAACATTTCTGATTCAGACTCGGCTTTGCCAAGAGCTGCA 1123
OY 1124 TCTTATCAGCGTTCTTGAAGATGATGACGCTCTTCCGACAGTGAAGAGCTGGAAT 1183
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1124 TCTTATCAGCGTTCTTGAAGATGATGACGCTCTTCCGACAGTGAAGAGCTGGAAT 1183
OY 1184 CTTTCAAGCGCAATTAAGAGATGGATCGCTCCGCGATGGAATGCTTCCAGAAATATAT 1243
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1184 CTTTCAAGCGCAATTAAGAGATGGATCGCTCCGCGATGGAATGCTTCCAGAAATATAT 1243
OY 1244 GAAAGAGTGTATGATGTTTATACACCGTAAATGAATGGCTGAGTGGCAGAGAA 1303
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1244 GAAAGAGTGTATGATGTTTATACACCGTAAATGAATGGCTGAGTGGCAGAGAA 1303
OY 1304 GGGTCAAGCGCGAGACACGCTCAACTATGCAAGACAGGCTTGGAGGCGTCTTTGATTC 1363
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1304 GGGTCAAGCGCGAGATACGCTCAACTATGCTCGGGAAGCTTGGAGGCTTATTTGATTC 1363
OY 1364 GTATATGCAAGAACAAAGTGGATCGCCACTGGTTATCTGCCACGTTTGAAGAGTACTT 1423
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1364 GTATATGCAAGAACAAAGTGGATCGCCACTGGTTATCTGCCACGTTTGAAGAGTACTT 1423
OY 1424 GGAGAACGGGAAAGTTAGCTGTGCTATGCGCCATGCGCACTGCAACCCATTCTGACGTT 1483
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1424 CGAGAAATGGGAAAGTTAGCTGTGCTATGCTATCCGCAATGCAACCCATTCTGACAAAT 1483
OY 1484 GGACATCCCTTCTCTGATCACAATCTCAAGGAAGTTGACTTCCCATCAAAAGCTTAAACGA 1543
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1484 GGACATCCCTTCTCTGATCACAATCTCAAGGAAGTTGACTTCCCATCAAAAGCTTAAACGA 1543
OY 1544 CTTGATATGTATCATCTTCTGATTAAGAGTGTATACAGGCTGTACAGGACAGACAGGCG 1603
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

```
DB 1544 CTTGGCATGTGCCATCTCTTCAATTAAGAGTGTATACGCGGTGTCAAGCGGACAGGCG 1603
OY 1604 CCGTGGAGAGAAAGCTTCTGCTATATCATGTTATATGAAGACAAATCCTGATTAACGGA 1663
DB 1604 TCGTGGAGAGAAAGCTTCTCTATATCATGTTATATGAAGACAAATCCTGAGTATCAGA 1663
OY 1664 AGAAGATGCTCTGAATCATATCAACTTCATGATCAGGAGACGCAATCAGAAATTAATTG 1723
DB 1664 GGAAGATGCTCTGATCATATCAAGCCATGATCAGTACGTAATCAAAAGATTAATTTG 1723
OY 1724 GGAGCTTTAAAGCCAGACACAGAGTTCCTCATCACTTCCAGAAACACGATTTGACAT 1783
DB 1724 GGAATCTTCAAAACAGACATCATGTTCCCATCTCGGCGAAGAAACATGCTTTGACAT 1783
OY 1784 AAGCAGAGTTTGGCATCACGCTTACAGATACCGAGATGCTTACAGCTTTGCCAACGTTGA 1843
DB 1784 CGCCAGAGCTTTCCATTAACGCTTACAAATACCGAGACGCTTACAGGCTTCCCAACGTTGA 1843
OY 1844 AACAAAGAGTTTGGTGTATGAGAACCGTCAATGAACTGTGCTTTGTAACAACACTTCAA 1903
DB 1844 AACGAAGAGTTTGGTGTATGAGAACCGTCAATGAACTGTGCTTTGTAACAACACTTCAA 1903
OY 1904 ATCTAATATTAATCACTGAGATGCCCTATGCGGTATATATAGGCAACAATAATATAT 1963
DB 1904 ATCTATGCCCTATGCTATGTGCGGTAAATATATATGTAAGAGTACCGCTTGATGTAGA 1963
OY 1964 GGTGTGTATGTAAGCTGTAAATTTAAGAAAAAATTTGAAAAAATTTGAAAAAATTTG 2013
DB 1964 GGATTAAGTTGTATATTAATTAATAAGTTGTAAATTTAATAAATAAATAAATAAATAA 2013
```

RESULT 8

```
US-09-360-545-77
; Sequence 77, Application US/09360545
; Patent No. 6429014
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B
; APPLICANT: Bohlmann, Jörg
; APPLICANT: Steele, Christopher L
; TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
; FILE REFERENCE: wsur13805
; CURRENT APPLICATION NUMBER: US/09/360,545
; EARLIER FILING DATE: 1999-07-26
; EARLIER APPLICATION NUMBER: 60/052,249
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: PCT/US98/14528
; EARLIER FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 77
; LENGTH: 1890
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1890)
; US-09-360-545-77
```

```
Query Match 54.3%; Score 1092.4; DB 4; Length 1890;
Best Local Similarity 76.8%; Pred. No. 2.7e-312;
Matches 1439; Conservative 0; Mismatches 396; Indels 39; Gaps 7;

OY 46 TTTCTATTAATCGCTGCTTTCCAGGCTGCTGCTCACTTCTTCTCATGAGATTAAAGCTC 105
DB 26 TGTCTTCAAAATCGGCTCTGCAAAATCGTGATCGTTTCTTACTTATGACATTAAGCTTA 85
OY 106 TCCGTAGAACATTCCTCAACTCTTGAATCTGCAGGCGCGGGAATCCGTCGCGCATTTCCA 165
DB 86 TCAGTGAACAATTCCTCAAAATCTTGAATTCGCTGGCGGAGGAATCTGTGACACATTTCCC 145
OY 166 TAAACATGTGTTTGAACAAGCGTGCATCTACTG--ATTCTGTACAGAGACGCGTGGCA 222
```

Db 146 TGAGATGAGTTTGAGCACCCGAGTCTCGATGATCATGCTGTACAAAGACGATAGTCG 205
Qy 223 ACTATCATTTCCAACCTGTGGAGCATGTTTCAACAGTCTCTGATCTCAACGCTTATG 282
Db 206 AGTTTCATTTCCAATCTGTGGAGCAGCATTTCAACAATCTC--TATCAACGCTTATG 262
Qy 283 GAGCACCCTGATTTACCGGGAACGTGTGACAGACTTATGGGGAAGTAAAGATATATGT 342
Db 263 GGGCACCCTTCATACCGTGAACGTCGTATGACTTATGTGGAAGTAAAGGCTATA--T 319
Qy 343 TCAATTTCAAGTCGCTGGAAGATGAG-----GCAATGATCTCCTTCAAC 387
Db 320 TCACTTCAATTTCAAGCAGAGATGAGAACTAATCACTCCCTCAATGATCTCATTCAAC 379
Qy 388 GACTTTTGTGCTCGATGACGTTGAACGTTTGGGAATCGACAGGCAATTCAAAAAAGAGA 447
Db 380 GCCTTTTATGTCGATACGTTGAACGTTAGGATGATAGACATTTCAAAAATGAGA 439
Qy 448 TAAAAACGGCACTCGATTATGTTAACAGTTATGGAAAGAAAAAGCATTTGATGTGGA 507
Db 440 TAAAAAGCAGCACTAGACTATGTTTACAGTTATGGAAAGAAAAAGCATTTGGCAGTGGA 499
Qy 508 GGGAGAGTGTGTGACTGACCTCAACCTCAACCGCTTGGGGCTTCCAACTCTCCGACTAC 567
Db 500 GTGATAGTGTGTGCTGATCTCAACTCAACCTGCGGCTTGGGTTTGAATTTCTTCGACTAC 559
Qy 568 ACGGATACACTGTGTCTTCAGATGTTTGAACGTTTAAAGACAAAAATGGGCA--AT 624
Db 560 ACGGATACAGTGTCTTCAGATGTTTGAACACTTCAAAAGAGAGAAAGGAGGAGGAGG 619
Qy 625 TTTCTCCACTGCCAATATTCAGATAGAGGAGAGATTAGAGCGTTCTCAATTATTTCA 684
Db 620 AGTTTGTATGTCGGCCATCCAAACAGAGAGAGATTAAGAAAGCGTTTGAATTATTTTC 679
Qy 685 GGGCTCCCTCGTCGCTTTTCCCGGAGAAAGTTATGATGAAGCTGAACATTCTCTA 744
Db 680 GGGCTCCCTCATGTCCTTCTCGGGAGAAAGTTATGAAAGGCTGAATCTTCTCTA 739
Qy 745 CAAATATTTAAGAGAAGCCCTGCAAAAGATTCGGCATCCAGTATACTTTCACTAGAGA 804
Db 740 AAATATATTTAAGAGAAGCCTTACAAATATTTGCTGTCTCCAGT---CTTTCAGAGAGA 796
Qy 805 TACGGGACGTTCTGGAATATGTTGGCACACCAATTTGCCACGCTTGAAGCAAGGAATT 864
Db 797 TAGAGTACGTTCTGGAGGATGTTGGCAACAATATGCCAAAGATTGGAACAAGGAAC 856
Qy 865 ACATGGACGTTCTTTGGAACAGCACATAAAAAATAG-----AACGCGCCGAGAAAC 915
Db 857 ACATCGATGATTTGGAGAGAGAACGATCGTATGAGACGTTATATATGAAATGAGAAAC 916
Qy 916 TTTTAGAATTCGAAAAATGGAATTCAATATATTTCACTCCTTACAAAGAGAGAGTTAA 975
Db 917 TTTTAGAAATTCGAAAAATGGAATTCAATATTTTCACTCCTTACAAAGAGAGAGCTAA 976
Qy 976 AACATGTTTCCGATGCTGGAAGAGCTGGGTTCTCTGAGATGACCTTCTGTGACATC 1035
Db 977 AAGACCTCTCCAGATGCTGGAAGAGATCGGGTTCTCTCACCTGACATTTTCTCGGCATC 1036
Qy 1036 GTCACTGGAATTAACGCTTTGGCTTCTGATTTGCCGTTGAGCCTCAACATTTCTGAT 1095
Db 1037 GTCATGTGAATTTCTACGCTCTGCGATCTTGCAATGAACTGATCGCAACATTTCCGAT 1096
Qy 1096 TCAGACTCGGCTTTTACCAAGATGTCTCATTTTATCAACGGTCTTGACGACATGTAGCAG 1155
Db 1097 TCAGACTCGGCTTTTCCAAAATGTCTCATTTTATCAACGGTTTGGACGATATATACACA 1156
Qy 1156 TCTTCGGCACAAGTACGAGCTGGAACCTTTCAAGCAGCAATTAAGAGATGGGATCCGT 1215
Db 1157 CCTTGGAAACAATGAGAGAGCTGGAACCTTTCACTGACGACATTTAAGAGATGGGATCCGT 1216
Qy 1216 CCGGATGGAATGCTTCCAGATATATGAAGAGATGTACATGATGTTTATCACACCG 1275

Db 1217 CTGCCACAGATTGCTTCCAGAGTATATGAAGGGTTGTACATGCTGCTTACGAACCG 1276
Qy 1276 TAAATGAATGGCTCGAGTGGCAGAGAGGCTCAAGGCCGAGACACGCTCAACTATGCA 1335
Db 1277 TAAATGAATTTGCTGAGAGGAGACAAGTCTCAAGGCCGAGAGACGCTCAACGATGCTC 1336
Qy 1336 GACAGCTTGGAGGCGTGTGTTGATTCGTATATGACAGAACAAAGTGATCGCCACTG 1395
Db 1337 GACAGCTTGGAGGCTTATCTGATTCGTATATGAAGAACTGAGTGATCTCCAGTG 1396
Qy 1396 GTTATGCCCCACGTTTGAAGTACTTGAGAACGGGAAAGTTAGCTCTGCTCATCGCC 1455
Db 1397 GTTATGCCCCAACGTTTGAAGTATCATGAGAACCAAGAAAGTTAGTTTGTATCGCA 1456
Qy 1456 CATGCGCACTGCAACCCATCTGACGTTGACATCCCTTCTGATCACATCCTCAAGG 1515
Db 1457 TATTCGCAATTGCAACCCATCTTCACTATGATGTTCCCTTACTCACACATCCTGCAG 1516
Qy 1516 AAGTTGACTTCCCATCGAAGCTCAATGACTGTATATGTATCATCTTCGATTAAGAGTG 1575
Db 1517 AAATAGACTTTCATTTGAGGTTTAAATGACTTAATATGTTCCATCTTCGACTTAAAAATG 1576
Qy 1576 ATACAGGTGCTACAAAGGACAGAGGCCCCGTGAGAGAAAGCTTGTCTATATCATGTT 1635
Db 1577 ACACCTGCTGTACAAAGGCGGACAGGCCCCGTGAGAGAAAGCTTGTGTATATCGTGT 1636
Qy 1636 ATATGAAGACAATCCTGATTTAAGGAAGATGCTCTGAATCATATCAACTTCATGA 1695
Db 1637 ATATGAAGAGAAATCCTGATTCACAGAGAAAGATGCTATCAATCATATCAACGCTATG 1696
Qy 1696 TCAGGACGCAATCAGAAATTAATTGGAGCTTCTAAAGCCAGACAACAGTGTCCCA 1755
Db 1697 TCAATTAATTAATCAAGAAAGTATGGAGCTTCTCCGACAGAGACGCGCTCATATA 1756
Qy 1756 TCATTTCCAAGAAACACGATTTGACATTAAGCAGAGTTTGGCATCACGGTTACAGATACC 1815
Db 1757 TTGCTTGAAGAAACACGCTTTGACATCTCTCAAGGTTCCCTTACGCGCTACAAATACC 1816
Qy 1816 GAGATGCTACAGCTTTGCCAACGTTGAACAAAGAGTTTGGTATGAGAACCGTCATTG 1875
Db 1817 GAGATGGGTTACGCGTTGCCAACAGAGAAACCAAGAAATTTGGTGAAGAGAACAGTCTTG 1876
Qy 1876 AACCTGTGCTTTG 1889
Db 1877 AGTCTGTGCTTTG 1890

RESULT 9
US-09-360-545-66
; Sequence 66, Application US/09360545
; Patent No. 6429014
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B
; APPLICANT: Bohlmann, Jorg
; APPLICANT: Steele, Christopher L
; APPLICANT: Phillips, Michael A
; TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
; FILE REFERENCE: wbur13885
; CURRENT APPLICATION NUMBER: US/09/360,545
; EARLIER FILING DATE: 1999-07-26
; EARLIER APPLICATION NUMBER: 60/052,249
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: PCT/US98/14528
; EARLIER FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 2186
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (34)..(1923)

US-09-360-545-66

| | | | | | |
|----------------------------|--------|---------------------|-------|--------------|-----------|
| Query Match | 53.3% | Score 1072.4; | DB 4; | Length 2186; | Indels 71 |
| Best Local Similarity | 76.4%; | Pred. No. 2.4e-306; | | | |
| Matches 1428; Conservative | 0; | Mismatches 391; | | Indels 51; | Gaps 7, |

| | | | |
|----|------|--|------|
| QY | 83 | TTCTTCTCATGAGATTAAAGCTCTCCGTAGAACAAATCCCACTCTTGAATCTGACGCC | 142 |
| | | | |
| Db | 90 | TACTCATCATGAGCTCAAGCCTCTGCGCAGAACCATCCCAACTCTTGAATGTAGCGC | 149 |
| | | | |
| QY | 143 | GGGGAATCCGTCCGCATTCCATAAACATGTGTTTGACAAGCGTCGATCTACTGATTC | 202 |
| | | | |
| Db | 150 | AGGGAATCTTTCAACCTCTGTGAGCATGAGTTTGACCAACCGCTGTATCTGATGATCG | 209 |
| | | | |
| QY | 203 | TGTACAGAGACCGGTGGCACTATCATTTCCAACTGTGGACGATGATTTTCATACAGTC | 262 |
| | | | |
| Db | 210 | TCTACAAAGACGCATAGGTGACTATCATTTCCAACTCTGTGGACGACGATTTTCATACAGTC | 269 |
| | | | |
| QY | 263 | TCTGATCTCAACGCCCTTATGAGCACCCTGATTACCGGGAACGTGCTGACAGACTTATTGG | 322 |
| | | | |
| Db | 270 | TC--TATCAACGCCCTTATGGGAGCCTTCTTACCAGAAAGCTGTGAGAAACTGATTGG | 326 |
| | | | |
| QY | 323 | GGAAGTAAAGGATATAATGTTCAATTTCAAGTCGCTGGAAGTGGAG----- | 369 |
| | | | |
| Db | 327 | GGAAGTGAAGG--GATGTTCAATTCATGCCATCGGAAGATGGAAGATCAATGAGTCC | 383 |
| | | | |
| QY | 370 | --GCAATGATCTCTTCAACGACTTTTGTCTGTCGATGACGTTGAACGTTTGGAAATCGA | 427 |
| | | | |
| Db | 384 | CCTCAATGATCTTATTGAACGACTTTGGATGGTCGATAGCGTTGAACGTTTGGGATTTGA | 443 |
| | | | |
| QY | 428 | CAGGCATTTCAAAAAAGAGATAAAAAACGGCACTCGATTATGTTAAACGTTATTGGAACGA | 487 |
| | | | |
| Db | 444 | TAGACATTTCAAAAAAGAGATAAAATCAGCCCTTGATATGTTTAAACGTTATTGGAACGA | 503 |
| | | | |
| QY | 488 | AAAAGCATTTGATGTGGAGGGAGAGTGTGTGACTGACCTCAACTCAACCGCCTTGGG | 547 |
| | | | |
| Db | 504 | AAAAGTATTGGATGCGGTAGAGATAGTGTTTTCTGATGTCACCTGACTGCCTCGGG | 563 |
| | | | |
| QY | 548 | GCTTCGAACCTCCGACTACACGGATACACTGTGTCTTCAGATGTTTGAACGTTTAA | 607 |
| | | | |
| Db | 564 | GTTTCGAACCTTCGCCCTACACGGATACAGTGTCTCTTCAGAGCTTTTGAAGTATTTCA | 623 |
| | | | |
| QY | 608 | AGACAAAAATGGGCAATTTCTCTCACTGCCAATATTCAAGTAGAGGAGAGATTAGAGG | 667 |
| | | | |
| Db | 624 | AGACAAAAATGGGCAATTTGCAATCTCTCC--TAGTACAAAAGAGAGACATCAGAAC | 680 |
| | | | |
| QY | 668 | CGTTCATATTATTACAGGCGCTCCCTGTCGCCCTTCCCGGAGAAAAGTTATGATGA | 727 |
| | | | |
| Db | 681 | CGTTCGAATTTATATCGGCGCTTCTTTCATTGCCCTTCCGCGGAGAAAAGTTATGAAGA | 740 |
| | | | |
| QY | 728 | AGCTGAAACATTTCTTACAAATATTTAAGAGAAGCCCTGCAAAAGATTCCGGCATCCAG | 787 |
| | | | |
| Db | 741 | GGCTGAATTTTCTCTCAAGATATTGAAAAGAAGCCGTGCAAAAGATTCGGTCTCCAG | 800 |
| | | | |
| QY | 788 | TATACTTTCACTAGAGATACGGGACGTTCTGGAATATGTTGGCACACCAATTTGCCACG | 847 |
| | | | |
| Db | 801 | T---CTTTCACAGAATAGACTACACTTTTGAATATGTTGGCACACAATATATGCCAAG | 857 |
| | | | |
| QY | 848 | CTTGAAGCAAGGAATTACATGCAAGCTTTTGACAGCACACTA-----AA | 893 |
| | | | |
| Db | 858 | ATTGGAACAAGGAATTACTTAGATGTATTTGGACATCTCTACCACTCCATGGCTCAAGAA | 917 |
| | | | |
| QY | 894 | AATTAAGAACGC-----CGCCGAGAAACTTTTGAACCTTGCAAAATTGGAATTCAA | 943 |
| | | | |
| Db | 918 | GAAAAGGACGCAATATCTGACACCGGAAAAGCTTTTAGAACTTCGCAAAATTGGAATTCAA | 977 |
| | | | |
| QY | 944 | TATATTTCACTCCTTACAGAGAGAGAGTTAAAACATGTTTCCCGATGGTGGAAAAGACTC | 1003 |
| | | | |
| Db | 978 | CATCTTTCACTCCCTTCAACAGAGAAGAGTTACAGTATCTCTCCAGATGGGTGATACATTC | 1037 |
| | | | |
| QY | 1004 | GGGTTCTCTGAGATGACCTTCTGTGACATCGTCAACGTGAAATACTACGCTTGGCTTC | 1063 |
| | | | |
| Db | 1038 | GGGTTTCCCTGAACTGACCTTTGGTGGCATCGTCAACGTGAAATACTACACCTGAGCTC | 1097 |
| | | | |

| | | | |
|----|------|--|------|
| QY | 1064 | CTGCATTGCCGTTCCAGCTCAACATCTCTGATTGACACTCGGCTTTACCAAGATGCTCA | 1123 |
| Db | 1098 | TTGCATTGCGACTGAGCCCAACATTCTGCATTGAGATTGGGCTTGGCCAAACGTGTCA | 1157 |
| QY | 1124 | TCTTATCAGCGTTCTTTGACGACATGTACGACGTCTTCCGACAGTAGACGAGCTGAACT | 1183 |
| Db | 1158 | TCTTATCAGCGTTCTGACGATATCTACGACACTTTCGGAACGATGATGAAATCGAACT | 1217 |
| QY | 1184 | CTTCACAGCGCAATTAAGATGGATCCGTCGCGATGGAATGCCCTCCAGAAATATAT | 1243 |
| Db | 1218 | CTTCAACGAGCGAGTTAGAGATGGAATCCGTCGGAGAAAGAACGCCCTCCAGAAATATAT | 1277 |
| QY | 1244 | GAAAGAGTGTACATGATGTTTATCACAACCCTAATGAATGGCTCGAGTGGCAGAGA | 1303 |
| Db | 1278 | GAAAGAAATCTACATGGCACTCTACGAAGCCTTAACTGACATGGCGCGAGAGGCAAGAA | 1337 |
| QY | 1304 | GGCTCAAGGCCGAGACACGCTCAACTATGTCAAGACAGGCTTGGAGGCGTGTTCATTC | 1363 |
| Db | 1338 | GACACAAGGCCGAGACACGCTCAATTATGTAGAAAGGCTTGGAGTTATCTTGATTC | 1397 |
| QY | 1364 | GTATATGACGAAGCAAGTGGATCGCCACTGGTTATCTGCCACGTTGAGAGTACTT | 1423 |
| Db | 1398 | GTATACACAAGAGCAAGTGGATCGCCAGCGTTATCTGCCAACTTTCGAGAGTACTT | 1457 |
| QY | 1424 | GGAGAACGGGAAGTTAGCTCTGCTCATCGCCACTGCGCACTGCAACCCATTCGACGTT | 1483 |
| Db | 1458 | AGAGAACGGGAAGTTAGCTCTGCTCATCGCCAGCGGCAATTGACACCCCTCTGACATT | 1517 |
| QY | 1484 | GGAATCCCCCTTCTCTGATCACATCCTCAAGGAAGTTGACTTCCCATCGAAGCTCAATGA | 1543 |
| Db | 1518 | GGAATCCCCCTTCTCTGATGACGCTTGAAGGGAATAGATTTCCATCGAGATTTAATGA | 1577 |
| QY | 1544 | CTTGATATGTATCATCTCTCGATTAAAGAGTGATACACGGTGCTACAGGCAGACAGGC | 1603 |
| Db | 1578 | TTTGGCATCTTCCTTCTTGAAGGAGTGAACAGATGCTTCAAGGCAGACAGGGA | 1637 |
| QY | 1604 | CCGTGGAGAAAGAGCTTCGTCTATATCATGTATTATGAAGAAACAATCCTGATTTAACGA | 1663 |
| Db | 1638 | CCGAGGAGAAAGAGCTTCAGCATATCGTGTACATGAAGAAACAATCCCGGATTTAACGA | 1697 |
| QY | 1664 | AGAAGATGCTCTGAATCATATCAACTTCATGATCAGGGAAGCAATCAGAGAATTAAATTG | 1723 |
| Db | 1698 | GGAAGATGCTCTGAATCATATCAATGCAATGATCAAGCAATTAATCAAGAAATTAAATTG | 1757 |
| QY | 1724 | GGAGCTTCTAAAGCCAGACAACAGTGTTCCTCATCTTCCAAAGAAACAGCATTTGACAT | 1783 |
| Db | 1758 | GGAATCTCTAAAGCCAGATAGCAATATTTCAATGACTGCAAGGAACATGCTTATGAGAT | 1817 |
| QY | 1784 | AAGCAGAGTTGGCATCAACGTTACAGATACGAGATGGCTACAGCTTTGGCAACGTTGA | 1843 |
| Db | 1818 | AACCAAGAGCTTCCACCAACTTTACAATATAGAGATGGCTTCAAGCGTTGCCACTCAAGA | 1877 |
| QY | 1844 | AACAAAGAGTTGGTATGAGAACCGTCATTGAACCTGTGCTTGTAAACAACACTTCA | 1903 |
| Db | 1878 | AACGAAAGAGTTGGTATGAGAACCGTCCTTGAACCAAGTGCCTCTTTAACAATTAAACC | 1937 |
| QY | 1904 | ATCTACAATA 1913 | |
| Db | 1938 | TTCCTATAATA 1947 | |

```

RESULT 10
US-09-360-545-1
; Sequence 1, Application: US/09360545
; Patent No. 6429014
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B
; APPLICANT: Bohlmann, Jörg
; APPLICANT: Steele, Christopher L
; APPLICANT: Phillips, Michael A
; TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
; FILE REFERENCE: wsur13385

```


| | | | |
|----|------|--|------|
| Qy | 1904 | ATCTACAATATTAACTGAGATGCCCTATGGGTATATATAGGCACA | 1950 |
| | | | |
| Db | 1964 | TCCATATATATAAGCTCATTAATGCTAAATTATTTGGCCCTTATGACATA | 2010 |

RESULT 11
US-09-398-395A-29

; Sequence 29, Application US/09398395A

; Patent No. 6468772

; GENERAL INFORMATION:

APPLICANT: Chappell, Joseph

APPLICANT: No. 64687721, Joseph P.

APPLICANT: Starks, Courtney M.

APPLICANT: Manna, KATHLEEN R.

; TITLE OF INVENTION: SYNTHASES

FILE REFERENCE: 07678-025001

; CURRENT APPLICATION NUMBER: US/09/398,395A

CURRENT FILING DATE: 1999-09-17

PRIOR APPLICATION NUMBER: 60/100,993

PRIOR FILING DATE: 1998-09-18

PRIOR APPLICATION NUMBER: 60/130,628

PRIOR FILING DATE: 1999-04-22

PRIOR APPLICATION NUMBER: 60/150,262

PRIOR FILING DATE: 1999-08-23

; NUMBER OF SEQ ID NOS: 58

```

; SOFTWARE: FastSeq for Windows Version 3.0

```

; SEQ ID NO 29

; LENGTH: 2196

TYPE: DNA

ORGANISM: *Abies grandis*

FEATURE:

; NAME/KEY: CDS

LOCATION: (69) ... (1949)

OTHER INFORMATION: myrcene synthase

US-09-398-395A-29

| | | | | |
|----------------------------|-------|---------------------|------------|--------------|
| Query Match | 53.2% | Score 1071.6; | DB 4; | Length 2196; |
| Best Local Similarity | 75.0% | Pred. No. 4.1e-306; | | |
| Matches 1430; Conservative | 0; | Mismatches 441; | Indels 36; | Gaps 6. |

| | | | | |
|----|--|-----|---|-----|
| Oy | | 68 | CAGGTCGTGCCTCAGTTCCTTCTCATGAGTTAAGGCTCTCCGTAGAACAATCCAACTCT | 127 |
| Dp | | 116 | CAAGTCGTGATCAGTTCATTCATGACATAAGCCTCCCTATAGAACAAATCCAAATCT | 175 |
| Oy | | 128 | TGGAATCTGCAGGCCGGGAAATCCGTCCGCATTCCATAAACATGTGTTGACAAAGCT | 187 |
| Dp | | 176 | TGGAATGCCGTAGCGGAGGAATCTGTCAAGCCTTCCATGAGCATCAGTTTGCCACC | 235 |
| Oy | | 188 | CGCATCTACTGATTCTGTACAGAGACGCGTGGGCAACTATCATTTCCAACCTGTGGACGA | 247 |
| Dp | | 236 | TGCACCTGATGATGTTGTACAAAGACGCATAGGTGACTACCATTTCCAATATCTGGACGA | 295 |
| Oy | | 248 | TGATTTTCATACAGTCTCTGATCTCAAAGCCTTATGGAGCACCTGATTACCGGGAACGTGC | 307 |
| Dp | | 296 | TGATTTTCATACAGTCTC--TATCAACGCTTATGGGGAACCTCTTACCAAGAACGTGC | 352 |
| Oy | | 308 | TGACAGACTTATGGGGAAGTAAGATTAATGTTCAATTTCAAGTCGTCGAAGATGG | 367 |
| Dp | | 353 | TGAGAGATTAAATTGTGAGAGTAAGAAAGATA--TTCAATTCATGTACTGTGATGATGG | 409 |
| Oy | | 368 | AGG-----CAATGATCTCCTTCAACGACTTTGCTGTGATGACGTGA | 412 |
| Dp | | 410 | AAGATTAAATGAGTTCCTTAAATGATCTCATGCAACGCTTTGATAGTGAATGCGTGA | 469 |
| Oy | | 413 | ACGTTTGGGAATGCACAGGCATTTCAAAAAAGAGATAAAAAGGCACCTGATTAATGTTAA | 472 |
| Dp | | 470 | ACGTTTGGGGATAGCTAGACATTTCAAGAACGAGATAACATCAAGCTCTGGATTATGTTTT | 529 |
| Oy | | 473 | CAGTTATTGGAACGAAAAAGGCATTGGATGTGGGAGGAGAGTGTGTGACTGACCTCAA | 532 |
| Dp | | 530 | CCGTTACTGGGAGGAAAAACGGCATTGGATGTGGGAGAGACAGTATTGTTACTGATCTCAA | 589 |
| Oy | | 533 | CTCAACCGCCTTGGGGCTTGAACCTCCGCACTACACGAGTACACTGTGTCTTCAGATGT | 592 |

| | | | |
|----|------|---|------|
| Db | 590 | CTCAACTGCGTTGGGGTTTCGAACTCTTCGATTACACGGGTACACTGTATCTCCAGAGT | 649 |
| Qy | 593 | TTTGAACGTTTTTAAAGACAAAATGGGCAATTTTCCTCCACTGCCAATATTCCAGATAGA | 652 |
| Db | 650 | TTTAAAGCTTTTCAAGATCAAAATGGACAGTTGTATGCTCCCC--GGTCAGACAGA | 706 |
| Qy | 653 | GGAGAGATTAGAGCGCTTCTCAATTTATTCAGGGCTCCCTCGTCGCTTTCCCGCGA | 712 |
| Db | 707 | GGGTAGATCAGAGCGTCTTAATTATTCGGGCTCCCTCATTCGCTTCCCTGGTGA | 766 |
| Qy | 713 | GAAAGTTATGATGAAGCTGAACATTTCTACAAAATATTTAAGAGAAGCCCTGCAAAA | 772 |
| Db | 767 | GAAAGTTATGGAAGAGCTGAATCTTCTCCACAGATATTTGAAAAGAGCTCTACAAA | 826 |
| Qy | 773 | GATTCGGGCATCCAGTATACCTTTCAGTAGAGATACGGGACGTTCTGGAATATGCTTGGCA | 832 |
| Db | 827 | GATTCAGTCTCCGCT--CTTCACAGAGATAAAGTTTGTATGGAATATGGCTGGCA | 883 |
| Qy | 833 | CACCAATTTGCCACGCTTGGAAAGCAAGAAATTACATGGAACGTCTTTGGACAGACACTA- | 891 |
| Db | 884 | CACAATTTGCCAAGATTGGAAGCAAGAAATTACATAGACACACTTGAGAAGACACAG | 943 |
| Qy | 892 | -----AAATTAAGACGCGCCGAGAACTTTAGAACTTGCAAAATTGGAATTCAA | 943 |
| Db | 944 | TGCATGGCTCAATTAATAAATGCTGGAGAGAGCTTTAGAACTTGCAAAATTGGAGTTCAA | 1003 |
| Qy | 944 | TATATTCACTCCTTACAGAAGAGAGATTAAACATGTTTCCCGATGTTGAAAGACTC | 1003 |
| Db | 1004 | TATATTAACTCCTTACAACAAAAAGAAATTACAATCTTTTGAGATGTTGAAAGAGTTC | 1063 |
| Qy | 1004 | GGGTTCTCCTGAATGACCTTCTGTGCACATCGTCAAGTGAATACTACGCTTTGGCTTC | 1063 |
| Db | 1064 | GGATTTGCCCTAATGACATTTGCTCGGCATCGTCAATGGAATTTCTACACTTTGGCTTC | 1123 |
| Qy | 1064 | CTGCATTGCGTTGAGCCTCAACATTTCTGATTTCAGACTCGGCTTTACCAAGATGTCTCA | 1123 |
| Db | 1124 | TTGTATTGCCATTCGCCAATAACATTCTGCATTCAAGACTAGGCTTCGCCAATGTGTCA | 1183 |
| Qy | 1124 | TCTTATCAGCGTCTTTGACGACATGTACGACGCTTTGGCACAAGTAGACGCTGGAAT | 1183 |
| Db | 1184 | TCTGTACAGTTTGGACGATATTACGACACTTTTGAACGATTGACGAGCTTGAAT | 1243 |
| Qy | 1184 | CTTCACAGCGACAATTAAGAGATGGATCCGTCGCGATGGAATGCTTCAGAAATATAT | 1243 |
| Db | 1244 | CTTCACATCTGCATTAAGAGATGGAATTCATCAGAGATAGAACACCTTCAGAAATATAT | 1303 |
| Qy | 1244 | GAAAGAGTACATGATGTTTATCACACCGTAAATGAATGGCTCGAGTGCAGAGAA | 1303 |
| Db | 1304 | GAAATGTGTGTAATGATGCTGTTGAAACTGTAAATGAATGACACGAGAGCGGAGAA | 1363 |
| Qy | 1304 | GGCTCAAGGCCGAGACACGCTCAACTATGCAAGACAGGCTTGGAGGCGTGTGTTGATTC | 1363 |
| Db | 1364 | GACTCAAGGGAGAAACACTCAACTATGTTCGAAAGCGTTGGAGGCTTATTTTGATTC | 1423 |
| Qy | 1364 | GTATATGCAAGCAAGCAAGTGGATCGCCACTGTTATCTGCCACGTTTGAGAGTACTT | 1423 |
| Db | 1424 | ATATATGGAAGAGCAAAATGGAATCTTAATGTGTAATCTGCCAATGTTGAAAGATACCA | 1483 |
| Qy | 1424 | GGAGAACGGAAAGTTAGCTGTGCTCATCGCCCATGGGCACTGCAACCCATTTGACGTT | 1483 |
| Db | 1484 | TGAGAATGGGAAGTAGCTGTGATATCGCGTAGCAACATGCAACCCATCTCACTTT | 1543 |
| Qy | 1484 | GGAATCCCTTTTCTGATCAATCTCTCAAGGAAGTTGACTTCCCATCGAAGCTCAATGA | 1543 |
| Db | 1544 | GAAATGATGGCTTCTGATTAATCTTGAAGGGAATTTGATTTCCATCCAGGTTCAATGA | 1603 |
| Qy | 1544 | CTTGATATGTAACATCTTGCATTAAGAGGTGATACAGGTGCTACAAAGCAGACAGGCG | 1603 |
| Db | 1604 | TTTGGCATCGTCTTCTTCGCGCTACGAGGTGACACGCTGCTACAAAGCCGATAGGGA | 1663 |
| Qy | 1604 | CCGTGAGAGAGCTTCTATATATCATGTTATATGAAGCAATCTCGATTAAAGGA | 1663 |

Db 1664 TCGTGTGAAGAAGCTTCGTATATCATGTATATGAAAGACAATCCTGGATCAACCGA 1723
Qy 1664 AGAAGATGCTCTGAATCATATCACTTCAATGATCAGGAGCGCAATGAGAATTAATTG 1723
Db 1724 AGAAGATGCTCTCAATCATATCAATGCCATGGTCAATGACATTAATCAAGAATTAATTG 1783
Qy 1724 GGAGCTTCTAAAGCCAGACAACAGTGTGCTCCATCACTTCCAAGAAAACGCAATTGACAT 1783
Db 1784 GGAATCTTAAAGATCCAACGACAATATTCGAATGCTGGCCAAAGAAACATGCTTTTGACAT 1843
Qy 1784 AAGCAGAGTTTGGCATCAACGTTACAGATACCGAGATGGCTACAGCTTTGGCCAACGTTGA 1843
Db 1844 AACAAAGAGCTCTCCACCATCTACATATATCGAGATGGCTTTAGTGTGCGCAACAAGGA 1903
Qy 1844 AACAAAGAGTTTGGTATGAGAACCGTCAATTGAACCTGTGCTTTGTAACAACACTTCAA 1903
Db 1904 AACAAAAAATGGTATGGAACACCTCTTGAATCTATGCTTTTAACTATAACCATATA 1963
Qy 1904 ATCTACATATTAATGAGATGCCCTATGGGTATATAGGCGACA 1950
Db 1964 TCCATATATTAAGCTCATATATGCTAAATTAATTGGCCTTATGACATA 2010

RESULT 12

US-09-887-586A-29
; Sequence 29, Application US/09887586A
; Patent No. 6495354
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64953541, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/887,586A
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for windows Version 3.0
; SEQ ID NO 29
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (69)...(1949)
; OTHER INFORMATION: myrcene synthase
US-09-887-586A-29

Query Match 53.2%; Score 1071.6; DB 4; Length 2196;
Best local Similarity 75.0%; Pred. No. 4.1e-306;
Matches 1430; Conservative 0; Mismatches 441; Indels 36; Gaps 6;

Qy 68 CAGGTGTCCTCAGTCTTCTCATGAGATTAAGGCTCTCCGTAGAACAAATCCCACTCT 127
Db 116 CAAGTCGTTGATCAGTTCAATTCAATGACATTAAGCCTCCCTATAGAACAAATCCCAATCT 175
Qy 128 TGAATCTGAGGCGCGGGAATCCGTCGCGCATTCATTAACATGTGTTGACAAAGCGT 187
Db 176 TGAATGCGTAGGCGAGGGAATCTGTACGCCCTTCATGAGCATCAGTTTGGCCACCGC 235
Qy 188 CGCATCTACTGATTTCTGTACAGAGACGCGTGGCAACTATCATTTCCAACCTGTGGAGCA 247
Db 236 TGCACTGATGATGTGTACAAAGACGCAATAGTGACTACCATTTCAATATCTGGAGCA 295
Qy 248 TGATTTCAATCAGTCTCTGATCTCAAGCGCTTATGAGACACCTGATTAACGGGAACGTGC 307
Db 296 TGATTTCAATCAGTCTC--TATCAAGCGCTTATGGGGAACCCCTTACCAAGGAACGTGC 352

Qy 308 TGACAGACTTATTTGGGAAGTAAAGATATATATGTTCAATTTCAAGTCGCTGGAAGATGG 367
Db 353 TGAGAGATTAATTGTGAGGTTAAAGAAGATA--TTCAATTCGAATGTACCTGGATGATGG 409
Qy 368 AGG-----CAATGATCTCCTTCAACGACTTTTGCTGTGATGACGTTGA 412
Db 410 AAGATTAATGAGTTCCTTAATGATCTCATGCAACGCCCTTGGATAGTCGATAGCGTTGA 469
Qy 413 ACGTTGGGAATCGACAGGCAATTCAAAAAGAGATAAACCACCTCGATTATGTTAA 472
Db 470 ACGTTGGGATAGCTAGACATTTCAAGAACGAGATTAACATCAGCTCTGATTATGTTT 529
Qy 473 CAGTTATTTGAACGAAAAAGCAATTTGATGTGGAGGGAGAGTGTGTGACTGACCTCAA 532
Db 530 CCGTTACTGGAGGAAAAACGGCAATTGGAATGTGGAGAGACAGTATTTACTGATCTCAA 589
Qy 533 CTCAACCGCCTTGGGCTTCGAATCTCCGACTACACGAGTACATGTGCTTCAGATGT 592
Db 590 CTCAACTGCGTTGGGCTTCGAATCTTCGATTACACGGGTACATGTATCTCCAGAGGT 649
Qy 593 TTTGAACGTTTTTAAAGACAAAATGGGCAATTTCTCCACTGCCAATATTACAGATAGA 652
Db 650 TTTAAAGCTTTTCAAGATCAAAATGGAACAGTTTGTATGCTCCCCC--GGTCAGACAGA 706
Qy 653 GGGAGATTTAGAGCGCTTCATTTATTCAGGCGCTCCCTCGCTTCCCGCGGA 712
Db 707 GGGTGATCAAGAGCGTCTTAATCTTATATCGGCTTCCCTCATGTGCTTCCCTGTGA 766
Qy 713 GAAAGTTATGATGAAGCTGAACATTTCTCAAAAATTTAAGAGAAAGCCCTGCAAA 772
Db 767 GAAAGTTATGGAAGAGCTGAATCTTCTCCACAAAGATATTGAAAGAAAGCTCTACAAA 826
Qy 773 GATTCGGCATCCAGTATACTTTCACTAGATACGGAGCTTCTGGAATATGTTGGCA 832
Db 827 GATTCAGTCTCCGCT--CTTCAAGAGATAAAGTTTGTATGGAATATGCTGGCA 883
Qy 833 CACCAATTTGCCACGCTTGAAGCAAGAAATTACATGACGCTTTGGACAGCACACTA- 891
Db 884 CACAAATTTGCCAAGATTTGAAGCAAGAAATTACATAGACACACTTGAGAAAGACACAG 943
Qy 892 -----AAATAAGAACGCCCGAGAAACTTTAGAACTTGCAAAATTTGAATTCAA 943
Db 944 TGCATGGCTCAATAAAATGCTGGGAAGAAGCTTTTAGAATCTGCAAAATTTGAAGTTCAA 1003
Qy 944 TATATTTCACTCCTTACAGAGAGAGAGTTAAACATGTTCCCGATGCTGGAAGACTC 1003
Db 1004 TATATTTAACTCCTTACACAAAGAAATTACATATCTTTTGAGATGCTGGAAGAGTCT 1063
Qy 1004 GGGTCTCTGAGATGACCTTCTGTGCAATCGTCAACGTGGAATACTACGCTTTGGCTTC 1063
Db 1064 GGATTTGCCTTAAATTGACATTTGCTGGCATCGTCAATGGAATTTCTACACTTTGGCTTC 1123
Qy 1064 CTGCATTCGCTTCGAGCCTCAACTTCTGATTAGACTCGGCTTTACCAAGATGCTCA 1123
Db 1124 TTGTATGGCATTGACCACCAAAACATTTCTGATTAGACTAGGCTTCCCAAAATGTGCA 1183
Qy 1124 TCTTATCAGGTTCTTGACGACATGTACGACGCTTTCGGCAGTAGACGAGCTGGAAT 1183
Db 1184 TCTTGTACAGTTTGGACGATTTTACGACACTTTTGAACGATTGACGAGCTTGAAT 1243
Qy 1184 CTTCACAGCGAATTAAGAGATGGGATCCGTCGCGAGTGAATGCCCTTCAGAAATATAT 1243
Db 1244 CTTCACATCTGCAATTAAGATGAATTCATCAGAGATGAAACACCTTCAGAAATATAT 1303
Qy 1244 GAAAGAGTGATCATGATGTTTATCACACCGTAAATGAATGGCTCGAGTGCAGAGAA 1303
Db 1304 GAAATGTGTATCATGTGCTGTGTTGAAACTGTAAATGAATGACACGAGAGCGGAGAA 1363
Qy 1304 GGGTCAAGGCCGAGACACGCTCAACTATGCAAGACAGGCTTGGAGCGGCTTTGATTC 1363
Db 1364 GACTCAAGGGAAGAAACACTCTCAACTATGTTGAAAAGGCTTGGAGGCTTATTTGATTC 1423

[illegible]

```

RESULT 13
US-09-895-752-29
; Sequence 29, Application US/09895752
; Patent No. 6559297
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 65592971, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/895,752
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (69)...(1949)
; OTHER INFORMATION: myrcene synthase
US-09-895-752-29

```

| | | | | |
|----------------------------|-------|---------------------|------------|--------------|
| Query Match | 53.2% | Score 1071.6; | DB 4; | Length 2196; |
| Best Local Similarity | 75.0% | Pred. No. 4.1e-306; | | |
| Matches 1430; Conservative | 0; | Mismatches 441; | Indels 36; | Gaps 6; |

| | | | |
|----|------|--|------|
| QY | 68 | CAGGTCGTGCTCAGTTCCTTCTCATGAGATTAAAGGCTCTCCGTAGAACAAATCCCAACTCT | 127 |
| Db | 116 | CAAGTCGTGATCAGTTCATTCATGAAACATTAAGCCCTCCTATAGAACAAATCCCAATCT | 175 |
| QY | 128 | TGGAATCTGCAGGCCGGGAAATCCGTGCGCATTCCTCAATTAACATGTGTTGACAAGCGT | 187 |
| Db | 176 | TGGAATGCGTAGGCGAGGAAATCTGTCAAGCCTTCATGAGCATCAGTTTGCCACCGC | 235 |
| QY | 188 | CGCATCTACTGATCTGTACAGAGACGCGTGGCACTATCATTCCAACTGTGGAGCA | 247 |
| Db | 236 | TGCACCTGATGATGGGTACAAAGACGCATAGTGATCAATCCATATCTGGAGCA | 295 |
| QY | 248 | TGATTTTCATACAGTCTTCATCTCAAGCCTTATGAGCACTGATTACCGGAACTGC | 307 |
| Db | 296 | TGATTTTCATACAGTCTC--TATCAACGCTTATGGGAACTCTTACCAGAACGTGC | 352 |
| QY | 308 | TGACAGACTTATTGGGGAAGTAAAGATATAATGTTCAATTTCAAGTCGCTGGAAGATGG | 367 |
| Db | 353 | TGAGAGATTAAATGTGAGGTAAAGAGATA--TTCAATTCAATGTACTGTGATGATGG | 409 |
| QY | 368 | AGG-----CAATGATCTCCTTCAACGACTTTGCTGTCGATGACGTTGA | 412 |
| Db | 410 | AAGATTAATGAGTTCCTTTAATGATCTCATGCAACGCTTTGATAGTCGATAGCGTTGA | 469 |
| QY | 413 | ACGTTTGGGAATGCACAGGCATTTCAAAAAAGAGATTAATAACGGCACTCGATTATGTTAA | 472 |
| Db | 470 | ACGTTTGGGATAGCTGACATTTCAAGAACGAGATTAACATCAGCTCTGATTAATGTTT | 529 |
| QY | 473 | CAGTTATTGGAACGAAAGGCAATTGATGTGGAGGAGAGTGTGTGACTGACCTCAA | 532 |
| Db | 530 | CCGTTACTGGAGCAAAACGGCATTTGATGTGGAGAGACAGATTTGTTACTGATCTCAA | 589 |
| QY | 533 | CTCAACCGCCTTGGGCTTCGAACCTCCGACTACACGGATACACTGTGTCTTCAGATGT | 592 |
| Db | 590 | CTCAACTGCGTTGGGTTTCGAACCTTCGATTACACGGTACACTGTATCTCCAGAGT | 649 |
| QY | 593 | TTTGAACGTTTAAAGACAAAATGGGCAATTTCTCTCCACTGCCAATATTCAGATAGA | 652 |
| Db | 650 | TTTAAAGCTTTCAAGATCAAAATGACAGTTTGTATGCTCCCC--GGTCAGACAGA | 706 |
| QY | 653 | GGGAGAGATTAGAGCGCTTCTCAATTTATTCAGGGCCTCCCTGTCGCTTCCGGCGA | 712 |
| Db | 707 | GGGTGAGATCAGAGCGTCTTAACTTATATCGGCTCCCTCATTTGCCCTTCCGTGTA | 766 |
| QY | 713 | GAAAGTTATGATGAGAGCTGAACATTTCTTACAAAATATTTAAGAGAGCCCTGCAAA | 772 |
| Db | 767 | GAAAGTTATGAGAGAGCTGAACATTTCTTCCACAGATATTTGAAAGAGCTTACAAA | 826 |
| QY | 773 | GATTCGCGCATCAGTATACTTCACTAGAGATACGGAGCTTCTGGAATATGTTGCA | 832 |
| Db | 827 | GATTCAGTCTCCGCT---CTTCAAGAGATAAAGTTGTATGGAATATGGCTGCA | 883 |
| QY | 833 | CACCAATTTGCCAGCGTTGGAAGCAAGGAATTACATGACGTCTTGACACACACTA- | 891 |
| Db | 884 | CACAATTTGCCAAGATTGGAAGCAAGAAATTACATAGACACACTTGAGAAAGACACAG | 943 |
| QY | 892 | -----AAAATPAAGACGCCCGCGAGAACTTTAGAACTTGCAAAATTGGAATTCAA | 943 |
| Db | 944 | TGCATGGCTCAATPAATAATGCTGGAGAGAGCTTTTAGAACTTGCAAAATTGAGTTCAA | 1003 |
| QY | 944 | TATATTTCACTCTTACAGAGAGAGAGTTAAACATGTTTCCCGATGGTGAAGACTC | 1003 |
| Db | 1004 | TATATTTAACTCTTACAACAAAAGGAATTACATATCTTTGAGATGTTGAAAGAGCTC | 1063 |
| QY | 1004 | GGGTTCTCTGAGATGACCTTCTGTGACATCGTACGTEGAATACTACGCTTTGGCTTC | 1063 |
| Db | 1064 | GGATTTGCCATAATGACATTTGCTCGGCATCGCATGTGGAATTTACACATTTGGCTTC | 1123 |

| | | | |
|----|------|--|------|
| QY | 1064 | CTGCATTGCGTTCCGAGCTCTCAACATTCTGAGTTCAGACTCGGCTTTTACCAAGATGTC | 1123 |
| Db | 1124 | TTGTATTGCCATTGACCCCAAAACATTCTGCAATTCAGACTAGGCTTCGCCAAAATGTCTCA | 1183 |
| QY | 1124 | TCTTATCAGCGTTCTTGAAGCATGTACGACGTCCTTCGGCACAAGTAGCAGCTGGA | 1183 |
| Db | 1184 | TCTTGTACAGTTTGGACGATATTTCAGACACTTTTGAACGATTGACGAGCTTGA | 1243 |
| QY | 1184 | CTTCACAGCGACAATTAAAGATGGATCCGTCGCGATGGAATGCTTCCAGAAATAT | 1243 |
| Db | 1244 | CTTCACATCTGCAATTAAAGATGGAATTCATCAGAGATGACAACCTTCAGAAATAT | 1303 |
| QY | 1244 | GAAAGAGTGATCATGATGGTTTATCACACCGTAATGAATGGCTCGAGTGCAAGAA | 1303 |
| Db | 1304 | GAAATGTGTATCATGTGTCGTCTTGAACCTGTAATGAAGTGAACAGAGAGCGGAGAA | 1363 |
| QY | 1304 | GGCTCAAGGCCGAGACACGCTCACTATGCAAGACAGGCTTGGAGGCGTGTGATTTC | 1363 |
| Db | 1364 | GACTCAAGGGAGAAACACTCTCACTATGTTCGAAAGGCTTGGAGGCTTATTTGATTTC | 1423 |
| QY | 1364 | GTAATATGCAAGCAAGCAAGTGGATCGCCACTGTTATCTGCCACGTTGAGAGTACTT | 1423 |
| Db | 1424 | ATATATGGAAGAACAAAATGATCTCTAATGTTATCTGCCAATGTTTGAAGAGTACA | 1483 |
| QY | 1424 | GGAGAACGGGAAAGTTAGCTCTGCTCATCGCCCATGCGCACTGCAACCCATTCTGACGT | 1483 |
| Db | 1484 | TGAGAATGGGAAAGTAGCTCTGATATCGCGTAGCAACATGCAACCCATCTCATT | 1543 |
| QY | 1484 | GGAATCCCTTTCTGATCAATCTCAGGAAGTTACTTCCATCGAAGCTCAATGA | 1543 |
| Db | 1544 | GAATGCATGGCTTCTGATTAATCTTGAAGGAATTGATTTCCATCCAGTTCAATGA | 1603 |
| QY | 1544 | CTTGATATGTATCATCTCTTCGATTAAAGAGTGATACACGCTCTACAAGGCAGACAGGC | 1603 |
| Db | 1604 | TTTGGCATCGTCTTCTTCGCTACGAGGTGACACACGCTGCTACAAGGCCGATAGGGA | 1663 |
| QY | 1604 | CCGTGAGAGAAAGCTTCGTCTATATCATGTATATGAAGACAATCCTGGATTAAAGGA | 1663 |
| Db | 1664 | TCGTGTGAAGAGCTTCGTGTATATCATGTTATATGAAGACAATCCTGGATCAACGGA | 1723 |
| QY | 1664 | AGAAAGATGCTCTGAATCATATCAACTTCATGATCAGGACGCAATCAGAGAATTAAATTG | 1723 |
| Db | 1724 | AGAAAGATGCCCTCAATCATATCAATGCCATGTGCAATGACATTAATCAAGAATTAAATTG | 1783 |
| QY | 1724 | GGAGCTTCTAAAGCCAGACAAGTGTCCATCACTTCCAAGAAAACGCAATTGACAT | 1783 |
| Db | 1784 | GGAACCTCTTAAGATCCAAAGCAATATTCCAATGCTGGCCAAAGAAACATGCTTTGACAT | 1843 |
| QY | 1784 | AAGCAGAGTTTGGCATCAGCGTTACAGATACGAGATGGCTACAGCTTTGCCAAGCTTGA | 1843 |
| Db | 1844 | AACAAGAGCTCTCCACCATCTCTACATATATCGAGATGGCTTAAAGTTGCCAACAGGA | 1903 |
| QY | 1844 | AACAAGAGTTTGGTGATGAGAACCGTCATTGAACCTGTGCTTGTAAACACACTTCAA | 1903 |
| Db | 1904 | AACAACAAAATTGGTTATGGAACAACCTCCTGGAATCTATGCTTTTAACTATAACCAT | 1963 |
| QY | 1904 | ATCTACAATATTAATGAGATGCCCTATGGGTGTATATAGGCAACA | 1950 |
| Db | 1964 | TCCATATATATAGCTCATATGCTAAATTAATTGGCCCTTATGACATA | 2010 |

```

RESULT 14
US-09-903-012B-29
; Sequence 29, Application US/09903012B
; Patent No. 6569656
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 65696561, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903, 012B

```

```

; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for windows Version 3.0
; SEQ ID NO 29
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (69)..(1949)
; OTHER INFORMATION: myrcene synthase
US-09-903-012B-29

```

| | | | | |
|----------------------------|--------|---------------------|------------|--------------|
| Query Match | 53.2% | Score 1071.6; | DB 4; | Length 2196; |
| Best Local Similarity | 75.0%; | Pred. No. 4.1e-306; | | |
| Matches 1430; Conservative | 0; | Mismatches 441; | Indels 36; | Gaps 6; |

| | | | |
|----|-----|--|-----|
| QY | 68 | CAGCTGCTGCCTCAGTTCTTCTCATGAGATTAAAGGCTCTCCGTAGAACAAATCCCAACTCT | 127 |
| | | | |
| Db | 116 | CAAGTCGTTGATCAGTTCAATTCATGAACATTAAGCCCTCTATGAACAATCCCAATCT | 175 |
| | | | |
| QY | 128 | TGGAATCTGCAGGCCGGGAAATCCGTGCGCATTCCTCAATAAATGTGTTGACAAAGCGT | 187 |
| | | | |
| Db | 176 | TGGAATGCGTAGGCGAGGAAATCTGTCAAGCCCTTCATGAGCATCAGTTTGCCACCCGC | 235 |
| | | | |
| QY | 188 | CGCATCTACTGATTTCTGTACAGAGACGCGTGGGCACTATCTCAACCTGTGGAGCGA | 247 |
| | | | |
| Db | 236 | TGCACCTGATGATGGGTGTACAAAGACGATAGGTGACTACCATTCATATATCTGGAGCGA | 295 |
| | | | |
| QY | 248 | TGATTTTCATACAGTCTCTGATCTCAACGCCCTTATGAGACACTGATTAACCGGAACGTGC | 307 |
| | | | |
| Db | 296 | TGATTTTCATACAGTCTC---TATCAACGCCCTTATGGGGAACCTCTTACCAGGAACGTGC | 352 |
| | | | |
| QY | 308 | TGACAGACTTATTTGGGGAAGTAAAGATATATGTTCAATTTCAAGTCGCTGGAAGATGG | 367 |
| | | | |
| Db | 353 | TGAGAGATTAAATTTGGAGCTAAAGAAAGATA--TTCAATTCATATGTAACCTGATGATGG | 409 |
| | | | |
| QY | 368 | AGG-----CAATGATCTCCTTCAACGACTTTTGCTGCTGATGACGTTGA | 412 |
| | | | |
| Db | 410 | AAGATTAATGAGTTCCTTTAATGATCTCATGCAACGCTTTGGATAGTCGATAGCGTTGA | 469 |
| | | | |
| QY | 413 | ACGTTTGGGAATCGACAGCATTTCAAAAAAGAGATAAAAACGGCACTCGATTATGTTAA | 472 |
| | | | |
| Db | 470 | ACGTTTGGGATAGCTAGACATTTCAAGAACGAGATTAACATCAGCTCTGATTATGTTT | 529 |
| | | | |
| QY | 473 | CAGTTATTGGAACGAAAAAGGCATTGGATGTGGAGGAGAGTGTGTGACTGACCTCAA | 532 |
| | | | |
| Db | 530 | CCGTTACTGGAGGAAACGGCATTTGGATGTGGAGAGACAGTATTGTTACTGATCTCAA | 589 |
| | | | |
| QY | 533 | CTCAACCGCCTTGGGCTTCGAACCTCTCCGACTACAGCGATACACTGTGCTTCAGATGT | 592 |
| | | | |
| Db | 590 | CTCAACTGCGTTGGGTTTCGAACCTCTCGATTACAGGGGTACACTGTATCTCCAGAGGT | 649 |
| | | | |
| QY | 593 | TTTGAACGTTTTTAAGACAATAATGGGCAATTTCTCCCACTGCGCAATATTCAGATAGA | 652 |
| | | | |
| Db | 650 | TTTAAAGCTTTTCAAGATCAAAATGAGACAGTTTGTATGCTCCCCC--GGTCAGACAGA | 706 |
| | | | |
| QY | 653 | GGGAGAGATTAGAGGCGTTCTCAATTTATTCAGGGCCTCCCTGTCGCCCTTCCCGGCGA | 712 |
| | | | |
| Db | 707 | GGGTGAGATCAGAAAGCGTTCTTAACCTATATCGGGCTTCCTCATTTGCCCTTCCCTGCTGA | 766 |
| | | | |
| QY | 713 | GAAAGTTATGATGAAGCTGAAACATTTCTTACAAATAATTTAAGAGAAGCCCTGCAAAA | 772 |
| | | | |
| Db | 767 | GAAAGTTATGAAGAAAGCTGAAATCTTCTCCACAAGATATTTGAAAGAAAGCTCTACAAAA | 826 |
| | | | |
| QY | 773 | GATTCGGCATCCAGTATTACTTTCACTAGAGATACGGGAGCTTCTGGAATATGTTGGCA | 832 |
| | | | |

Db 827 GATTCAGTCTCGCT---CTTCAAGAGATAAAGTTGTTATGAAATAGGCTGGCA 883
QY 833 CACCAATTTGCCAGCTTGAAGCAGAAGATTACATGACGTCTTTGGACAGACACTA- 891
Db 884 CACAATTTGCCAAGATTGGAAGCAGAAGATTACATGACACTTGAGAAAGACACCAG 943
QY 892 -----AAATAAGAACGCCGCCGAGAACTTTAGAACTTGCAAAATTGGAATTCAA 943
Db 944 TGCATGGCTCAATAAAATGCTGGAGAGAGCTTTTAGAACTTGCAAAATTGGAATTCAA 1003
QY 944 TATATTTCACTCTTCAAGAGAGAGATTAAACATGTTCCCGATGGTGAAGAACTC 1003
Db 1004 TATATTTAACTCTTCAACAAAAGAAATTACATATCTTTGAGATGGTGAAGAGCTC 1063
QY 1004 GGGTCTCTGAGATGACCTTCTGTCGACATGTCACGTTGAATACCTGCTTGGCTTC 1063
Db 1064 GGATTTGCTTAAATTGACATTTGCTCGGCATGTCATGTGAATCTTCACTTTGGCCTC 1123
QY 1064 CTGCAATGCTTGAAGCTTCAACATTTCTGATTCAGACTCGGCTTTACCAAGATGCTCA 1123
Db 1124 TTGTATGGCAATGACCCAAAACATTTCTGCAATCAGACTAGGCTTCCGCAAAATGTGCA 1183
QY 1124 TCTTATCAGGTTCTTGAAGACATGTAGCAGCTTCCGCAACAGTACGAGCTGAACT 1183
Db 1184 TCTTGTACAGTTTGGACGATATTACGACACTTTTGGAAAGATGACGAGCTTGAAT 1243
QY 1184 CTTCAACAGCGCAATTAAGAGATGGATCCGTCGCGCATGGAATGCCCTTCCAGAATATAT 1243
Db 1244 CTTCAACATCTGCAATTAAGAGATGAATTCATCAGAGATAGAACACCTTCCAGAAATATAT 1303
QY 1244 GAAAGAGTGTATCATGATGTTTATCACACCGTAAATGAATGGCTGAGTGGCAGAGAA 1303
Db 1304 GAAATGTGTATCATGCTGCTGTTGAATGTAAATGAATGACAGAGAGCGGAGAA 1363
QY 1304 GGGTCAAGCGGAGACACGCTCAACTATGACAGAGCGCTTGGAGCGCTGTTGATTTC 1363
Db 1364 GACTCAAGGAGAAACACTCTCAACTATGTTGAAAGCGCTTGGAGCGCTTATTTGATTTC 1423
QY 1364 GTATATGACAGCAAAAGTGTATGCGCACTGTTATCTGCCACGTTGAGAGTACTT 1423
Db 1424 ATATATGAGAGCAAAATGATCTCTAATGTTATCTGCCAATGTTGAAGAAGTACCA 1483
QY 1424 GGAGAACGGGAAAGTTAGCTCTGCTATCGCCCATGCGCACTGCAACCATCTGACGTT 1483
Db 1484 TGAGAAATGGGAAAGTGAAGCTCTGCATATCGCGTAGCAACATTTGCAACCATCTTCACTTT 1543
QY 1484 GGACATCCCTTTCTCTGATCATCATCTCAAGAGAGTGAATCTCCCATGCAAGCTCAATGA 1543
Db 1544 GAATGCATGGCTTCTCTGATTCATCTTGAAGGGAATTTTCCATCCAGGTTCAATGA 1603
QY 1544 CTTGATATGATCATCTCTGATTAAGAGGTGATACAGGTGCTACAGGAGACAGAGGCG 1603
Db 1604 TTTGGCATGCTCTCTCTCGGCTACGAGGTGACACAGCGCTGCTACAGGCGGATAGGGA 1663
QY 1604 CCGTGAGAGAGAGCTTCTGCTATATCATGTTATATGAAGACAATCTGGAATTAACGGA 1663
Db 1664 TCGTGTGAGAGAGCTTCTGCTATATCATGTTATATGAAGACAATCTGGAATCAACGGA 1723
QY 1664 AGAAGATGCTTGAATCATATCACTTCAATGATCAGGAGCGCAATCAGAGAATTAATTTG 1723
Db 1724 AGAAGATGCTTCAATCATATCAATGCGATGCTCAATGATCAATCAAGAAATTAATTTG 1783
QY 1724 GGAGCTTCTAAAGCCAGACACAGTGTTCCTCACTTCCAGAGAAACAGCATTTGACAT 1783
Db 1784 GGAATCTTAAGATCCACAGCAATATTTCCAATGCTGGCCAGAGAAACATGCTTTGACAT 1843
QY 1784 AAGCAGAGTTTGGCATCAGGTTACAGATACCGAGATGGCTACAGCTTTGCCAAGTGA 1843
Db 1844 AACAGAGAGCTCTCCACCATCTCTACATATATGAGATGGCTTAGTGTGCCAACAAGGA 1903
QY 1844 AACAAAGAGTTTGGTATGAGAACCGTCACTGAACTGTGCTTTGTAACAACACTTCAA 1903
Db 1904 AACCAAAAAATGTTATGAGAACACTCTTGAATCTATGCTTTTAACTATTAACCATAT 1963

QY 1904 ATCTACATATTAATGAGAGATGCCCTATGGGTATATAGGGCACA 1950
Db 1964 TCATATATATTAAGCTCATATATGCTAAATTAATTGGCCTTATGACATA 2010

RESULT 15
US-09-900-797-29
; Sequence 29, Application US/09900797
; Patent No. 6645762
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 66457621; Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/900,797
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (69)...(1949)
; OTHER INFORMATION: myrcene synthase
US-09-900-797-29

Query Match 53.2%; Score 1071.6; DB 4; Length 2196;
Best Local Similarity 75.0%; Pred. No. 4.1e-306;
Matches 1430; Conservative 0; Mismatches 441; Indels 36; Gaps 6;

QY 68 CAGTCTGCTCAGTCTTCTCATGAGATTAAAGGCTCTCCGTAGAACAAATCCCACTCT 127
Db 116 CAAGTCGTGATCACTTCAATTCATGACATAAGCCCTCCCTATGAAACAATCCCAATCT 175
QY 128 TGAATCTGAGCGCGGGAATCCGTCGCGCATTCATTAACATGCTTGAACAAGCT 187
Db 176 TGAATGCGGTAAGCGAAGAAATCTGTACAGCGCTTCATGAGCATCAGTTGGCCACGCG 235
QY 188 CGCATCTACTGATTTGTACAGAGACGGGTGGCAACTATCATTCACAACCTGTGGAGCA 247
Db 236 TGACACCTGATGATGTGTACAAAGACGATAGGTGACTACCATTCATATCTGGAGCA 295
QY 248 TGATTTCAATACAGTCTCTGATCTCAAGCCTTATGAGGACCTGATTAACGGGAACGTGC 307
Db 296 TGATTTCAATACAGTCTC--TATCAAGCCTTATGAGGAACTCTTACCAAGGAACGTGC 352
QY 308 TGACAGACTTATTGGGGAAGTAAGATATATGTTCAATTTCAAGTCCGCTGGAAGATGG 367
Db 353 TGAGAGATTAAATGGAGGTAAGAGATTA--TTCAATTCATGTAACCTGATGATGG 409
QY 368 AGG-----CAATGATCTCTTCAACAGCACTTTGCTGCTGATGACGTTGA 412
Db 410 AAGATTATGAGTTGCTTTAATGATCTCATGCAACGCCCTTGGATGATGATGAGCGTTGA 469
QY 413 ACGTTGGGAATCGACAGCATTTCAAAAAAGAGATAAAAAAGCACTCGATTATGTTAA 472
Db 470 ACGTTGGGAGTAGTAGACATTTCAAGAAAGAGATTAACATCAGCTCTGATATGTTT 529
QY 473 CAGTTATTGAACGAAAAAGCATTTGATGTGGAGGAGAGAGTGTGTGACTGACCTCAA 532
Db 530 CCGTTACTGGAGGAAACGCGCATTTGATGTGGAGAGACAGATATTGTTACTGATCTCAA 589


```
QY 533 CTCAACCGCCTGGGCTTCGAACCTCCGACTACACGGATACACTGTCTTCAGATGT 592
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 590 CTCAATCGCTGGGTTTCGAACCTTCGATTACACGGGTACACTGTATCTCCAGAGGT 649
QY 593 TTTGAACGTTTTTAAAGCAAAAAATGGCAATTTCTCCACTGCCAATATTAGATAGA 652
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 650 TTTAAAGCTTTTCAAGATCAAAAATGACAGTTGTATGCTCCCC--GTCAGACAGA 706
QY 653 GGGAGATTAGAGCGCTTCTCAATTATTCAGGGCTCCCTCGTCCCTTTCCGCGCA 712
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 707 GGGTGAGATCAGAAAGCTTCTTAATAATCGGGCTCCCTCATGGCTTCCCTGTGA 766
QY 713 GAAAGTTATGATGAAGCTGAAACATTTCTTACAAAATATTAAAGAAAGCCCTGCAAA 772
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 767 GAAAGTTATGGAAGAAAGCTGAAATCTTCCACAAAGATATTGAAGAAGCTCTACAAA 826
QY 773 GATTCCGGCATCCAGTATACCTTCACTAGAGATACGGGACGTTCTGGAATATGTTGCA 832
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 827 GATTCCAGTCTCCGCT--CTTCAAGAGATTAAGTTGTATGGAATATGGCTGGCA 883
QY 833 CACCAATTTGCCACGCTTGGAAAGAAATTACATGAGCGTCTTTGACAGCACACTA- 891
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 884 CACAAATTTGCCAAGATTGGAAGCAAAATTAATAGACACACTTGAGAAAGACACCAG 943
QY 892 -----AAATTAAGAACGCCCGCGAAACTTTTGAACCTTGCAAAATTGGAATTCAA 943
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 944 TGCATGGCTCAATAAAATGCTGGGAAGACTTTTGAACCTTGCAAAATTGGAATTCAA 1003
QY 944 TATATTTCACTCCTTACAGAGAGAGATTAACAATGTTCCGATGGTGAAGACTC 1003
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1004 TATATTTAACTCCTTACACAAAAGAAATTACAATATCTTTGAGATGTTGGAAGAAGTC 1063
QY 1004 GGGTTCCTGAGATGACCTTCTGTGCACTCGTCACGTGGAATACTACGCTTTGGCTTC 1063
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1064 GGATTTGCCCTAAATTGACATTTGCTCGGCATCGTCATGTGAATTTCTACACTTTGGCTTC 1123
QY 1064 CTGCATTGGCTTCGAGCCTCAACATTTCTGGAATTCAGACTCGGCTTTACCAAGATGTCCTCA 1123
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1124 TTGTATGTCATGTGACCCAAAACATTTGCAATTCAGACTAGGCTTCGCAAAATGTCTCA 1183
QY 1124 TCTTATCAGGTTCTTGACGACATGTACGCTCTTCGGCACAGTAGACGAGCTGGAACCT 1183
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1184 TCTTGTACAGTTTGGACGATATTTAGACACTTTTGGAAAGATTGACGAGCTTGAACCT 1243
QY 1184 CTTACAGCGCAATTAAGAGATGGATCCGTCGCGATGGAATGCCCTTCAGATATATAT 1243
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1244 CTTACATCTGCAATTAAGAGATGGAATTCAGAGATAGAAACACTTCAGATATATAT 1303
QY 1244 GAAAGAGTGTACATGATGTTTATCACACCGTAAATGAATGGCTCGAGTGGCAGAGAA 1303
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1304 GAAATGTGTGTACATGCTGTGTTGAAACTGTAAATGAAGTGAACGAGAGCGGAGAA 1363
QY 1304 GGCCTCAAGCGCGAGACACGCTCAACTATGCAAGACAGGCTTGGAGGCGTGTGATTTC 1363
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1364 GACTCAAGGGGAGAAACACTCTCAACTATGTTCGAAAAGGCTTGGAGGCTTATTTGATTTC 1423
QY 1364 GTATATGAGAGCAAGCAAGTGGATCGCACTGGTATCTGCCACGTTTGAAGAGTACTT 1423
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1424 ATATATGAGAGAAAGCAAAATGATCTTAATGTTATCTGCCAATGTTGAAGAGTACCA 1483
QY 1424 GGAGAACGGGAAAAGTTAGCTCTGCTCATCGCCCATGCGCACTGCAACCATTTCTGACGTT 1483
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1484 TGAGAAATGGAAAGTGAGCTCTGCAATGCGGTAGCAACATTTGCAACCATCTCACTTT 1543
QY 1484 GGACATCCCTTTCTGATCACATCTCAAGGAAGTTGACTTCCCATCGAAGCTCAATGA 1543
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1544 GAATGCATGGCTTCTGATTACATCTGAAGGAATTGATTTCCATCCAGGTTCAATGA 1603
QY 1544 CTTGATATGTATCATCTCTTGATTAAGAGTGTATACACGGTGCTACAAAGCAGACAGGCG 1603
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1604 TTTGGCATCGTCTTCTTCCGCTACGAGGTGACACACGCTGCTACAAAGCCGATAGGGA 1663
QY 1604 CCGTGAGAAAGAGCTTCTGTATATCATGTATATGAAAGCAATCTTGATTTAACGGA 1663
```

```
Db 1664 TCGTGTGAAGAGCTTCGTGTATATCATGTATATAGAAAGCAATCCTGATCAACCGA 1723
QY 1664 AGAAGATGCTCTGAATCATATCAACTTCATGATCAGGAGCGCAATCAGAGAATTAATTG 1723
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1724 AGAAGATGCCCTCATATCATATCAATGCCATGTGTCATATGACATTAATCAAGAATTAATTG 1783
QY 1724 GAGCTTCTAAAGCCAGACACAGTGTTCCTCATCTTCCAGAAACACGATTTGACAT 1783
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1784 GGAATTTCTAAGATCCAAACGACAAATATTTCCAATGCTGGCCAGAAACATGCTTTGACAT 1843
QY 1784 AAGCAGATTGGCATCACGGTTACAGATACCGAGATGGCTACAGCTTTGCCAACGTTGA 1843
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1844 AACAGAGCTCTCCACCATCTCTACATATATCGAGATGGCTTTAGTGTGCCAACAGGA 1903
QY 1844 AACAGAGTTTGGTATGAGAACCGTCATTTGAACCTGTGCTTTGTAAACAACACTTCAA 1903
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1904 AACAAAAAATTGGTATGAAACACTCCTTGAATCTATGCTTTTAACTATTAACATA 1963
QY 1904 ATCTACAATATTAACTGAGATGCCCTATGGGTATATATAGGGCACA 1950
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1964 TCCATATAATAAGCTCATATATGTAATTATTGGCTTATGACATA 2010
```

Search completed: July 26, 2004, 10:19:43
Job time : 174 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 26, 2004, 10:19:48 ; Search time 3693 Seconds
(without alignment)
2664.540 Million cell updates/sec

Title: US-10-025-145A-64
Perfect score: 2013
Sequence: 1 ttctgacgtgccttctatc.....aaaaaaaaaaaaaa 2013

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3216467 seqs, 2444149694 residues

Total number of hits satisfying chosen parameters: 6432934

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------------|
| 1 | 2013 | 100.0 | 2013 | 15 | US-10-025-145A-64 |
| 2 | 1306.8 | 64.9 | 2018 | 9 | US-09-887-586A-19 |
| 3 | 1306.8 | 64.9 | 2018 | 9 | US-09-903-012-19 |
| 4 | 1306.8 | 64.9 | 2018 | 10 | US-09-900-797-19 |
| 5 | 1306.8 | 64.9 | 2018 | 13 | US-09-893-820-19 |
| 6 | 1306.8 | 64.9 | 2018 | 14 | US-10-041-007-21 |
| 7 | 1306.8 | 64.9 | 2018 | 15 | US-10-025-145A-3 |
| 8 | 1092.4 | 54.3 | 1890 | 15 | US-10-025-145A-77 |
| 9 | 1072.4 | 53.3 | 2186 | 15 | US-10-025-145A-66 |
| 10 | 1071.6 | 53.2 | 2196 | 9 | US-09-887-586A-29 |
| 11 | 1071.6 | 53.2 | 2196 | 9 | US-09-903-012-29 |
| 12 | 1071.6 | 53.2 | 2196 | 10 | US-09-900-797-29 |
| 13 | 1071.6 | 53.2 | 2196 | 13 | US-09-893-820-29 |
| 14 | 1071.6 | 53.2 | 2196 | 14 | US-10-041-007-25 |

| | | | | | | |
|----|--------|------|------|----|-------------------|-------------------|
| 15 | 1071.6 | 53.2 | 2196 | 15 | US-10-025-145A-1 | Sequence 1, Appl |
| 16 | 1071.6 | 53.2 | 2205 | 15 | US-10-025-145A-31 | Sequence 31, Appl |
| 17 | 929.4 | 46.2 | 2429 | 14 | US-10-041-007-27 | Sequence 27, Appl |
| 18 | 929.4 | 46.2 | 2429 | 15 | US-10-025-145A-68 | Sequence 68, Appl |
| 19 | 925.4 | 46.0 | 2089 | 9 | US-09-887-586A-57 | Sequence 57, Appl |
| 20 | 925.4 | 46.0 | 2089 | 9 | US-09-903-012-57 | Sequence 57, Appl |
| 21 | 925.4 | 46.0 | 2089 | 10 | US-09-900-797-57 | Sequence 57, Appl |
| 22 | 925.4 | 46.0 | 2089 | 13 | US-09-893-820-57 | Sequence 57, Appl |
| 23 | 925.4 | 46.0 | 2089 | 14 | US-10-041-007-23 | Sequence 23, Appl |
| 24 | 925.4 | 46.0 | 2089 | 15 | US-10-025-145A-5 | Sequence 5, Appl |
| 25 | 471 | 23.4 | 696 | 15 | US-10-025-145A-70 | Sequence 70, Appl |
| 26 | 445.8 | 22.1 | 1865 | 9 | US-09-887-586A-47 | Sequence 47, Appl |
| 27 | 445.8 | 22.1 | 1865 | 9 | US-09-903-012-47 | Sequence 47, Appl |
| 28 | 445.8 | 22.1 | 1865 | 10 | US-09-900-797-47 | Sequence 47, Appl |
| 29 | 445.8 | 22.1 | 1865 | 13 | US-09-893-820-47 | Sequence 47, Appl |
| 30 | 445.8 | 22.1 | 1865 | 14 | US-10-041-007-17 | Sequence 17, Appl |
| 31 | 429.6 | 21.3 | 1967 | 15 | US-10-025-145A-17 | Sequence 17, Appl |
| 32 | 427 | 21.2 | 2700 | 9 | US-09-887-586A-43 | Sequence 43, Appl |
| 33 | 427 | 21.2 | 2700 | 9 | US-09-903-012-43 | Sequence 43, Appl |
| 34 | 427 | 21.2 | 2700 | 10 | US-09-900-797-43 | Sequence 43, Appl |
| 35 | 427 | 21.2 | 2700 | 12 | US-10-041-018-363 | Sequence 363, App |
| 36 | 427 | 21.2 | 2700 | 13 | US-09-893-820-43 | Sequence 43, Appl |
| 37 | 391.6 | 19.5 | 2424 | 9 | US-09-887-586A-45 | Sequence 45, Appl |
| 38 | 391.6 | 19.5 | 2424 | 9 | US-09-903-012-45 | Sequence 45, Appl |
| 39 | 391.6 | 19.5 | 2424 | 10 | US-09-900-797-45 | Sequence 45, Appl |
| 40 | 391.6 | 19.5 | 2424 | 13 | US-09-893-820-45 | Sequence 45, Appl |
| 41 | 391.6 | 19.5 | 2424 | 14 | US-10-041-007-14 | Sequence 14, Appl |
| 42 | 391.6 | 19.5 | 2424 | 15 | US-10-025-145A-15 | Sequence 15, Appl |
| 43 | 391.6 | 19.5 | 2528 | 14 | US-10-041-007-13 | Sequence 13, Appl |
| 44 | 390.2 | 19.4 | 1735 | 9 | US-09-887-586A-49 | Sequence 49, Appl |
| 45 | 390.2 | 19.4 | 1735 | 9 | US-09-903-012-49 | Sequence 49, Appl |

ALIGNMENTS

RESULT 1

US-10-025-145A-64

; Sequence 64, Application US/10025145A

; Publication No. US20030175861A1

; GENERAL INFORMATION:

; APPLICANT: Croteau, Rodney B.

; APPLICANT: Bohlmann, Joerg

; APPLICANT: Steele, Christopher L.

; APPLICANT: Phillips, Michael A.

; TITLE OF INVENTION: Monoterpane Synthases from Grand Fir (Abies Grandis)

; FILE REFERENCE: WSIU18414

; CURRENT APPLICATION NUMBER: US/10/025,145A

; CURRENT FILING DATE: 2002-06-28

; PRIOR APPLICATION NUMBER: US 09/360,545

; PRIOR FILING DATE: 1999-07-26

; PRIOR APPLICATION NUMBER: PCT/US98/14528

; PRIOR FILING DATE: 1998-07-10

; PRIOR APPLICATION NUMBER: US 60/052,249

; PRIOR FILING DATE: 1997-07-11

; NUMBER OF SEQ ID NOS: 107

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 64

; LENGTH: 2013

; TYPE: DNA

; ORGANISM: Abies Grandis

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (36)..(1889)

; OTHER INFORMATION:

US-10-025-145A-64

Query Match 100.0%; Score 2013; DB 15; Length 2013;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2013; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTTTGACGTGCTTCTATCTGATGACAGCTGAATGCGCTTCTTCTATCTACTCCGC 60
|||||

Db 1 TTTTGAGTGCCCTTCTTATCTGATAGCAAGCTGAAATGGCTCTTCTTTCTATTACTCCGC 60
QY 61 TGGTTCCAGSTGTCGCTCAGTTCTTCTCATGAGATTAAGGCTCTCCGTAGAACAAATCC 120
Db 61 TGGTTCCAGSTGTCGCTCAGTTCTTCTCATGAGATTAAGGCTCTCCGTAGAACAAATCC 120
QY 121 CAACCTCTTGAATCTTGACGCGCGGGAATCCGTCGCGCATTCATTAACATGTGTTGA 180
Db 121 CAACCTCTTGAATCTTGACGCGCGGGAATCCGTCGCGCATTCATTAACATGTGTTGA 180
QY 181 CAAGCGTCGATCTACTGATTTCTGTACAGAGACGCGTGGCACTATCATTTCCAACTGT 240
Db 181 CAAGCGTCGATCTACTGATTTCTGTGTACAGAGACGCGTGGCACTATCATTTCCAACTGT 240
QY 241 GGGACGATGATTTTCATACAGTCTCTGATCTCAACGCCCTTATGGAGCACTGATTACC 300
Db 241 GGGACGATGATTTTCATACAGTCTCTGATCTCAACGCCCTTATGGAGCACTGATTACC 300
QY 301 AACGTGCTGACAGACTTATTTGGGGAAGTAAGGATATATGTTCAATTTCAAGTCGCTGG 360
Db 301 AACGTGCTGACAGACTTATTTGGGGAAGTAAGGATATATGTTCAATTTCAAGTCGCTGG 360
QY 361 AAGATGAGGCAATGATCTCTTCAACGACTTTTGCTGTGATGACGTGAACGTTTGG 420
Db 361 AAGATGAGGCAATGATCTCTTCAACGACTTTTGCTGTGATGACGTGAACGTTTGG 420
QY 421 GAATCGACGCAATTTCAAAAAAGAGATAAAACGGCACTCGATTAATGTTAACATTAAT 480
Db 421 GAATCGACGCAATTTCAAAAAAGAGATAAAACGGCACTCGATTAATGTTAACATTAAT 480
QY 481 GGAACGAAAAAGGCATTGGATGTGGAGGAGAGAGTGTGTGACTGACTCACTCAACCG 540
Db 481 GGAACGAAAAAGGCATTGGATGTGGAGGAGAGAGTGTGTGACTGACTCACTCAACCG 540
QY 541 CCTGGGGCTTCGAACCTCCGACTACACGGATACACTGTGTCTTCAAGTGTTTGAAACG 600
Db 541 CCTGGGGCTTCGAACCTCCGACTACACGGATACACTGTGTCTTCAAGTGTTTGAAACG 600
QY 601 TTTTAAAGACAAAAATGGGCAATTTCTCCACTGCCAATATTCAGATAGAGGAGAGA 660
Db 601 TTTTAAAGACAAAAATGGGCAATTTCTCCACTGCCAATATTCAGATAGAGGAGAGA 660
QY 661 TTAGAGCGTCTCAATTTATTCAGGCGCTCCCTGCTGCTTCCGGCGAGAAAAGTTA 720
Db 661 TTAGAGCGTCTCAATTTATTCAGGCGCTCCCTGCTGCTTCCGGCGAGAAAAGTTA 720
QY 721 TGGATGAAGCTGAAAATCTCTCAAAAATATTTAAGAGAAGCCCTGCAAAAAGATTCCGG 780
Db 721 TGGATGAAGCTGAAAATCTCTCAAAAATATTTAAGAGAAGCCCTGCAAAAAGATTCCGG 780
QY 781 CATCCAGTATCTTCTACTAGAGTACGGGACGTTCTGGAATATGTTGGCACACCAATT 840
Db 781 CATCCAGTATCTTCTACTAGAGTACGGGACGTTCTGGAATATGTTGGCACACCAATT 840
QY 841 TGCCACGCTTGAAGCAAGGAATTAATGACGCTTTGACAGCACACTAAAAATAGA 900
Db 841 TGCCACGCTTGAAGCAAGGAATTAATGACGCTTTGACAGCACACTAAAAATAGA 900
QY 901 ACGCCGCGAGAAAATTTAGAACTTGAAAATTGGAATTCAATATATTTCACTCCTTAC 960
Db 901 ACGCCGCGAGAAAATTTAGAACTTGAAAATTGGAATTCAATATATTTCACTCCTTAC 960
QY 961 AAGAGAGAGTTAAAAATGTTCCCGATGCTGAAAAGACTCGGTTCTCTGAGATGA 1020
Db 961 AAGAGAGAGTTAAAAATGTTCCCGATGCTGAAAAGACTCGGTTCTCTGAGATGA 1020
QY 1021 CCTTCTGTCATCGTCAAGTGAATACGCTTTGGCTTCTGATGCGTTGCGTTCGAGC 1080
Db 1021 CCTTCTGTCATCGTCAAGTGAATACGCTTTGGCTTCTGATGCGTTGCGTTCGAGC 1080
QY 1081 CTCAACATTTCTGATTTCAGACTCGGCTTTACCAAGATGTCTCATCTTATCACGGTCTTG 1140
Db 1081 CTCAACATTTCTGATTTCAGACTCGGCTTTACCAAGATGTCTCATCTTATCACGGTCTTG 1140

QY 1141 ACGACATGTACGACGTTCTTCCGCAAGTAGACGAGCTGGAATCTTTCACAGCGACAAATTA 1200
Db 1141 ACGACATGTACGACGTTCTTCCGCAAGTAGACGAGCTGGAATCTTTCACAGCGACAAATTA 1200
QY 1201 AGAGATGGGATCCGTCGCGCATGGAATGCCCTTCCAGAAATATGAAGAGGTATACATGA 1260
Db 1201 AGAGATGGGATCCGTCGCGCATGGAATGCCCTTCCAGAAATATGAAGAGGTATACATGA 1260
QY 1261 TGGTTTATCACACCGTAATGAAAATGGCTCGAGTGGCAGAGAAAGGCTCAAGCCGAGACA 1320
Db 1261 TGGTTTATCACACCGTAATGAAAATGGCTCGAGTGGCAGAGAAAGGCTCAAGCCGAGACA 1320
QY 1321 CGCTCACTATGCAAGACAGGCTTGGAGCGGTGTTTGAATTCGTATATGCAAGAACAA 1380
Db 1321 CGCTCACTATGCAAGACAGGCTTGGAGCGGTGTTTGAATTCGTATATGCAAGAACAA 1380
QY 1381 AGTGAATCGCCACTGTTATCTGCCCAAGTTGAGAGTACTTGAAGAACGGAAGTTA 1440
Db 1381 AGTGAATCGCCACTGTTATCTGCCCAAGTTGAGAGTACTTGAAGAACGGAAGTTA 1440
QY 1441 GCTTGTCTATCGCCCATGCGCACTGCAACCCATTCTGACGTTGACATCCCTTCTCTG 1500
Db 1441 GCTTGTCTATCGCCCATGCGCACTGCAACCCATTCTGACGTTGAGACATCCCTTCTCTG 1500
QY 1501 ATCAATCTCTCAAGGAAGTTGACTTCCCATCGAAGCTCAATGACTTGATATGATCATCC 1560
Db 1501 ATCAATCTCTCAAGGAAGTTGACTTCCCATCGAAGCTCAATGACTTGATATGATCATCC 1560
QY 1561 TTGATTAAGAGGTGATACACGGTGTCTCAAGGCAGACAGGCCCCGTGAGAAAGACTT 1620
Db 1561 TTGATTAAGAGGTGATACACGGTGTCTCAAGGCAGACAGGCCCCGTGAGAAAGACTT 1620
QY 1621 CGTCTATATCATGTTATATGAAGCAATCCTGGATTAAACGAAAGATGCTCTGAATC 1680
Db 1621 CGTCTATATCATGTTATATGAAGCAATCCTGGATTAAACGAAAGATGCTCTGAATC 1680
QY 1681 ATATCAATCTCATGATCAGGAGCGCAATCAGAGAAATTAATTGGAGCTTCTAAAGCCAG 1740
Db 1681 ATATCAATCTCATGATCAGGAGCGCAATCAGAGAAATTAATTGGAGCTTCTAAAGCCAG 1740
QY 1741 ACAACAGTGTCCCATCACTTCCAAGAAAACAGCATTTGACATAAGAGTTTGCATC 1800
Db 1741 ACAACAGTGTCCCATCACTTCCAAGAAAACAGCATTTGACATAAGAGTTTGCATC 1800
QY 1801 ACGGTTACAGATACCGAGATGGCTACAGCTTTGCCAACGTTGAAAACAAAGAGTTGTGA 1860
Db 1801 ACGGTTACAGATACCGAGATGGCTACAGCTTTGCCAACGTTGAAAACAAAGAGTTGTGA 1860
QY 1861 TGAGAACCGTCATTGAACTGTGCTTTGTAAACAACATTCATAATATTAATCTG 1920
Db 1861 TGAGAACCGTCATTGAACTGTGCTTTGTAAACAACATTCATAATATTAATCTG 1920
QY 1921 AGGATGCCCTATGGGTGATATAGGGCACAAAAATTAATATGTTGTGTAGTAAAGC 1980
Db 1921 AGGATGCCCTATGGGTGATATAGGGCACAAAAATTAATATGTTGTGTAGTAAAGC 1980
QY 1981 TGTAAATTATGAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2040
Db 1981 TGTAAATTATGAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2040

RESULT 2
US-09-887-586A-19
; Sequence 19, Application us/09887586A
; Patent No. US20020094556A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20020094556A1, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001


```

; CURRENT APPLICATION NUMBER: US/09/887,586A
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 2018
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)...(1889)
; OTHER INFORMATION: pinene synthase
US-09-887-586A-19

```

| | | | | |
|----------------------------|-------|-----------------|------------|--------------|
| Query Match | 64.9% | Score 1306.8; | DB 9; | Length 2018; |
| Best Local Similarity | 81.0% | Pred. No. 0; | | |
| Matches 1595; Conservative | 0; | Mismatches 342; | Indels 33; | Gaps 5 |

| | | | |
|----|-----|---|-----|
| Qy | 68 | CAGGTCGTGCTCAGTTCCTTCTCATGAGATTAAAGGCTCTCCGTAGAACAAATCCCACTCT | 127 |
| Db | 53 | CAAAATCGTTGATCAGTTCTAACCCATGAGCTTAAAGCTCTCTTAGAACAAATTCAGCTCT | 112 |
| Qy | 128 | TGGAATCTGCAGGCCGGGAAATCCGTCGCGCATTCATMAACATGTTTGAACAAGCGT | 187 |
| Db | 113 | AGGAATGAGTAGCGGAGGAAATCTATCACTCTTCATCAGCATGAGCTCTACCAACCGT | 172 |
| Qy | 188 | CGCATCTACTGATTCTGTACAGAGACGCTGGGCAACTATCATTTCCAACCTGTGGAGCA | 247 |
| Db | 173 | TGTAACCGATGATGTTGTACGAAGACGATGGGCGATTTCCATTCCAACCTGTGGAGCA | 232 |
| Qy | 248 | TGATTTCATACAGTCTCTGATCTCAACGCTTATGAGCACCTGATTAACGGGAACGTGC | 307 |
| Db | 233 | TGATGTCATACAGTCT--TTACCAACGCTTATGAGGAAATCGTACTCGAGCGTGC | 289 |
| Qy | 308 | TGACAGACTTATTGGGGAAGTAAGGATATAATGTTCAATTCCAAGTCGCTGCAAGATGG | 367 |
| Db | 290 | TGAGAACTGATCGGGGAAGTAAG--AACATGTTCAATTGATGTCTATTAGAAAGATGG | 346 |
| Qy | 368 | AG-----GCAATGATCTCTTCAACGACTTTGCTGTGTCATGACGTGA | 412 |
| Db | 347 | AGAGTTAATGAGTCCGCTCAATGATCTCATTCACGCTTTGATGTGCACAGCCTTGA | 406 |
| Qy | 413 | ACGTTTGGGAATCGACAGGCATTTCAAAAAAGAGATMAAAACGGCACTCGATTATGTTAA | 472 |
| Db | 407 | ACGTTTGGGATCCATAGACATTTCAAGATGAGATAAAATCGCGCTTGATTAATGTTTA | 466 |
| Qy | 473 | CAGTTATTGGAACGAAAAAGGCAATTGATGTGGAGGGAGAGAGTGTGTACTGACCTCAA | 532 |
| Db | 467 | CAGTTATTGGGGCGAAAAATGGCATCGGATGCGGAGGAGAGAGTGTGTAATGATCTGAA | 526 |
| Qy | 533 | CTCAACCGCCTTGGGGCTTCGAATCTCCGACTACACGATACACTGTGCTTCAGATGT | 592 |
| Db | 527 | CTCACTGCGTTGGGGCTTCGAACCTACGACTACACGATACCCGGTGTCTTCAGATGT | 586 |
| Qy | 593 | TTTGAACGTTTTTAAGA CAAAAATGGGCAATTTTCTCCA CTGCCAATATTCAGATAGA | 652 |
| Db | 587 | TTTCAAGCTTTCAAAAGGCCAAAAATGGGCAATTTTCTGCTCTGA AATATTCAGACAGA | 646 |
| Qy | 653 | GGGAGAGATTAGAGCGCTTCTCAATTTATTCAAGGGCTCCCTCGCTTTTCCCGGGCA | 712 |
| Db | 647 | TGAAGAGATCAGAGCGCTTCTGAATTTATTCCGGGCTCCCTCATTTGCTTTCCAGGGGA | 706 |
| Qy | 713 | GAAAGTTATGATGAGAGCTGAAACATTTCTACAA AATATTTAAGAGAAAGCCCTGCAAAA | 772 |
| Db | 707 | GAA AATTATGATGAGCGCTGA AATCTTCTCTACCA AATATTTAAAGAAAGCCCTGCAAAA | 766 |
| Qy | 773 | GATTCGGGCATCCAGTATACTTTCACTAGAGATACGGGACGTTCTGGAATATGTTGGCA | 832 |

| | | | | |
|----|------|---|--|------|
| Db | 767 | GATTCGGTCTCCAGT--- | CTTTCGGAGAGATCGGGGACGTTTGGAAATATGGTTGGCA | 823 |
| QY | 833 | CACCAATTTGGCAGCGCTTGAAGCAAGAAATTACATGACGTCTTTGGACAGACACTAA | | 892 |
| Db | 824 | CACATATTTGCCGFEGATTTGGAAGCAAGGAATTACATCCAACTCTTTGGACAGACACTGA | | 883 |
| QY | 893 | AAATAAGAACGC-----CGCCGAGAACTTTTAGAACTTGCAAAATTGGAATTCAA | | 943 |
| Db | 884 | GAAACAGAAAGTCATATGTGAAGAGCAAAAAAATTTTAGAACTCGCAAAATTGGAGTTCAA | | 943 |
| QY | 944 | TATATTTCACTCCCTTACAGAGAGAGAGATTAAAAACATGTTTCCGATGTTGGAAGACTC | | 1003 |
| Db | 944 | CATCTTCAATCCTTACAAAGAGAGAGATTAGAAAGTCTGTGATAGTTGGAAGAAATC | | 1003 |
| QY | 1004 | GGGTTCTCCTGAGATGACCTTCTGTGACATCGTCAAGTGAATACTACGCTTTGGCTTC | | 1063 |
| Db | 1004 | GGGTTTCTCTGAGATGACCTTCTGCCGACATCGTCAAGTGAATACTACACTTTGGCTTC | | 1063 |
| QY | 1064 | CTGCATTGCGTTTGAAGCTCAACATTTCTGATTCAGACTCGGCTTTACCAAGATGTCTCA | | 1123 |
| Db | 1064 | CTGCATTGCGTTTGAAGCTCAACATTTCTGATTCAGACTCGGCTTTGCCAAGAGCTGTCA | | 1123 |
| QY | 1124 | TCTTATCAGCGTTTCTTGACGACATGTACGACGTTCTTGCGCACAGTAGACGAGCTGAACT | | 1183 |
| Db | 1124 | TCTTATCAGCGTTTCTTGACGATATGTACGACACTTTCGGCACAGTAGACGAGCTGAACT | | 1183 |
| QY | 1184 | CTTCACAGCGACIATTAAGATGGGATCCGTCGGGATGGAATGCTTCAGAAATATAT | | 1243 |
| Db | 1184 | CTTCACAGCGACIATGAGAGATGGGATCCGTCCTCGATAGATTGCTTCAGAAATATAT | | 1243 |
| QY | 1244 | GAAAGAGTGTACATGATGTTTATCACACCGTAAATGAATGCTCGAGTGCAGAGAA | | 1303 |
| Db | 1244 | GAAAGAGTGTACATGACGGTTTACGACACCGTAAATGAATGCTCGAGAGCAGAGGA | | 1303 |
| QY | 1304 | GGCTCAAGGCCGAGACACGCTCAACTATGCAAGACAGGCTTGGAGGCGTGTGATTTC | | 1363 |
| Db | 1304 | GGCTCAAGGCCGAGATACGCTCACATATGCTCGGGAAGCTTGGAGGCTTATATGATTTC | | 1363 |
| QY | 1364 | GTAATGCAAGAGCAAGTAGTGATCGCCACTGCTTATCTGCCACGTTTGAGGAGTACTT | | 1423 |
| Db | 1364 | GTAATGCAAGAGCAAGTGGATCGCCACTGCTTATCTGCCACTGCTTATGATGAGTACTA | | 1423 |
| QY | 1424 | GGAGAAACGGGAAAGTTAGCTCTGCTCATCGCCCATGCGCACTGCAACCCATTCTGACGTT | | 1483 |
| Db | 1424 | CGAATGGAAGTTAGTGTGTGTCATCGCATATCCGATTCGCAACCCATTCTGCAAT | | 1483 |
| QY | 1484 | GGACATCCCCCTTCTCTGATCACATCTCAAGGAAAGTTGACTTCCCATCGAAGCTCAATGA | | 1543 |
| Db | 1484 | GGACATCCCCCTTCTCTGATCATATCTCAAGGAAAGTTGACTTCCCATCGAAGCTTAACGA | | 1543 |
| QY | 1544 | CTTGATATGTATCATCTTCGATTAGAGGTGATACAGGTGCTACAGGCGACAGGGC | | 1603 |
| Db | 1544 | CTTGATATGTATCATCTTCGATTAGAGGTGATACAGGTGCTACAGGCGGACAGGGC | | 1603 |
| QY | 1604 | CCGTGAGAAAGAGCTTCTCTATATCATGTTATATGAAGAACAATCCTGATTAACGA | | 1663 |
| Db | 1604 | TCGTGAGAAAGAGCTTCTCTATATCATGTTATATGAAGAACAATCCTGAGATATCAGA | | 1663 |
| QY | 1664 | AGAAGATGCTCTGAATCATATCAACTTCATGATCAGGAGCGCAATCAGAGAAATTAATTG | | 1723 |
| Db | 1664 | AGAAGATGCTCTGAATCATATCAACGCCATGATCAGTGAAGTAAATTAATTG | | 1723 |
| QY | 1724 | GGAGCTTCTTAAGCCAGACAACAGTGTTCCTCATCACTTCCAAAGAAACAGCATTTGACAT | | 1783 |
| Db | 1724 | GGAACTTCTTAAGCCAGACAACATGTTCCCATCTCGGCAAGAAACATGCTTTGACAT | | 1783 |
| QY | 1784 | AAGCAGAGTTTGCATCAAGCTTACAGATACCGAGTGGCTACAGCTTTGCCAAGCTTGA | | 1843 |
| Db | 1784 | CGCCAGAGCTTTCATTAACGGCTACAAATACCGAGACGGCTACAGCGTTGCCAAGCTTGA | | 1843 |
| QY | 1844 | AACAAGAGTTTGGTGATGGAACCGTCATTGAACCTGTGCTTTGTAACAACACTTCAA | | 1903 |

Db 1844 AACGAAGTTTGGTCACGAGAACCTCTCTTGAATCTGTGCCTTTGTAGCAACAGCTCAA 1903
Qy 1904 ATCTACAATAATTAAGTCTGAGATGCCCTATGGGTGTATATAGGGCACACAATAAATATAT 1963
Db 1904 ATCTATGCCCTATGCTATGTGCGGTAAATAATATATGTGGAAGGTAGCCGTGATGTAGA 1963
Qy 1964 GGTGTGTAGTAAAGCTGTAATTTATGAAAAAATGAAAAAATGAAAAAATGAAAAAATG 2013
Db 1964 GGATAGTTGTATATTAATTTAATTAAGTTGTAATTTAATAAATGAAAAAATGAAAAA 2013

RESULT 3
US-09-903-012-19
; Sequence 19, Application US/09903012
; Patent No. US20020094557A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20020094557A11, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903,012
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 05/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 2018
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6) ... (1889)
; OTHER INFORMATION: pinene synthase
US-09-903-012-19

Query Match 64.9%; Score 1306.8; DB 9; Length 2018;
Best Local Similarity 81.0%; Pred. No. 0;
Matches 1595; Conservative 0; Mismatches 342; Indels 33; Gaps 5;

Qy 68 CAGTGTGCTCAGTCTTCTCATGAGATTAAAGCTCTCCGTAGAACAAATCCAACTCT 127
Db 53 CAAATCGTGTATCAGTTCTACCCATGAGCTTAAGGCTCTCTAGAACAAATCCAGCTCT 112
Qy 128 TGAATCTGCAGGCCGGGGAATCCGTCGCATTCATTAACATGTGTTGACAAGCGT 187
Db 113 AGGAATGAGTAGCGGAGGAATCTATCACTCTTCATCAAGCATGAGCTCTACCAACCGT 172
Qy 188 CGCATCTACTGATTTCTGTACAGACGCGGTGGGCAACTATCATTTCCAACTGTGGACGA 247
Db 173 TGTAAACCGATGATGGTGTACGAAGACGATGGGCGATTTCATTCCAACTCTGGGACGA 232
Qy 248 TGATTTCAATCAGTCTCTGATCTCAACGCGCTTATGAGCACCCTGATTAACGGGAACGTGC 307
Db 233 TGATGTCAATCAGTCT--TTACCACGCGCTTATGAGAAAAATCGTACTGTGAGCGTGC 289
Qy 308 TGACAGACTTAATGGGGAAGTAAGGATTAATGTTCATTTCAAGTCCGTGGAAGATGG 367
Db 290 TGAGAAACTGATCGGGGAAGTAAG--AACATGTTCATTCGATGTCAATTAAGAAGATGG 346
Qy 368 AG-----GCAATGATCTCCTTCAACGACTTTTGTGCTGATGACGTTGA 412
Db 347 AGAGTTAATGATCCGCTCAATGATCTCAATTCACGCGCTTGGATTGTGACAGCCTTGA 406
Qy 413 ACGTTTGGGAATCGACAGGCATTTCAAAAAAGAGATAAAAAACGGCACTCGATTATGTTAA 472

Db 407 ACGTTGGGGATCCATAGACATTTCAAGATGAGATAAATCGCGCTTGATTATGTTTA 466
Qy 473 CAGTTATTGAACGAAAAAGCAATTGATGTGGAGGGAGAGTGTGTGACTGACCTCAA 532
Db 467 CAGTTATTGGGGCGAAATGGCATCGGATGCGGAGGAGAGTGTGTACTGATCTGAA 526
Qy 533 CTCAACCGCTTGGGCTTGCAGTCTCCGACTACACGGATACACTGTGCTTCAGATGT 592
Db 527 CTCACTGCGTGGGGCTTCGAACCTTACGACTACACGGATACCCGGTGTCTTCAGATGT 586
Qy 593 TTTGAAGCTTTTAAAGACAAAAATGGGCAATTTCTCCACTGCCAATATTCAGATAGA 652
Db 587 TTTCAAGCTTTCAAAAGCCAAATGGGCAAGTTTCTGCTCTGAAAAATATTCAGACAGA 646
Qy 653 GGGAGATTAGAGGCGTTCTCAATTATTCAGGGCTCCCTGCTGCTTCCCGCGCA 712
Db 647 TGAAGAGATCAGAGCGTTCGAATTTATTCGGGCTCCCTCAATGCTTCCAGGGGA 706
Qy 713 GAAAGTTATGATGAGAGCTGAAACATTTCTCAAAAAATATTTAAGAAAGCCCTGCAAAA 772
Db 707 GAAATATATGATGAGAGCTGAAATCTTCTCTACCAATATTTAAGAAAGCCCTGCAAAA 766
Qy 773 GATTCGGCATCCAGTATACCTTCACTAGAGATACGGGACGTTCTGGAATATGTTGCA 832
Db 767 GATTCGGCTCCAGT--CTTCGCGAGAGATCGGGGACGTTTGAATATGTTGCA 823
Qy 833 CACCAATTTGCCACGCTTGGAGCAAGAAATTACATGAGACGTCCTTTGGACAGCACACTAA 892
Db 824 CACATATTTGCCGCGATTGGAGCAAGAAATTACATCCAAATCTTTGGACAGCACACTGA 883
Qy 893 AAATAAGAACGC-----CGCGAGAACTTTAGAACTTGCAAAATTTGGAATTCAA 943
Db 884 GAACACGAAGTCATATGTGAAGACCAAAAACTTTAGAACTTCGCAAAATTTGAGTTCAA 943
Qy 944 TATATTTCACTCCTTACAGAGAGAGATTAAACATGTTCCGATGCTGGAAGAGACTC 1003
Db 944 CATCTTCAATCCTTACAAAAAGGAGATTAGAAAGTCTGTCAGATGTGGAAGAATC 1003
Qy 1004 GGGTTCCTGAGATGACCTTCTGACATCGTCAAGTGAATACTACGCTTGGCTTC 1063
Db 1004 GGGTTTCTGAGATGACCTTCTGCGGACATCGTCAAGTGAATACTACACTTGGCTTC 1063
Qy 1064 CTGCATTCGCTTGCAGCTCAACATTTCTGATTCAAGCTCGGCTTGCAGAGCTGTCA 1123
Db 1124 TCTTATCAGGTTCTTGACGACATGTACGACGCTTCGGCACAGTACGAGCTGAACT 1183
Qy 1184 CTTCAAGGCAATTAAGAGATGGATCCGTCGCGATGGAATGCTTCCAGATATAT 1243
Db 1184 CTTCAAGGCAATGAAGAGATGGATCCGTCGATAGATTGCTTCCAGATATAT 1243
Qy 1244 GAAAGAGTGTACATGATGTTTATCAACCGTAAATGAATGGCTCGAGTGAGAGAA 1303
Db 1244 GAAAGAGTGTACATAGCGGTTTACGACACCGTAAATGAATGGCTCGAGTGAGAGAA 1303
Qy 1304 GGTCAAGCGCGAGACAGCTCAACTATGCAAGACAGGCTTGGGAGGCGTGTGATTC 1363
Db 1304 GGTCAAGCGCGAGATACGCTCAATATGCTCGGAAGCTTGGGAGGCTTATATGATTC 1363
Qy 1364 GTATATGCAAGAAAGTGAATGCGCCACTGTTATCTGCCACGTTTGAGAGTACTT 1423
Db 1364 GTATATGCAAGAAAGTGAATGCGCCACTGTTATCTGCTGCTTGTGATGACTACTA 1423
Qy 1424 GGAGAAAGGGAAGTTAGCTTGTCTATCGCCCATGCGCACTGCAACCCATTCTGACGTT 1483
Db 1424 CGAGAAATGGGAAAGTTAGCTGTGTCTATCGCATATCCGCAATGCAACCCATTCTGACAA 1483
Qy 1484 GGACATCCCTTCTCTGATCAATCTCAAGGAAGTTGACTTCCATCGAAAGCTCAATGA 1543

Db 1484 GGACATCCCTTCTCTGATCATATCCTGAAGAGTGACTTCCCATCAAGCTTAACGA 1543
QY 1544 CTGTATATGATCATCTCTTGATTAAGAGTGATACACGGTGCTACAGCAGACAGGGC 1603
Db 1544 CTGGCATGTGCCATCTTCGATTACGAGGTGATACGGGTGCTACAGCGCAGACAGGGC 1603
QY 1604 CCGTGAGAGAGAGCTTCGTCTATATCATGTATATGAAAGACAATCTCGATTAAACGA 1663
Db 1604 TCGTGAGAGAGAGCTTCCTCTATATCATGTATATGAAAGACAATCTCGAGTATCAGA 1663
QY 1664 AGAAGATGCTCTGAATCATATCAACTTCATGATCAGGAGCGCAATCAGAGATTAAATTG 1723
Db 1664 GGAAGATGCTCTGATCATATCAACGCCATGATCAGTACGTAATCAAGAGATTAAATTG 1723
QY 1724 GGAGCTTCTAAAGCCAGACAACAGTGTCCCATCACTTCCAAGAAACAGCATTTGACAT 1783
Db 1724 GGAATCTTCAAAACAGACATCAATGTCCCATCTCGCGAAGAAACATGCTTTGACAT 1783
QY 1784 AAGCAGATTGGCATCAGGTTACAGATACGAGATGGCTACAGCTTTGCCAAGCTTGA 1843
Db 1784 CGCCAGAGCTTTCCATTAACGGCTACAAATACGAGACGGCTACAGCGTTGCCAAGCTTGA 1843
QY 1844 AACAAAGAGTTTGGTGTATGAGAACCGTCAATGAACTGTGCTTTGTAAACAACACTTCA 1903
Db 1844 AACGAAGAGTTTGGTGTACAGAAACCTCTTGAATCTGTGCTTTGTAGCAACAGCTCAA 1903
QY 1904 ATCTACAATATTAATCTGAGATGCCCTATGGGTATATATAGGCGACACAAAATAATAT 1963
Db 1904 ATCTATGCCCTATGCTATGTGCGGTTAAATAATATGTGAAGGTAGCCGTGGATGTAGA 1963
QY 1964 GGTGTGTAGTAAAGCTGTATTTATGAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAA 2013
Db 1964 GGATAGTGTGTATTAATTTAATTAAGTTGTAAATTTTAAAAAATTTTAAAAAATTTTAAAAA 2013

RESULT 4

US-09-900-797-19

; Sequence 19, Application US/09900797
; Publication No. US20030087406A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20030087406A1, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/900,797
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for windows Version 3.0
; SEQ ID NO 19
; LENGTH: 2018
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)...(1889)
; OTHER INFORMATION: pinene synthase
US-09-900-797-19

Query Match 64.9%; Score 1306.8; DB 10; Length 2018;
Best Local Similarity 81.0%; Pred. No. 0;
Matches 1595; Conservative 0; Mismatches 342; Indels 33; Gaps 5;
QY 68 CAGTGTGCTCAGTCTCTCTCATGAGATTAAAGCTCTCCGTAGAACAAATCCCAACTCT 127
Db 53 CAAATCGTGTATCATCTTCAACCATGAGCTTAAAGCTCTCTCTAGAACAAATTCAGCTCT 112

QY 128 TGAATCTGACAGGCGCGGGAATCCGTGCGCATTCATTAACATGTGTTGACAAAGCCT 187
Db 113 AGAATGATAGAGCGAGGGAATCTATCACTCTTCATCAGCATGAGCTCTACCAACCT 172
QY 188 CGCATCTAATCTCTGTACAGAGCGGTGGCAACTATCATTTCAACCTGTGGAGCA 247
Db 173 TGTAAACGATGATGTGTACGAAGCAGATGGCGATTTCATTCCAACCTCTGGAGCA 232
QY 248 TGATTTCAACAGTCTCTGATCTCAACGCTTATGAGACCTGATTAACCGGAACGTGC 307
Db 233 TGATGTCAACAGTCT--TTACCAACGCTTATGAGGAATAATCGTACCTGAGCGTGC 289
QY 308 TGACAGACTTATTTGGGAAGTAAAGATATAATGTTCAATTTCAAGTCCCTGGAAGATGG 367
Db 290 TGAGAAACTGATCGGGGAAGTAAAG--AACATGTTCAATTCGATGTCAATTAGAAGATGG 346
QY 368 AG-----GCAATGATCTCTTCAACGACTTTTGTGCTGATGACGTGA 412
Db 347 AGAGTTAATGAGTCCGCTCAATGATCTCAACGCTTTGATGTCGACAGCCTTGA 406
QY 413 ACGTTTGGGAATGACAGGCAATTTCAAAAAGAGATAAAAACGCACTCGATTATGTAA 472
Db 407 ACGTTTGGGATTCATAGACATTTCAAGATGAGATAAATCGCGCTGATTATGTTA 466
QY 473 CAGTTATGGAACGAAAAAGCATGTGAGGAGGAGAGAGATGTTGTGACCTCAA 532
Db 467 CAGTTATTTGGGCGAAATGCGATCGGATGCGGAGGAGAGAGATGTTGTACTGATCTGAA 526
QY 533 CTCAACCGCTTGGGGCTTCGAACTCTCCACTACACGGATACACTGTGCTTCAGATGT 592
Db 527 CTCAACTGCGTTGGGCTTCGAACCTTACGACTACACGGATACCGGCTGCTTCAGATGT 586
QY 593 TTTGAACGTTTAAAGACAAAATGGGCAATTTCTCTCCACTGCAATATTCAGATGA 652
Db 587 TTTCAAGCTTTCAAAAGGCCAAAATGGGCAATTTCTCTGCTTGAATAATTCAGACAGA 646
QY 653 GGGAGATTAAGGCGCTTCTCAATTTATTCAGGGCTCCCTGCTGCTTCCCGGCGA 712
Db 647 TGAAGATGACAGGCGTTCTGAATTTATTCGGGCTCCCTCAATGCTTCCAGGGGA 706
QY 713 GAAAGTTATGATGAAGCTGAACATTTCTCAAAAATATTTAAGAAAGCCCTGCAAA 772
Db 707 GAAATTTATGATGAAGCTGAACATTTCTCAAAAATATTTAAGAAAGCCCTGCAAA 766
QY 773 GATTCGGCATTCAGTATACCTTCTACTAGATACGGAGCTTCTGAATATGTTGCA 832
Db 767 GATTCGGCTTCAGT---CTTCCGAGAGATCGGGAGCTTTGGAATATGTTGCA 823
QY 833 CACCAATTTGCCACGCTTGAAGCAAGAAATTACATGAGCGTCTTTGACAGACACTAA 892
Db 824 CACATATTTGCCCGCATTTGAAGCAAGAAATTACATCCAAAGTCTTTGACAGACACTGA 883
QY 893 AAATAAGAACGC-----CGCCGAGAACTTTAGAACTTGCAAAATTGGAATCAA 943
Db 884 GAACACGAGTCTATGTGAAGAGCAAAAACCTTTAGAACTCGCAAAATTGAGTTCAA 943
QY 944 TATATTTCACTCTTACAGAGAGAGATTAAACATGTTTCCGATGGTGAAAGACTC 1003
Db 944 CATCTTTCAATCTTACAAAAGAGGAGTTAAGAAAGTCTGTGATGTGGAAGAAATC 1003
QY 1004 GGGTTCCTGAGATGACCTTCTGTGACATCGTCAAGTGAATTAACGCTTTGGCTTC 1063
Db 1004 GGGTTTCTGAGATGACCTTCTGTGACATCGTCAAGTGAATTAACGCTTTGGCTTC 1063
QY 1064 CTGATTCGCTTGAAGCTCAACATCTGATTACAGACTCGGCTTAAACAAAGATGTCTCA 1123
Db 1064 CTGATTCGCTTGAAGCTCAACATCTGATTACAGACTCGGCTTAAACAAAGATGTCTCA 1123
QY 1124 TCTTATCAAGGTCTTGACGACATTAAGAGCTTCCGCAAGTAAAGAGCTGGAAT 1183
Db 1124 TCTTATCAAGGTCTTGACGATATTAAGAGCAACCTTCCGCAAGTAAAGAGCTGGAAT 1183

| | | | | | |
|----|--|------|----------------------|---|------|
| OY | | 1184 | CTTCACAGCGACAATTAAGA | GATGGGATCCGTCGCCCATGGAATGCCTTCCAGATAATAT | 1243 |
| Dd | | 1184 | CTTCACAGCGACAATGAAG | ATGGGATCCGTCCTCGATAGATTGCCCTTCCAGATAATAT | 1243 |
| OY | | 1244 | GAAAGAGGTGTACATGATG | GGTTTATCACACCCTAATATGAATGGCTCGAGTGCGACAGAA | 1303 |
| Dd | | 1244 | GAAAGAGGTGTACATAGC | GGTTTTACGACACCCTAATATGAATGGCTCGAGAGGCGACAGGA | 1303 |
| OY | | 1304 | GGCTCAAGGCCGAGACA | CGCTCAACTATGCAAGCAGGCTTGGAGGCGGTGTTTGAATTC | 1363 |
| Dd | | 1304 | GGCTCAAGGCCGAGATAC | GCTCAATATGCTCGGGAAGCTTGGAGGCTTATATTGATTC | 1363 |
| OY | | 1364 | GTATATGACAGAAAGCAA | AGTGGATCGCCACTGGTTATCTGCCACGTTTGAGAGTACTT | 1423 |
| Dd | | 1364 | GTATATGCAAGAACAGCA | AGGTGGATCGCCACTGGTTACTGCCCTCTTGATGATGACTA | 1423 |
| OY | | 1424 | GGAGAACGGGAAAGTTA | CTCTGCTCATCGCCCATGCGCACTGCAACCCATTCTGACGTT | 1483 |
| Dd | | 1424 | CGAGAAATGGGAAAGTTA | CTGTGTCATCGCATATCCGCATTGCAACCCATTCTGACAT | 1483 |
| OY | | 1484 | GGACATCCCCCTTCTG | ATCACAATCCTCAAGGAAGTTGACTTCCCATTGGAAGCTCAATGA | 1543 |
| Dd | | 1484 | GGACATCCCCCTTCTGAT | CATATCCTCAAGGAAGTTGACTTCCCATTCAAGCTTAAAGCA | 1543 |
| OY | | 1544 | CTTGATATGTATCATCT | TTCGATTAAAGGTGATACACGGTGTCTACAAGGCAGACAGGC | 1603 |
| Dd | | 1544 | CTTGCAATGTGCCATCT | CTTCGATTACGAGGTGATACGGGTGCTACAAGGCAGACAGGC | 1603 |
| OY | | 1604 | CCGTGAGAGAAGAGCTT | CGTCTATATCATGTTATATGAACAACAATCCGTGATTAAAGGA | 1663 |
| Dd | | 1604 | TCGTGAGAGAAGAGCTT | CCTCTATATCATGTTATATGAACAACAATCCGTGAGTATCAGA | 1663 |
| OY | | 1664 | AGAAGATGCTCTGATCA | TATCAACTTCATGATCAGGAGCGCAATCAGAGATTAAATTG | 1723 |
| Dd | | 1664 | GGAAGATGCTCTCGATCA | TATCAACGCCATGATCAGTGCAGTAATCAAAAGATTAAATTG | 1723 |
| OY | | 1724 | GGAGCTTCTAAAGCCCA | GACAGAGTGTTCCCATCACTTCCAAGAAACACGCAATTGACAT | 1783 |
| Dd | | 1724 | GGAACCTTCTCAAAACCA | GACATCAATGTTCCCATCTCGCGGAAGAAAACATGCTTTTGACAT | 1783 |
| OY | | 1784 | AAGCAGAGTTTGGCATCA | CGSJTACAGATACCGAGATGGCTACAGCTTTGCCAACGTTGA | 1843 |
| Dd | | 1784 | CGCCAGAGCTTTCATTTA | CGGCTACAATAACCGAGACGGCTACAGCGTTGCCAACGTTGA | 1843 |
| OY | | 1844 | AACAAAGAGTTTGGTGA | TGAGAAACCGTCATTGAACCTGTGCTTTGTAAACAACACTTCAA | 1903 |
| Dd | | 1844 | AACGAAGAGTTTGGTGA | CGAGAAACCCCTCCTTGAATCTGTGCTTTGTAGCAACAGCTCAA | 1903 |
| OY | | 1904 | ATCTACATATTTAATCA | TGAGGATGCCCTATGGGTGTATATAGGGCACACAAAAATAAATAT | 1963 |
| Dd | | 1904 | ATCTATGCCCTATGCTAT | GTCTCGGGTTAAATATATATGTGGAAGGTAGCCGTTGGATGTAGA | 1963 |
| OY | | 1964 | GGTGTGTAGTAAAGCTG | TAAATTTATGAAAAAAAAAAAAAAAAAAAAA 2013 | |
| Dd | | 1964 | GGATTAAGTTTGTATAT | TTTAAATTAAGTTGTAAATTTTAAAAAAAAAAAAA 2013 | |

RESULT 5
US-09-893-820-19
; Sequence 19, Application US/09893820
; Publication No. US20040053386A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20040053386A1, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/893,820
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US/09/398,395A
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993

```

; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 2018
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6) ...(1889)
; OTHER INFORMATION: pinene synthase
US-09-093-820-19

```

| | | | | |
|----------------------------|-------|-----------------|------------|--------------|
| Query Match | 64.9% | Score 1306.8; | DB 13; | Length 2018; |
| Best Local Similarity | 81.0% | Pred. No. 0; | | |
| Matches 1595; Conservative | 0; | Mismatches 342; | Indels 33; | Gaps 5; |

| | | | |
|----|-----|--|-----|
| QY | 68 | CAGGTCGTGCTCAGTTCTTCTCATGAGATTAAAGCTCTCCGTAGAACCAATCCCACTCT | 127 |
| Db | 53 | CAAAATCGTTGATCAGTTCTACCCATGAGCTTAAAGCTCTCTCTAGAACCAATTCACGCTCT | 112 |
| QY | 128 | TGGAATCTGCAGCGCGGGGAAATCCGTCGCGCATTCATAAATCATGTGTTGACAAGCGT | 187 |
| Db | 113 | AGGAATGAGTAGCGGAGGAAATCTATCACTCTTCCATCAGCATGAGCTCTACCAACCGT | 172 |
| QY | 188 | CGCATCTACTGATTCTGTACAGAGACGCGTGGGCACTATCATTCCAACCTGTGGACGA | 247 |
| Db | 173 | TGTAACCGATGATGGGTGTACGAAGACGCATGGGCGATTCCATTCCAACCTGTGGACGA | 232 |
| QY | 248 | TGATTTCATACAGTCTCTGATCTCAACGCTTATGAGCACTGATTACCGGAACGTGC | 307 |
| Db | 233 | TGATGTCATACAGTCT---TTACCAACGCTTATGAGGAAATACTGACCTGAGCGTGC | 289 |
| QY | 308 | TGACAGACTTATTTGGGGAAGTAAAGATATATGTTCATTTCAGTCGCTGGAAGATGG | 367 |
| Db | 290 | TGAGAACTGATCGGGGAAGTAAAG--AACATGTTCAATTCCATGTCTATTAGAAAGATGG | 346 |
| QY | 368 | AG-----GCAATGATCTCTTCAACGACTTTTGCTGCTGATGACGTTGA | 412 |
| Db | 347 | AGAGTTAATGAGTCGCGCTCAATGATCTCATTCACGCTTTGGATGTGACACAGCCTTGA | 406 |
| QY | 413 | ACGTTTGGGAATCGACAGGCATTTCAAAAAAGAGATAAACCGCACTCGATTATGTTAA | 472 |
| Db | 407 | ACGTTTGGGATCCATAGACATTTCAAAAGATGAGATAAATCGCGCTTGATTATGTTAA | 466 |
| QY | 473 | CAGTTATTGGAACGAAAAAGCATTTGATGTGGAGGAGAGTGTGTGACTGACCTCAA | 532 |
| Db | 467 | CAGTTATTGGGGCGGAAATGCGATCGGATCGGGAAGGAGAGTGTGTACTGATCTGAA | 526 |
| QY | 533 | CTCAACCGCCTTGGGGCTTCGAACCTCTCCGACTACACGGAATACACTGTGTCTTCAGATGT | 592 |
| Db | 527 | CTCAACTGCGTTGGGGCTTCGAACCCCTACGACTACACGGATACCCGGTGTCTTCAGATGT | 586 |
| QY | 593 | TTTGAACGTTTAAAGACAAAAATGGGCAATTTTCTCTCACTGCCAATATTCAGATAGA | 652 |
| Db | 587 | TTTCAAAAGCTTTCAAGGCCAAAAATGGGCAATTTCTGCTCTGAAAAATATTCAGACAGA | 646 |
| QY | 653 | GGGAGAGATTAGAGCGCTTCTCAATTTATTCAGGGCCTCCCTGTCGCTTTCCCGGCGA | 712 |
| Db | 647 | TGAAGAGATCAGAGCGCTTCTGAATTTATTCGGGCTCCCTCATTTGCCCTTCCAGGGGA | 706 |
| QY | 713 | GAAAGTTATGATGAGCTGAAACATTTCTACAAATAATTTAAGAGAAGCCCTGCAAAA | 772 |
| Db | 707 | GAAATTTATGATGAGCTGAAATCTTCTCTACCAATAATTTAAGAAGCCCTGCAAAA | 766 |
| QY | 773 | GATTCCGGCATCCAGTATACTTTCACCTAGAGATACGGGACGTTCTGGAATATGTTGGCA | 832 |
| Db | 767 | GATTCCGGTCTCCAGT---CTTTCCGAGAGATCCGGGACGTTTTCGAATATGTTGGCA | 823 |

| | | | |
|----|------|---|------|
| QY | 833 | CACCAATTGGCCACGCTTGGAAGCAAGGAATTACATGACGCTTTGGACAGCACACTAA | 892 |
| Db | 824 | CACATATTGGCCGCGATGGAAAGCAAGGAATTACATCCAAGTCTTTGGACAGCACACTGA | 883 |
| QY | 893 | AAATAAGAACGC-----CGCCGAGAAACTTTTAGAACTTGCAAAATTGGAATTCAA | 943 |
| Db | 884 | GAACACGAAAGTCATATGTGAAGACAAAACCTTTTAGAACTCGCAAAATTGGAATTCAA | 943 |
| QY | 944 | TATATTTCACTCCTTACAGAGAGAGATTAAACA TGTTCCCGATGCTGGAAGAAGACTC | 1003 |
| Db | 944 | CATCTTTCAATCCTTACAAAAGAGGAGATTAGAAAAGTCTGCTCAGATGGTGGAAAAGATC | 1003 |
| QY | 1004 | GGGTTCTCCTGAGATGACCTTCTGTGCAATCGTCACGTTGAAATACTACGCTTTGGCTTC | 1063 |
| Db | 1004 | GGGTTTCTCGAGATGACCTTCTGCCGACATCGTCACGTGGAATACTACACTTTGGCTTC | 1063 |
| QY | 1064 | CTGCATTGCGTTGAGCGCTCAACATTCTGGATTCAGACTCGGCTTTACCAAGATGTCTCA | 1123 |
| Db | 1064 | CTGCATTGCGTTGAGCGCTCAACATTCTGATTCACTCGGCTTTGCCAAGACGTCTCA | 1123 |
| QY | 1124 | TCTTATCACGCTTCTTGAAGACATGTACGACGCTCTTGGCACAAGTACGAGCTGAACT | 1183 |
| Db | 1124 | TCTTATCACGCTTCTTGAAGATGTACGACACTTGGCACAAGTACGAGCTGAACT | 1183 |
| QY | 1184 | CTTACAGCGACAATTAAAGATGGGATCCGTCGGGATGGAATGCCTTCCAGAATATAT | 1243 |
| Db | 1184 | CTTACAGCGACAATTAAAGATGGGATCCGTCCTCGATATGCTTCCAGAATATAT | 1243 |
| QY | 1244 | GAAAGAGTGTCATGATGGTTTTATCACACCGTAAATGGAATGGCTCGAGTGGCAGAGAA | 1303 |
| Db | 1244 | GAAAGAGTGTCATAGCGGTTTTACGACACCGTAAATGGAATGGCTCGAGAGGCAGAGGA | 1303 |
| QY | 1304 | GGCTCAAGGCCGAGACACGCTCAACTATGCAAGACAGGCTTGGGAGGCGTGTATTGATTTC | 1363 |
| Db | 1304 | GGCTCAAGGCCGAGATACGCTCACTATGCTCGGAAAGCTTGGGAGGCTTATATTGATTTC | 1363 |
| QY | 1364 | GTATATGCAGGAAGCAAGTGGATCGCCACTGGTTATCTGCCACGTTTGAGAGTACTT | 1423 |
| Db | 1364 | GTATATGCAGGAAGCAAGTGGATCGCCACTGGTTACTGCTCTTGTGATGATACTTA | 1423 |
| QY | 1424 | GGAGAACGGGAAAGTTAGCTGTGCTCATCGCCATGCGCACTGCAACCCATTCTGACGT | 1483 |
| Db | 1424 | CGAGAAATGGGAAAGTTAGCTGTGTCATCGCATATCCGCAATTGCAACCCATTCTGACAT | 1483 |
| QY | 1484 | GGAATCCCCCTTCCGTGATCACTCCTCAAGGAAGTTGACTTCCCATCGAAGCTCAATGA | 1543 |
| Db | 1484 | GGAATCCCCCTTCCGTGATCAATCTCTCAAGGAAGTTGACTTCCCATCAAGCTTAAAGCA | 1543 |
| QY | 1544 | CTTGATATGTATCATCTCTTGCATTAAAGAGGTGATACACGGTGTCTACAAGGCACAGGCG | 1603 |
| Db | 1544 | CTTGCAATGTGCATCTCTTGATTACGAGGTGATACGGGTGTCTACAAGGCGGACAGGCG | 1603 |
| QY | 1604 | CCGTGAGAGAAGCTTCGTCTATATCATGTTATATGAAGCAATCCTGATTAAACGA | 1663 |
| Db | 1604 | TGCTGAGAGAAGCTTCCTATATCATGTTATATGAAGCAATCCTGAGATTACGA | 1663 |
| QY | 1664 | AGAAGATGCTCTGAATCAATCAACTTCATGATCAGGACGCAATCAGAGATTAAATTG | 1723 |
| Db | 1664 | GGAAGATGCTCTGATCAATCAACGCCATGATCAGTGAGTAAATCAAAAGATTAAATTG | 1723 |
| QY | 1724 | GGAGCTTCTAAAGCCAGACAAGTGTCCCATCACTTCAAGAAAACAGCATTTGACAT | 1783 |
| Db | 1724 | GGAATCTTCAAAACGACATCAATGTTCCCATCTCGCGAAGAAAACATGCTTTGACAT | 1783 |
| QY | 1784 | AAGCAGAGTTTGGCATCACGGTTACAGATACCGAGATGGCTTACAGCTTTGCCAAGCTTGA | 1843 |
| Db | 1784 | CGCCAGAGCTTTCATTAACGCTTACAATTAACGAGACGGCTTACAGCGTTGCCAAGCTTGA | 1843 |
| QY | 1844 | AAACAAAGATTGGTGATGAGAAACCGTCATTGAACCTGTGCTTTGTAAACAACACTTCAA | 1903 |
| Db | 1844 | AAACAAAGATTGGTGATGAGAAACCGCTCTTGAATCTGTGCTTTGTAGCAACAGCTCAA | 1903 |
| QY | 1904 | ATCTACAATATTAATGAGATGCCCTATGGGTGTATATAGGGCACACAAAATAATAT | 1963 |

Db 1904 ATCTATGCCCTATGCTATGTCGGGTAAATATATATGTGGAAGTAGCCGTTGGATGTAGA 1963

QY 1964 GGTGTGTTAGTAAGCTGTAATTTATGAAAAAAAAAAAAAAAAAAAA 2013

Db 1964 GGATAAGTTTGTTATTAATTTAATAAAGTTGTAATTTAAAAAAAAAAAAA 2013

RESULT 6

```

US-10-041-007-21
; Sequence 21, Application US/10041007
; Publication No. US20020161736A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seichi P.T.
; APPLICANT: Schepmann, Hala G
; TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase
; FILE REFERENCE: P02081US1
; CURRENT APPLICATION NUMBER: US/10/041, 007
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259,881
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 2018
; TYPE: DNA
; ORGANISM: Abies grandis
US-10-041-007-21

```

| | |
|-------------|--|
| Query Match | 64.98; Score 1306.8; DB 14; Length 2018; |
|-------------|--|

| | | | |
|----------------------------|--------|----------------|--------------------|
| Best Local Similarity | \$1.04 | Pred. No. 0 | |
| Matches 1595; Conservative | 0 | Mismatches 342 | Indels 33; Gaps 5; |

| | | | | |
|----|--|-----|--|-----|
| OY | | 68 | CAGTCGCTGACCTGAGTTCTTCTCATGAGATTAAAGCCTCTCCGTAGAACAATCCCAACTCT | 127 |
| Db | | 53 | CAATCGTTGATGAGTTCTAACCATGAGCTTAAGGCTCTCTTAGAACAATCCAGCTCT | 112 |
| OY | | 128 | TGGAATCTGCAGGCCGGGGAATCCGTCGGCATTCCATAAACAATGTTTGACAAGCGT | 187 |
| Db | | 113 | AGGAATGAGTAGGCCGAGGGAATCTATCACTCCTTCATCAGCATGAGCTCTACCACCGT | 172 |
| OY | | 188 | CGCATCTACTGATTTCTGTACAGAGACGCCGTGGCACTATCATTTCCAACCTGTGGACGA | 247 |
| Db | | 173 | TGTAACCGATGATGGTGTACGAAGACGCATGGCGATTTCATTCCAACCTCTGGAGCGA | 232 |
| OY | | 248 | TGATTTCATACAATCTCTGATCTCAACGCCCTTATGAGAGCACCTGATTAACGGGAACGTGC | 307 |
| Db | | 233 | TGATGTCATACAATCTCT--TTACCAACGCCCTTATGAGAAAAATCGTACCTGAGCGTGC | 289 |
| OY | | 308 | TGACAGACTTATTTGGGGAAGTAAAGATATATATGTTCAATTTCAAGTCGCTGGAAGATGG | 367 |
| Db | | 290 | TGAGAACTGATCGGGGAAGTAAAG--AACATGTTCAATTGCATGCTATTAGAAGATGG | 346 |
| OY | | 368 | AG-----GCAATGATCTCTCTTCAACGACTTTTGTGCTGCGATGACGCTTGA | 412 |
| Db | | 347 | AGAGTTAATGAGTCCGCTCAAATGATCTCATTTCAACGCCCTTTGATTTGACAGCCTTGA | 406 |
| OY | | 413 | ACGTTTGGGAATCGACAGGATTTCAAAAAAGAGATMAAAACGGCACTCGATTATGTTAA | 472 |
| Db | | 407 | ACGTTTGGGATCCATAGACATTTCAAAAGATGAGATMAAATCGGCGCTTGATTATGTTTA | 466 |
| OY | | 473 | CAGTTATTGGAACGA AAAAGCATTTGATGTGGAGAGAGATTTGTGACTGACCTCAA | 532 |
| Db | | 467 | CAGTTATTGGGCGGA AAATGGCATCGATGCGGAGGAGAGATGTTGTA CTGATCTGAA | 526 |
| OY | | 533 | CTCAACCGCCTTGGGGCTTCCAACTCTCCGACTACACGATACACTGTGTCTTCAGATGT | 592 |
| Db | | 527 | CTCAACTGCGTTGGGGCTTCCGAACCCCTACGACTACACGATACCCGCGTCTTCAGATGT | 586 |
| OY | | 593 | TTTGAACGTTTTTAAGACAAAATGGGCAATTTTCTCCACTGCGCAATATTTCAGATAGA | 652 |
| Db | | 587 | TTTCAAGCTTTCA AAGCCAAAATGGGCAATTTTCTGCTCTGTA AAAATATTTCAGACAGA | 646 |

| | | | |
|----|------|---|------|
| QY | 653 | GGGAGAGATTAGAGCGCTTCTCAATTTATTATTCAGGGCCTCCCTGTCGCTTTCCCGGCA | 712 |
| Db | 647 | TGAAGAGATCAGAGCGCTTCTGAATTTATTTCCGGCCCTCCATTTGCCCTTCCAGGGGA | 706 |
| QY | 713 | GAAAGTTATGATGAAGCTGAAACATTTCTCTACAAATATTTAAAGAAAGCCCTGCAAA | 772 |
| Db | 707 | GAAATTTATGATGAGCGCTGAATCTTCTCTACCAATATTTAAAGAAGCCCTGCAAAA | 766 |
| QY | 773 | GATTCCGCGATCCAGTATACTTTCACTAGAGATACGGACGTTCTGGAATATGTTGGCA | 832 |
| Db | 767 | GATTCGGGTCTCCAGT---CTTTCCGAGAGATCCGGGACGTTTGGAAATATGTTGGCA | 823 |
| QY | 833 | CACCAATTTGGCACCGCTTGGAAAGCAAGGAATTACATGACGCTTTTGGACAGCACACTAA | 892 |
| Db | 824 | CACATATTTGGCCCGGATTTGGAAAGCAAGGAATTACATCCAGTCTTTTGGACAGCACACTGA | 883 |
| QY | 893 | AAATAAGAACGC-----CGCCGAGAAACTTTTAGAACTTGCAAAATTGGAATTCAA | 943 |
| Db | 884 | GAAACAGAAAGTCATATGTAGAGAGCAAAAACTTTTAGAACTCGCAAAATTGAGATTCAA | 943 |
| QY | 944 | TATATTTCACTCCTTACAGAGAGAGAGATTAAACATGTTTCCGATGTTGGAAGACTC | 1003 |
| Db | 944 | CATCTTTCAATCCTTACAAAGAGAGGAGATTAGAAAGTCTGTCAGATGTTGGAAGAAATC | 1003 |
| QY | 1004 | GGGTTCTCCTGAGATGACCTTCTGTGACATCGTCAAGTGAATACTACGCTTTGGCTTC | 1063 |
| Db | 1004 | GGGTTTCTCTGAGATGACCTTCTGCCGACATCGTCAAGTGAATACTACACTTTGGCTTC | 1063 |
| QY | 1064 | CTGCATTGCGTTTCGAGCCCTCAACATTTCTGATTCAAGCTCGGCTTTACCAAGATGTCA | 1123 |
| Db | 1064 | CTGCATTGCGTTTCGAGCCCTCAACATTTCTGATTCAAGCTCGGCTTTGCCAAGACGTCTCA | 1123 |
| QY | 1124 | TCTTATCAAGGTTCTTGACGACATGTAACGACGTCTTCCGACAGTAGACGAGCTGGAAT | 1183 |
| Db | 1124 | TCTTATCAAGGTTCTTGACGATATGTAACGACACCTTCGGCACAGTAGACGAGCTGGAAT | 1183 |
| QY | 1184 | CTTCACAGCGACAATTAAAGATGGGATCCGTCGCGGATGGAATGCTTCCAGAATATAT | 1243 |
| Db | 1184 | CTTCACAGCGACAATGAAGATGGGATCCGTCCTGATGATTTGCCCTCCAGAATATAT | 1243 |
| QY | 1244 | GAAAGAGTGTACATGATGGTTTATCAACCCGTAATGAAATGGCTCGAGTGACAGAA | 1303 |
| Db | 1244 | GAAAGAGTGTACATAGCGGTTTACGACACCGTAATGAAATGGCTCGAGAGCAGAGGA | 1303 |
| QY | 1304 | GGCTCAAGGCCGAGACACGCTCAACTATGCAAGACAGGCTTGGGAGCGTGTTTGATTC | 1363 |
| Db | 1304 | GGCTCAAGGCCGAGATACGCTCACATATGCTCGGGAAGCTTGGGAGGCTTATATTGATTC | 1363 |
| QY | 1364 | GTATATGCAGGAAGCAAGTGCATCCCACTGGTTATCTGCCACGTTTGAGGAGTACTT | 1423 |
| Db | 1364 | GTATATGCAGAAGCAAGTGCATCCCACTGGTTACTCTGCCCTCTTTGATGAGTACTTA | 1423 |
| QY | 1424 | GGAGAACGGGAAAGTTAGCTCTGCTCATCCGCCCATGCGCACTGCAACCATTCTGACGTT | 1483 |
| Db | 1424 | CGAGAATGGGAAAGTTAGCTGTGTGTCATCCGATATCCGCAATTGCAACCATTCTGACAAT | 1483 |
| QY | 1484 | GGACATCCCTTCTCTGATCAATCTCAAGGAAGTTGACTTTCCCATCGAAGCTCAATGA | 1543 |
| Db | 1484 | GGACATCCCTTCTCTGATCAATCTCAAGGAAGTTGACTTTCCCATCAAAAGCTTAACGA | 1543 |
| QY | 1544 | CTTGATATGTATCATCTTCGATTTAAGAGGTGATACACGCTGCTACAAGGCAGACAGGC | 1603 |
| Db | 1544 | CTTGGCATGTGCATCTTCGATTTACGAGGTGATACGCGGTCTACAAGGCAGACAGGC | 1603 |
| QY | 1604 | CCGTGAGAGAAGACTTCGTCTATATCATGTTATATGAAGAACAATCCTGATTAAACGA | 1663 |
| Db | 1604 | TCGTGAGAGAAGACTTCCTCTATATCATGTTATATGAAGAACAATCCTGAGATATCAGA | 1663 |
| QY | 1664 | AGAAGATGCTCTGAATCATATCAACTTCATGATCAGGAGCGCAATCAGAGATTTAAATTG | 1723 |
| Db | 1664 | GGAAGATGCTCTCGATCATATCAACGCCATGATCAAGTACGTAATCAAAAGATTTAAATTG | 1723 |
| QY | 1724 | GGAAGCTTTAAAGCCAGACAAAGTGTTCCTCATCTTCCAAAGAAACAGCATTTGACAT | 1783 |

```

Db      1724 GGAAGTCTCAAAACAGACATCAATGTTCCATCTCGGCGAAGAAACATGCTTTGACAT 1783
QY      1784 AAGCAGAGTTTGGCATCACGGTTACAGATACCGAGATGGCTACAGCTTTGGCAACGTTGA 1843
Db      1784 CGCCAGAGCTTTCCATTAACGGCTACAAATACCGAGACGGCTACAGCGTTGCCAACGTTGA 1843
QY      1844 AACAAAGAGTTTGGTGATGAGAACCGCTCATTTGAACCTGTGCCCTTTGTACAAACACTTCAA 1903
Db      1844 AACGAAAGATTGGTGACGAGAACCCCTCCTTGAATCTGTGCCCTTTGTAGCAACAGCTCAA 1903
QY      1904 ATCTACAATATTAACGTAGAGATGCCCTATGGGTGATATAGGGCACACAAAATATAAT 1963
Db      1904 ATCTATGCCCTATGCTATGTGCGGTTAAATATATGTGAAAGGTAGCCGTTGATGTAGA 1963
QY      1964 GGTGTGTTAGTAAAGCTGTAAATTTATGAAAAAAAAAAAAAAAAAAAAA 2013
Db      1964 GGATAAGTTTGTATTAATTTAATAAAGTTGTAATTTAAAAAAAAAAAAA 2013

RESULT 7
US-10-025-145A-3
; Sequence 3, Application US/10025145A
; Publication No. US20030175861A1
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B.
; APPLICANT: Bohlmann, Joerg
; APPLICANT: Steele, Christopher L.
; APPLICANT: Phillips, Michael A.
; TITLE OF INVENTION: Monoterpene Synthases from Grand Fir (Abies Grandis)
; FILE REFERENCE: WSUR118414
; CURRENT APPLICATION NUMBER: US/10/025,145A
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 09/360,545
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: PCT/US98/14528
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: US 60/052,249
; PRIOR FILING DATE: 1997-07-11
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2018
; TYPE: DNA
; ORGANISM: Abies Grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)..(1892)
; OTHER INFORMATION:
; US-10-025-145A-3

Query Match      64.9%; Score 1306.8; DB 15; Length 2018;
Best Local Similarity 81.0%; Pred. No. 0;
Matches 1595; Conservative 0; Mismatches 342; Indels 33; Gaps 5;

QY      68 CAGTGCCTCAGTCTTCTCATGAGATTAAGGCTCTCCGTAGAAACAATCCAACTCT 127
Db      53 CAATCGTTGATCAGTTCTAACCCATGAGCTTAAGGCTCTCTAGAACAAATCCAGCTCT 112
QY      128 TGAATCTGCAGGCCGGGAAATCCGTCGCGCATTCATAAACAATGTTTGACAGCGT 187
Db      113 AGGAATGAGTAGGCGGAGGAAATCTATCACTCTTCCATCAGCATGAGCTCTACACCGT 172
QY      188 CGCATCTACTGATTTCTGTACAGAGACGCGTGGGCAACTATCATTTCCAAACCTGTGGAGCA 247
Db      173 TGTAAACGATGATGTTGTACGAAAGACGATGGGCGAATTTCCATTCCAAACCTGTGGAGCA 232
QY      248 TGATTTCATACAGTCTCTGATCTCAACGCCCTTATGAGACACCTGATTACCGGGAACGTGC 307
Db      233 TGATGTATACAGTCT--TTACCAACGCGTTATGAGAAAAATCGTACCTGGAGCGTGC 289
QY      308 TGACAGACTTATTGGGGAAGTAAAGATATATGTTCAATTTCAGTCGCTGGAAGATGG 367

```


Db 290 TGAGAACTGATCGGGGAAGTAAAG---AACATGTTCAATTCGATGTGATAGAAGATGG 346
QY 368 AG-----GCAATGATCTCTTCAACGACTTTTGCTGGTGAGAGCTTGA 412
Db 347 AGAGTTAATGATCGGCTCAATGATCTCATTCACGCCCTTGATGTGACAGCCTTGA 406
QY 413 ACGTTGGGAATCGACAGGCATTTCAAAAAAGAGATTAATAACGGCACTCGATTATGTTAA 472
Db 407 ACGTTGGGATCCATAGACATTTCAAAAGATGAGATTAATAATCGGCCCTTGATTAATGTTTAA 466
QY 473 CAGTTATTGGAAAGAAAAAGCATTGGATGGGAGGAGAGTGTGTGACTGACTGAA 532
Db 467 CAGTTATTGGGCGAAAAATGGCATCGGATGCGGAGGAGAGTGTGTGACTGACTGAA 526
QY 533 CTCACCGCCTTGGGGCTTCGAACCTCTCGACTACACGAGTACACTGTGCTTCAGATGT 592
Db 527 CTCACCTGCGTTGGGGCTTCGAACCTACGACTACACGAGTACCCGGTCTTCAGATGT 586
QY 593 TTTGAACGTTTAAAGCAAAATGGGCAATTTCTCCACTGCCAATATTCAGATAGA 652
Db 587 TTTCAAGCTTTCAAAGGCCAAATGGGCAAGTTTCTGCTCTGAATAATTCAGACAGA 646
QY 653 GGGAGAGATTAGAGCGCTTCTCAATTTATTCAGGGCTCCCTCGCTTCCCGCGA 712
Db 647 TGAAGAGATCAGAGCGCTTCTGAATTTATTCGGGCTCCCTCATTTGCCCTTTCAGGGGA 706
QY 713 GAAAGTTATGATGAAGCTGAAACATTTCTTCAAAATATTTAAGAGAACCTTGCAAAA 772
Db 707 GAAATATATGATGAGCGCTGAATCTTCTTCAAAATATTTAAGAGAACCTTGCAAAA 766
QY 773 GATTCCGGCATCCAGTATACCTTCACTAGAGATACGGGACGTTCTGGAATATGTTGCA 832
Db 767 GATTCCGGCTCCAGT---CTTTCGAGAGATCGGGGACGTTTGGAAATATGTTGCA 823
QY 833 CACCAATTTGCCACGCTTGGAGCAAGAAATTAATGAGCGTCTTGGACAGCACTAA 892
Db 824 CACATATTTGCCCGATTTGGAGCAAGAAATTAATCCAAAGTCTTGGACAGCACTGA 883
QY 893 AAATAAGAACGC-----CGCCGAGAACTTTTGAACCTTGCAAAATTTGAATTCAA 943
Db 884 GAAACAGAGTCATATGTGAAGAGCAAAAACTTTTGAACCTTGCAAAATTTGAAGTTCAA 943
QY 944 TATATTTCACTCTTCAAGAGAGAGATTAAACATGTTTCCCGATGGTGAAGACTC 1003
Db 944 CATCTTTCAATCCTTACAAAAGAGGAGTTAGAAAGTCTGGTCAAGTGTGAGAAAGATC 1003
QY 1004 GGGTCTCTGAGATGACCTTCTGTGACATCTGTCACGTGGAATACTACGCTTGGCTTC 1063
Db 1004 GGGTCTCTGAGATGACCTTCTGTGACATCTGTCACGTGGAATACTACGCTTGGCTTC 1063
QY 1064 CTGCATGCGCTTCGAGCCTCAACATTTCTGGAATTCAGACTCGGCTTTCGAAGACTGTCA 1123
Db 1064 CTGCATGCGCTTCGAGCCTCAACATTTCTGGAATTCAGACTCGGCTTTCGAAGACTGTCA 1123
QY 1124 TCTTATCAGCGTCTTTCGAGACATGTACGACGTCTTCGACAGTACGAGCTGGAATC 1183
Db 1124 TCTTATCAGCGTCTTTCGAGACATGTACGACGTCTTCGACAGTACGAGCTGGAATC 1183
QY 1184 CTTCAAGCGACAATTAAGAGATGGGATCCGCTCCGCGATGGAATGCTTCCAGAATATAT 1243
Db 1184 CTTCAAGCGACAATTAAGAGATGGGATCCGCTCCGCGATGGAATGCTTCCAGAATATAT 1243
QY 1244 GAAAGAGTGTACATGATGTTTATCACACCGTAAATGAATGGCTGAGAGGCGAGAGAA 1303
Db 1244 GAAAGAGTGTACATGATGTTTATCACACCGTAAATGAATGGCTGAGAGGCGAGAGAA 1303
QY 1304 GGGTCAAGGCGGAGACACGCTCAACTATGCAAGACAGGCTTGGAGGCGTGTGATTTC 1363
Db 1304 GGGTCAAGGCGGAGATACGCTCACATATGCTCGGAGAGCTTGGAGGCTTATATGATTTC 1363
QY 1364 GTATATGAGGAAGCAAAAGTGATCGCCACTGTTATCTGCCACGTTGAGGAGTACTT 1423
Db 1364 GTATATGCAAGAAAGCAAGGTGATCGCCACTGTTTAACTGCTTCTTGAATGAGTACTA 1423

QY 1424 GGAGAACGGGAAATTTAGCTCTGCTCATCGCCCATGCGCACTGCAACCCATTCTGACGTT 1483
Db 1424 CGAGAAATGGGAAATTTAGCTGTGTGTCATCGCATATCCGCAATTGCAACCCATTCTGACAAAT 1483
QY 1484 GGACATCCCTTTCTCTGATCACATCTCGAAGAAAGTTGACTTCCCATCGAAGCTCAATGA 1543
Db 1484 GGACATCCCTTTCTCTGATCATATCTCGAAGAAAGTTGACTTCCCATCGAAGCTTAAACA 1543
QY 1544 CTTGATATGATCATCTCTGATTAAGAGTGATACACGCTGCTACAGGCGAGACAGGGC 1603
Db 1544 CTTGATATGATCATCTCTGATTAAGAGTGATACACGCTGCTACAGGCGAGACAGGGC 1603
QY 1604 CCGTGAGAGAAAGCTTCTGCTATATCATGTTATATGAAGACAATCTCGATTAAACGA 1663
Db 1604 TCGTGAGAGAAAGCTTCTGCTATATCATGTTATATGAAGACAATCTCGATTAAACGA 1663
QY 1664 AGAAGATGCTGTGAATCATATCATCACTTCATGATCAGGAGCGCAATCAGAGAAATTAATG 1723
Db 1664 GGAAGATGCTGTGATCATATCAACGCCATGATCAGTACGCTAATCAAGAAATTAATG 1723
QY 1724 GGAGCTTCTAAAGCCAGACAAAGTGTCCCATCACTTCCAAAGAAACAGCAATTGACAT 1783
Db 1724 GGAACCTTCTAAACAGACATCAATGTTCATCTCGGCGAAGAAACATGCTTTTGACAT 1783
QY 1784 AAGCAGATTTCGATCAGCGTTACAGATACCGAGATGCTACAGCTTTCGCAACGTTGA 1843
Db 1784 CGCAGAGCTTTCATTAACGCTACAAATAACGAGACGCTACAGCGTTGCAACGTTGA 1843
QY 1844 AACAAAGATTTCGTGATGAGAACCGTCAATTGAACCTGTGCTTGTAAACAACACTTCAA 1903
Db 1844 AACGAAGATTTCGTGATGAGAACCGTCAATTGAACCTGTGCTTGTAAACAACACTTCAA 1903
QY 1904 ATCTACAATATTAACAGGATGCCCTATGGGTATATAGGCGACAAAAATAATAT 1963
Db 1904 ATCTATGCCCTTAAGCTATGTGCGGTTAAATATATGTGGAAGGTAGCCGTTGATGTAGA 1963
QY 1964 GGTGTGTTAGTAAAGCTGTAATTTATGAAAAAATTTGAAAAAATTTGAAAAAATTTGAAAAA 2013
Db 1964 GGATAGTTGTTATTAATTAATTAAGTTGTAATTTGAAAAAATTTGAAAAAATTTGAAAAA 2013

RESULT 8
US-10-025-145A-77
; Sequence 77, Application US/10025145A
; Publication No. US20030175861A1
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B.
; APPLICANT: Bohlmann, Joerg
; APPLICANT: Steele, Christopher L.
; APPLICANT: Phillips, Michael A.
; TITLE OF INVENTION: Monoterpene Syntheses from Grand Fir (Abies Grandis)
; FILE REFERENCE: WSUR118414
; CURRENT APPLICATION NUMBER: US/10/025, 145A
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 09/360, 545
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: PCT/US98/14528
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: US 60/052, 249
; PRIOR FILING DATE: 1997-07-11
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77
; LENGTH: 1890
; TYPE: DNA
; ORGANISM: Abies Grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1890)
; OTHER INFORMATION:
US-10-025-145A-77

| | | | | | |
|-----------------------|------|--|---------------------|------------|--------------|
| Query Match | | 54.3%; | Score 1092.4; | DB 15; | Length 1890; |
| Best Local Similarity | | 76.8%; | Pred. No. 8.6e-313; | | |
| Matches 1439; | | Conservative 0; | Mismatches 396; | Indels 39; | Gaps 7; |
| QY | 46 | TTTCTATTACTCCGCTGGTTTCCAGGTGCTGCTCAGTTCCTTCATGAGATTAAAGGCTC | 105 | | |
| DB | 26 | TGCTTCCAAATCGGCTCGACAAATCGTGATCGTTCTACTTAAGACATAAGGCTA | 85 | | |
| QY | 106 | TCCGTGAACAATCCCAACTCTTGAAATCTGCAGCGCGGGAATCCGTCGCGATTCCA | 165 | | |
| DB | 86 | TCAGTGAACAATCCCAATCTTGAAATGCGTGGCGAGGAAATCTGTGACACATTCCC | 145 | | |
| QY | 166 | TAAACATGTTTGACAAGCGTGCATCTACTG--ATTCTGTACAGACGCGTGCGCA | 222 | | |
| DB | 146 | TGAGATGAGTTTGAGCACCAGCTCTGATGATCATGCTGTACAAAGACGATAGTCG | 205 | | |
| QY | 223 | ACTATCATTTCCAACCTGTGGACGATATTTCATACAGTCTCTGATCTCAACGCTTATG | 282 | | |
| DB | 206 | AGTTTCATTTCCAATCTGTGGACGACGATTTCAACAATCTC--TATCAACGCTTATG | 262 | | |
| QY | 283 | GAGCACCCTGATTAACCGGGAACGTGCTGACAGACTTATTTGGGGAAGTAAGATATATGT | 342 | | |
| DB | 263 | GGGACCTTCATACCGTGAAACGTGCTGATAGACTTATTTGGAAGTAAAGGTATA--T | 319 | | |
| QY | 343 | TCAATTTCAAGTCGCTGGAAGATGAG-----GCAATGATCTCCTTCAAC | 387 | | |
| DB | 320 | TCACTTCATTTCAAGCGAAGATGGAACATACTACCTCCCTCAATGATCTCATTCAC | 379 | | |
| QY | 388 | GACTTTGCTGTGATGATGACGTGGAACGTTTGGGAATCGACAGGCAATTCAAAAAGAGA | 447 | | |
| DB | 380 | GCCTTTATGCTCGATAACGTTGACGTTTAGGATTGATAGACATTTCAAAATGAGA | 439 | | |
| QY | 448 | TAAAAACGCACTCGATTATGTTAACGTTATTGGAAACGAAAAAGCATTTGGATGTGGA | 507 | | |
| DB | 440 | TAAAAACGCACTAGACTATGTTTACGTTATTGGAAACGAAAAAGCATTTGGCAGTGAA | 499 | | |
| QY | 508 | GGGAGAGTGTGACTGACCTCAACTCAACCGCTTGGGGCTTCAACTCTCCGACTAC | 567 | | |
| DB | 500 | GTGATAGTGTGTGCTGATCTCAACTCAACTGCGCTGGGTTTCGAATTTCTTCGACTAC | 559 | | |
| QY | 568 | ACGATACACTGTGTCTTCAGATGTTTGAACGTTTAAAGACAAAAATGGGCA--AT | 624 | | |
| DB | 560 | ACGATACAGTGTCTTCAGATGTTTGAACACTTCAAAGAGAGAAAGAGAGAGGCGC | 619 | | |
| QY | 625 | TTTCTCCACTGCCAATATTTCAGATAGAGGAGATTAGAGCGCTTCTCAATTATTTCA | 684 | | |
| DB | 620 | AGTTTGAATGTGGCCATCCAAACAGAGAAAGATAAAAAGCGTTCTGAATTTATTTTC | 679 | | |
| QY | 685 | GGGCTCCCTCGTCGCTTTCCCGCGAAGAAAGTTATGATGAAGCTGAACATTCTCTA | 744 | | |
| DB | 680 | GGGCTCCCTCATTCGCTTTCCGCGAAGAAAGTTATGGAAGCGCTGAATCTTCTCTA | 739 | | |
| QY | 745 | CAAAATATTAAAGAAAGCCCTGCAAAAGATTCGGGATCCAGTAACTTTCACTAGAGA | 804 | | |
| DB | 740 | AAATATATTAAAGAAAGCCCTTACAAAATATTGCTGTCTCCAGT---CTTTCACGAGAGA | 796 | | |
| QY | 805 | TACGGAGCTTCTGGAATATGTTGGACACCAATTGGCCACGCTTGGAAAGCAAGGAATT | 864 | | |
| DB | 797 | TAGAGTACGTTCTGGAGATGTTGGCAACAATATGCCAAAGATTGGAAAACAAGGAAC | 856 | | |
| QY | 865 | ACATGACGTCCTTTGGACAGACACTAAAAATAAG-----AACGCCCGAGAAAC | 915 | | |
| DB | 857 | ACATCGATGATTTGGAGAGAACGATCGTATGAGACGTTATATATGAACATGAGAAAC | 916 | | |
| QY | 916 | TTTTAGAACTTGCAAAATTGGAATTCATATATTCACTCCTTACAGAGAGAGATTAA | 975 | | |
| DB | 917 | TTTTAGAAATTGCAAAATTGAGATTCAATATTTTCACTCCTTACACAGAGAGACTAA | 976 | | |
| QY | 976 | AACATGTTCCCGATGTGGAAGACTGGGTTCTCTGAGATGACCTTCTGTGCACATC | 1035 | | |
| DB | 977 | AAGACCTCTCCAGATGTGGAAGATTCGGGTTCTCTCACCTGACATTTTCTCGGCATC | 1036 | | |
| QY | 1036 | GTACAGTGAATACTACGCTTTGGCTTCTTCATTTGCGTTGAGCCTCAACATTTCTGAT | 1095 | | |

| | | | | | |
|----|------|--|------|--|--|
| DB | 1037 | GTCAATGGAATTTCTACGCTCTGGCATCTTGCAATTGAACTGATCGCAACATTTCCGAT | 1096 | | |
| QY | 1096 | TCAGACTCGGCTTTACCAAGATGCTCATCTTATCACGGTTCTTGACGACATGACGACG | 1155 | | |
| DB | 1097 | TCAGACTCGGCTTTGCCAAATGTGTATCTTATCACGGTTTGGACGATATATACGACA | 1156 | | |
| QY | 1156 | TCTTCGCACAGTAGACGCTGGAATCTCTTCACAGCGACATTAAGATGGATCCGT | 1215 | | |
| DB | 1157 | CCTTGAACAATGAGAGAGCTGGAATCTTCACTGCAGCATTTAAGATGGATCCGT | 1216 | | |
| QY | 1216 | CCGCGATGGAATGCCCTTCCAGATATATGAAAGAGGTATCATGATGTTTATCACACCG | 1275 | | |
| DB | 1217 | CTGCCACAGATTTGCTTCAGAGTATATGAAAGGTTGTACATGGTGTACGAAACCG | 1276 | | |
| QY | 1276 | TAAATGAATGCTCGAGTGGCAGAGAAAGCTCAAGGCCGAGACACGCTCAACTATGCA | 1335 | | |
| DB | 1277 | TAAATGAATTTGCTCGAGAGCGACAAAGTCTCAAGGCCGAGACGCTCAACGATGCTC | 1336 | | |
| QY | 1336 | GACAGCTTGGAGGCGTGTGATTCGTATATGACAGAACCAAGTGATCGCCACTG | 1395 | | |
| DB | 1337 | GACGAGCTTGGAGGCGCTATCTGATTCGTATATGAAGAACTGAGTGATCTCCAGTG | 1396 | | |
| QY | 1396 | GTTATCTGCCACGTTTGAGAGTACTTGAGAACGGGAAAGTTAGCTCTGCTCATCGCC | 1455 | | |
| DB | 1397 | GTTATCTGCCAACGTTTGAGAGTACTGAGAACCAAGTTAGTTTGTGTTATCGCA | 1456 | | |
| QY | 1456 | CATGCGCACTGCAACCCATTTGACGTTGGACATCCCTTCTGATCACATCTCTCAAG | 1515 | | |
| DB | 1457 | TATTCGATTGCAACCCATCTTCACTATGATGTTCCCTTACTCACCAATCTCTCAGG | 1516 | | |
| QY | 1516 | AAGTTGACTTCCATCGAAGCTCAATGACTGTATATGATATCTTGCATTAAGAGTG | 1575 | | |
| DB | 1517 | AAATGACTTTCATTTAGGTTTAATGACTTAATATGTTTCATCTTCACTTAAAAATG | 1576 | | |
| QY | 1576 | ATACAGGTGTACAAAGCAGACAGGCGCGTGAGAAAGCTTCTGTATATCATGTT | 1635 | | |
| DB | 1577 | ACACTCGCTGTACAAAGCGGACAGGCGCGTGAGAAAGCTTCTGTATATCTGTT | 1636 | | |
| QY | 1636 | ATATGAAGACAATCCTGATTTAACGGAAGAGTCTTGAATCATATCAACTTCATGA | 1695 | | |
| DB | 1637 | ATATGAAGAGAAATCCTGATTCACAGAGAAAGATGCTATCATATCATACGCTATGG | 1696 | | |
| QY | 1696 | TCAGGACGCAATCAGAAATTAATTGGAGCTTCTAAAGCCAGACAACAGTGTCCCA | 1755 | | |
| DB | 1697 | TCAATAACTTATCAAGAAGTAAATTGGAGCTTCTCCGACAGACCGCACCTCATTA | 1756 | | |
| QY | 1756 | TCATTTCCAAAGAACCGCATTTGACATTAAGCAGATTTGGCATCAACGTTACAGATACC | 1815 | | |
| DB | 1757 | TTGCTTCAAGAAACACGCTTTTGAATCTCTCAAGGTTCCCTTCAACGCTACAAATACC | 1816 | | |
| QY | 1816 | GAGATGCTACAGCTTTGCCAACGTTGAAACCAAAGAGTTTGGTATGAGAACCGTCATTG | 1875 | | |
| DB | 1817 | GAGATGCTTACAGCTTTGCCAACGTTGAAACCAAAGAGTTTGGTATGAGAACCGTCATTG | 1876 | | |
| QY | 1876 | AACCTGTGCTTTG 1889 | | | |
| DB | 1877 | AGTCTGTGCTTTG 1890 | | | |

RESULT 9
US-10-025-145A-66
; Sequence 66, Application US/10025145A
; Publication No. US20030175861A1
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B.
; APPLICANT: Bohlmann, Joerg
; APPLICANT: Steele, Christopher L.
; APPLICANT: Phillips, Michael A.
; TITLE OF INVENTION: Monoterpene Synthases from Grand Fir (Abies Grandis)
; FILE REFERENCE: MSUR118414
; CURRENT APPLICATION NUMBER: US/10/025,145A
; CURRENT FILING DATE: 2002-06-28

PRIOR APPLICATION NUMBER: US 09/360,545
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: PCT/US98/14528
PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: US 60/052,249
PRIOR FILING DATE: 1997-07-11
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 66
LENGTH: 2186
TYPE: DNA
ORGANISM: Abies Grandis
FEATURE:
NAME/KEY: CDS
LOCATION: (34)..(1923)
OTHER INFORMATION:
US-10-025-145A-66

Query Match 53.3%; Score 1072.4; DB 15; Length 2186;
Best Local Similarity 76.4%; Pred. No. 8.2e-307;
Matches 1428; Conservative 0; Mismatches 391; Indels 51; Gaps 7;

QY 83 TTCTTCATGAGATTAAAGCTCTCCGTAGACAAATCCCACTCTTGGAACTGACAGCC 142
DB 90 TACTCATCATGAGCTCAAGCCTCTGCGCAGAACCACTCCCACTCTTGGAACTGAGGCG 149
QY 143 GGGGAATCCGTGCGGCATTCATTAACATGTGTTGACAAAGCGTCGATCTACTGATTC 202
DB 150 AGGGAATCTTCAACCTCTGTGAGCATGATTGACCACCGCTGTATCTGATGATGG 209
QY 203 TGTACAGAGACGCGTGGCAACTATCATTCCACTGTGGAGCATGATTTCATACAGTC 262
DB 210 TCTACAAAGACGATAGGTGACTATCATTCCAATCTCTGGAGCAGCATTTCAATACAGTC 269
QY 263 TCTGATCTCAACGCTTATGAGACACCTGATTAACGGGAACGTGCTGACAGACTTATTGG 322
DB 270 TC--TATCAACGCTTATGGGAGCCTTCTTACCGAAGACGTGAGAAACTGATTGG 326
QY 323 GGAAGTAAAGATATATGTTCAATTTCAAGTCGCTGGAAGATGAG----- 369
DB 327 GGAAGTAAAGATATATGTTCAATTTCAAGTCGCTGGAAGATGAGATGATGCC 383
QY 370 --GCAATGATCTCTTCAACGACTTTGCTGCTGATGACGTTGAACGTTGGGAATCGA 427
DB 384 CCTCAATGATCTTATGAAACGACTTTGATGCTGATGACGTTGAACGTTGGGGAATTGA 443
QY 428 CAGGCAATTTCAAAAAGAGATAAAAACGCACTCGATTATGTTAAAGATTGGAACGA 487
DB 444 TAGACATTTCAAAAAGAGATAAAAACGCACTCGATTATGTTAAAGATTGGAACGA 503
QY 488 AAAAGCATGATGATGAGGAGGAGAGATGTTGATGACCTCAACTCAACGCTTGGG 547
DB 504 AAAAGCATGATGATGAGGAGGAGAGATGTTGATGACCTCAACTCAACGCTTGGG 563
QY 548 GCTTGAACCTCCGACTACACGATACACTGTCTTCAAGATGTTGAAGCTTTTAA 607
DB 564 GTTTCGAACCTCCGACTACACGATACAGTGTCTTCAAGATGTTGAAGATTTCA 623
QY 608 AGACAAAATGGGCAATTTTCTCCACTGCCAATATTCAGATAGAGGAGAGATTAGAGG 667
DB 624 AGACAAAATGGGCAATTTTCTCCACTGCCAATATTCAGATAGAGGAGAGATTAGAGG 680
QY 668 CGTTCATATTTATTCAGGCGCTCCCTGCTGCTTCCCGGCGAAGATTATGATGA 727
DB 681 CGTTCATATTTATTCAGGCGCTCCCTGCTGCTTCCCGGCGAAGATTATGATGA 740
QY 728 AGCTGAACATTTCTTACAAAATATTTAAGAGAAAGCCCTGCAAAAAGATTCGGCATCCAG 787
DB 741 GGCTGAATTTCTCTTCAAGATATTTGAAGAAAGCCGTGCAAAAAGATTCGGCTCCAG 800
QY 788 TATACCTTCACTAGAGATACGGGACGTTCTGGAATATGTTGGACACCAATTTGCCACG 847
DB 801 T--CTTTCAGAAATAGACTACACTTTGGAATATGTTGGACACCAATATGCCAAG 857

QY 848 CTGGAAGCAAGAAATTACATGACGCTTTTGGACAGACACTA-----AA 893
DB 858 ATTGAACAGAGAAATTACTTAGATGATTTGGACATCTTACAGATGCTCAAGAA 917
QY 894 AATAAGAACG-----CGCCGAAACTTTAGAACTTGCAAAATTGGAATTCAA 943
DB 918 GAAAAGAGCAATATCTGACAGCGAAAGCTTTTGAAGCTCGCAAAATTGGAATTCAA 977
QY 944 TATATTTCACTCTTACAGAGAGAGATTAAACATGTTTCCCGATGTTGAAAGACTC 1003
DB 978 CATCTTCACTCTTCAACAGAGAGATTACAGTATCTCTCCAGATGTTGATACATTC 1037
QY 1004 GGGTCTCCTGAGATGACCTTCTGTGACATCGTCAAGTGAATACCTTTGGCTTC 1063
DB 1038 GGGTTGCTGAACTGACCTTTGGTCCGCACTGTCAGTGAATACCTTGAAGCTC 1097
QY 1064 CTGCAATGCGTTGAGCCTCAACATTTGGAATTGAGACTCGGCTTTACCAAGATGTC 1123
DB 1098 TTGATTTGCACTGAGCCCAACATTTGCAATTCAGATTGGGCTTTGCCAAACGTGTC 1157
QY 1124 TCTTATCAGGTTCTTGACGACATGTACAGCTCTTGGCAGATGACGAGCTGAACT 1183
DB 1158 TCTTATCAGGTTCTTGACGATATCTACGACATTTTGGAAAGATGATGAATGAACT 1217
QY 1184 CTTACAGCGCAATTAAGAGATGGATCCGTCGCGATGGAATGCTTCCAGAAATATAT 1243
DB 1218 CTTCAAGAGGAGTTAGAGATGGAATCCGTGGAAGAAAGACGCTCCAGAAATATAT 1277
QY 1244 GAAAGAGTTAGATGATGTTTATCAACCGTAAATGAATGGCTCGAGTGCAGAGAA 1303
DB 1278 GAAAGAAATCTAGATGCACTCTACGAAGCTTAACTGACATGGCGGAGAGAGAGAA 1337
QY 1304 GGTCAAGCGCGAGACACGCTCAACTATGCAAGACAGAGCTTGGAGCGCTTTGATTC 1363
DB 1338 GACACAGGCGGAGACACGCTCAATATGTTAGAAAGGCTTGGAGTTTATCTTGATTTC 1397
QY 1364 GTATATGACAGAGCAAGTGATGCGCACTGTTATCTGCCACGTTTGAAGAGTACTT 1423
DB 1398 GTATACACAGAGCAAGTGATGCGCAAGGTTATCTGCCAACTTTGAGAGATCTT 1457
QY 1424 GGAGAACGGGAAGTTAGCTCTGCTCATGCGCCATGCGCACTGCAACCATCTGACGTT 1483
DB 1458 AGAGAACGCGAAGTTAGCTCTGCTCATGCGCAGCGCATGACACCCCTCTGACATT 1517
QY 1484 GGACATCCCTTCTCTGATCACATCTCAAGAAAGTTGACTTCCCATCGAACTCAATGA 1543
DB 1518 GGACGATCCGCTTCTGATGACGCTTGAAGGAATAGATTTCATCGAGATTATATGA 1577
QY 1544 CTGATATGATATCTCTTCTGATTAGAGTGATACACGCTGCTACAGGACAGAGGC 1603
DB 1578 TTTGCAATCTTCTCTTCTGATTAGACTGACACAGATGCTTCAAGGACAGAGGGA 1637
QY 1604 CCGTGAGAGAGAGCTTCTGCTATATCATGTTATATGAAGACAAATCCTGATTAAAG 1663
DB 1638 CCGAGAGAGAGAGCTTCAAGCATATGCTGTTACATGAAGACAAATCCTGATTAAAG 1697
QY 1664 AGAAGATGCTCTAATCATATCAACTTCATGATCAGGAGCGCAATCAGAGATTAAATTG 1723
DB 1698 GGAAGATGCTCTAATCATATCAATGATGATCAACGACATATCAAGAAATTAAATTG 1757
QY 1724 GGAGCTTCTAAAGCCAGACAAAGTGTTCCTCACTTCCAAAGAAACAGCATTTGACAT 1783
DB 1758 GGAAGCTTCTAAAGCCAGATAGCAATATTCATGATGACGAGAAACATGCTTATGAGAT 1817
QY 1784 AAGCAGATTGCGATCAGGTTACAGATACGAGATGCTACAGCTTGGCCAAGCTTGA 1843
DB 1818 AACCAAGCTTTCACCACTTTACAAATATAGAGATGCTTCAAGGTTGCCACTCAAGA 1877
QY 1844 AACCAAGCTTGTGATGAGAACGCTCATTGAACCTGTGCTTTGTAACAACACTTCAA 1903
DB 1878 AACCAAGCTTGTGATGAGAACGCTCATTGAACCTGTGCTTTGTAACAACACTTCAA 1937

QY 1904 ATCTACATA 1913
Db 1938 TTCTATAATA 1947

RESULT 10

US-09-887-586A-29
; Sequence 29, Application US/09887586A
; Patent No. US20020094556A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20020094556A11, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/887, 586A
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for windows Version 3.0
; SEQ ID NO 29
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (69)...(1949)
; OTHER INFORMATION: myrcene synthase
US-09-887-586A-29

Query Match 53.2%; Score 1071.6; DB 9; Length 2196;
Best Local Similarity 75.0%; Pred. No. 1.4e-306;
Matches 1430; Conservative 0; Mismatches 441; Indels 36; Gaps 6;

QY 68 CAGTCTGCTCAGTCTTCTCATGAGATTAAAGGCTCTCCGTAGACAATCCCACTCT 127
Db 116 CAAGTCGTGATCAGTTCATTCATGACATTAAGCCTCCCTATAGACAATCCCAATCT 175
QY 128 TGAATCTGACGCGCGGGAATCCGTCGCGCATTCATTAACATGTTTGACAAGCGT 187
Db 176 TGAATGCGTAGGCGAGGAATCTGTACGCTTCATGAGCATCAGTTGGCCACCGC 235
QY 188 CGCATCTACTGATTTCTGTACAGAGCGGTGGCAACTATCATTCGAACCTGTGGAGCA 247
Db 236 TGACACCTGATGATGTTGTACAAGAAGCATAGTACTACCATTCGAATATCTGGAGCA 295
QY 248 TGATTTCAATACAGTCTCTGATCTCAAGCCTTATGAGACACCTGATTAACCGGAACGTG 307
Db 296 TGATTTCAATACAGTCTC--TATCAACGCTTATGGGAACCTCTTAACGAGAACGTGC 352
QY 308 TGACAGACTTATTTGGGGAAGTAAGGATATAATGTTCAATTTCAAGTCGCTGGAAGATGG 367
Db 353 TGAGAGATTAATTTGTGAGAGTTAAAGAGATA--TTCAATTCATGTACTTGATGATGG 409
QY 368 AGG-----CAATGATCTCTTCAACGACTTTTGTGCTGTGATGACGTTGA 412
Db 410 AAGATTAATGAGTTCCTTAAATGATCTCAAGCAACGCTTTGATAGTAGATAGCGTTGA 469
QY 413 ACGTTTGGGAATCGACAGGCAATTTCAAAAAAGAGATAAAAAAGGCACTGATTAATGTTAA 472
Db 470 ACGTTTGGGATAGCTAGACATTTCAAGAACAGATAACATCAGCTCGGATTAATGTTT 529
QY 473 CAGTTATTTGAAACGAAAAAGCATTTGAGTGGGAGGAGAGAGTGTGACTGACCTCAA 532
Db 530 CCGTTACTGGAGGAGAAAAAGCATTTGATGGGAGAGAGACAGTATTTACTGATCTCAA 589
QY 533 CTCAACCGCTTGGGGCTTCGAACCTCCGACTACACGAGATACATGTGTCTTCAGATGT 592

Db 590 CTCACTGCGTTGGGTTTGCACCTCTTCGATTACACGGGTACACTGTATCTCCAGAGGT 649
QY 593 TTGAACTTTTTTAAGACAAAAATGGCAATTTCTCCACTGCCAATATTACAGATAGA 652
Db 650 TTTAAAGCTTTTCAAGATCAAAATGAGACAGTTGTATGCTCCCC--GGTCAGACAGA 706
QY 653 GGGAGATTTAGAGCGCTTCTCAATTTATTCAGGGCTCCCTCGTCCCTTTCCCGCGCA 712
Db 707 GGGTAGATCAGAAAGCGTCTTAATTAATATATCGGGCTTCCCTCATGCTCCCTGTGA 766
QY 713 GAAAGTTATGATGAAGCTGAACATTTCTACAAAATATTTAAGAGAAAGCCCTGCAAAA 772
Db 767 GAAAGTTATGGAAGAGCTGAAATCTTCTCCACAAGATATTTGAAGAAAGCTTACAAAA 826
QY 773 GATTCGGCATCCAGTATACTTTCACTAGAGATACGGGACGTTCTGGAATATGTTGCA 832
Db 827 GATTCAGTCTCCGCT--CTTTCACAAGAGATAAAGTTTGTATGGAATATGCTGGCA 883
QY 833 CACCAATTTGCCACGCTTGAAGCAAGAAATTACATGAGCGTCTTGGACAGACACACTA- 891
Db 884 CACAAATTTGCCAAGATTGGAAGCAAGAAATTACATAGACACACTGAGAAAGACACAG 943
QY 892 -----AAATAAGAACGCCGCCGAGAAACTTTTAGAACTTGCAAAATTTGAATCAA 943
Db 944 TGCAATGCTCAATAAAAAATGCTGGAGAGAAAGCTTTAGAACTTGCAAAATTTGAGTTCAA 1003
QY 944 TATATTTCACTCCTTACAGAGAGAGAGATTAAACATGTTCCCGATGCTGGAAGACTC 1003
Db 1004 TATATTTAACTCCTTACACAAAGAAATTACAATATCTTTTGAAGATGCTGGAAGAGTC 1063
QY 1004 GGGTTCCTGAGATGACCTTCTGTGACATGCTGACAGTGAATACTACGCTTTGGCTTC 1063
Db 1064 GGATTCCTTAATTTGACATTTGCTGGCATGCTGATGGAATTTCTACACTTTGGCTTC 1123
QY 1064 CTGATTCGCTTGAGACCTTCAACTCTGATTCAGACTCGGCTTTACCAAGATGCTCA 1123
Db 1124 TTGTATGGCATTGACCCCAAAATCTCTGATTGAGACTGAGCTTGGCAAAATGTGTCA 1183
QY 1124 TCTTATCAGCGTTCTTGACGACATGTACGACGCTTTCGGCAGTAGACGAGCTGAAC 1183
Db 1184 TCTTGTACAGTTTGTGACGATATTACGACACTTTTGAAGCATGACGAGCTTGAAC 1243
QY 1184 CTTCAACGCAATTAAGAGATGCGTCCGCGATGGAATGCTTCCAGAATATAT 1243
Db 1244 CTTCAATCTGCAATTAAGAGATGGAATTCATCAGAGATGAACACCTTCCAGAATATAT 1303
QY 1244 GAAAGAGTGTACATGATGTTTATCACACCGTAATGAATGCTCGAGTGGCAGAGAA 1303
Db 1304 GAAATGTGTGTACATGCTGTGTTTGAATGTAATGAACTGACACGAGAGCGGAGAA 1363
QY 1304 GGTTCAGGCGGAGACACGCTCAACTATGCAAGACAGGCTTGGAGGCGGTGTTGATTC 1363
Db 1364 GACTCAAGGAGAAACACTCTCACTATGTTGAAAAGGCTTGGAGGCTTATTTGATTC 1423
QY 1364 GTATATGAGGAAAGCAAGTGAATGCGCACTGTTATCTGCCACGTTGAGAGTACTT 1423
Db 1424 ATATATGGAAGAAAGCAAAATGATCTTAATGTTATCTGCCAATGTTGAAGAGTACCA 1483
QY 1424 GGAGAACGGGAAAGTTAGCTGTGCTCATCGCCCATGCGCACTGCAACCCATTCTGACGTT 1483
Db 1484 TGAGAAATGGGAAAGTAGCTGTGATATCGCGTAGCAACATTTGCAACCCATCTCACTTT 1543
QY 1484 GGAATCCCTTCTCTGATCACAATCCTCAAGGAAGTTGACTTCCATCGAAGCTCAATGA 1543
Db 1544 GAATGCAATGCTTCTGATTAATCTTGAAGGAATGATTTTCCATCCAGGTTCAATGA 1603
QY 1544 CTTGATATGTATCATCTTGTGATTAAGAGGTATACACGGTGTACAAAGGACAGACAGGC 1603
Db 1604 TTTGGCATGCTCTTCTTGGGCTACGAGGTGACACACGCTGTCTACAAAGGCCGATAGGGA 1663
QY 1604 CCGTGGAGAGAAAGCTTGTCTATATCATGTTATGAAGACAAATCCTGATTAACGGA 1663

Db 1664 TCGGTGAAGAAGCTTCGTGTATATCATGTATATGAAGACAATCCGTGATCAACCGA 1723
QY 1664 AGAAGATGCTCTGAATCATATATCACTTCATGATGAGGAGCGCAATCAGAGATTAATG 1723
Db 1724 AGAAGATGCCCTCATCATATATCATATGATGATGATGATGATGATGATGATGATG 1783
QY 1724 GGAGCTTCTAAGCCAGACAACAGTGTTCCTCATCTTCCAGAGAAACAGCATTTGACAT 1783
Db 1784 GGAACTTCTAAGATCCAAACGACAATATTTCCAACTGCTGGCCAAAGAAACATGCTTTTGACAT 1843
QY 1784 AAGCAGATTTGGCATCAAGGTTACAGATACGAGATGCTACAGCTTTGCCAAGCTTGA 1843
Db 1844 AACAGAGCTCTCCACCATCTCTACATATATGAGATGCTTTAGTGTGGCAACAGGA 1903
QY 1844 AACAAAGAGTTGGTGTATGAGAACCGCTCATTTGAACCTGTGCTTTGTAACAACACTTCAA 1903
Db 1904 AACAAAAAATGTGTATGAGAAACACTCCTGAACTATGCTTTTAACTATAACCATATA 1963
QY 1904 ATCTACATATTAAGTATGAGATGCCCTATGGGTATATAGGCACA 1950
Db 1964 TCCATATAATTAAGCTCATATATGCTAATTAATGCGCTTATGACATA 2010

RESULT 11
US-09-903-012-29
; Sequence 29, Application US/09903012
; Patent No. US20020094557A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20020094557A1, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903,012
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (69)...(1949)
; OTHER INFORMATION: mycene synthase
US-09-903-012-29

Query Match 53.2%; Score 1071.6; DB 9; Length 2196;
Best Local Similarity 75.0%; Pred. No. 1.4e-306;
Matches 1430; Conservative 0; Mismatches 441; Indels 36; Gaps 6;

QY 68 CAGTCGTCCTGAGTTCTTCTCATGAGATTAAGGCTCTCCGTAAGACAATCCCACTCT 127
Db 116 CAAGTCGTTGATCAAGTTCAATTCATGAAACATTAAGCTCCCTATAGAACAAATCCCAATCT 175
QY 128 TGGAAATCGCAGCGCGGGAATCCGTCGCGCATTCATTAACATGTGTTGACAAAGCGT 187
Db 176 TGGAAATCGTAGCGAGGAAATCTGTACGCGCTTCATGAGCATCAGTTTGCCACCGC 235
QY 188 CGCATCTACTGATTTCTGTACAGAGACGCGTGGCACTATCATTTCCAACCTGTGGAGCA 247
Db 236 TGCACCTGATGATGTGTACAAAGACGATAGTACCATTTCCAATATCTGGAGCA 295
QY 248 TGATTTATACAGTCTCTGATCTCAACGCGCTTATGAGACACCTGATTAACCGGAACGTGC 307

Db 296 TGATTTATACAGTCTC--TATCAACGCTTATGCGGAACCCCTCTTAACAGGAACGTGC 352
QY 308 TGACAGACTTAATGGGGAAGTAAGATATATGTTCAATTTCAAGTCGCTGGAAGATG 367
Db 353 TGAGAGATTAATGTGAGGTAAAGAGATA--TTCAATTCATGTACCTGGATGATG 409
QY 368 AGG-----CAATGATCTCTCAACGACTTTGCTGTGATGATGATGATGATGATGATG 412
Db 410 AAGATTAATGAGTCTCTTAATGATCTCAACGACTTTGATGATGATGATGATGATGATG 469
QY 413 ACGTTGGGAATCGACAGGCAATTTCAAAAAGAGATAAAACGGCACTCGATTAATGTTAA 472
Db 470 ACGTTGGGGAATGCTAGACATTTCAAGACGAGATTAACATCAGCTCTGATTAATGTTT 529
QY 473 CAGTATTTGGAACGAAAAAGCATTTGATGAGGAGGAGAGAGTGTGATGATGATGATGATG 532
Db 530 CCGTTACTGGGAGGAAAAAGCATTTGATGAGGAGAGAGACAGTATTTGTTACTGATCTCAA 589
QY 533 CTCAACCGCTTGGGCTTGAAGCTCTCGACTACAGGATACAGTGTCTTCAAGATG 592
Db 590 CTCAACGCTTGGGCTTGAAGCTCTCGACTACAGGATACAGTGTCTTCAAGATG 649
QY 593 TTGAACGTTTAAAGACAAAATGGGCAATTTCTCCACTGCCAATATTCAGATAGA 652
Db 650 TTTAAAGCTTTCAAGATCAAAATGAGACGTTGTATGCTCCGCC--GATCAGACAGA 706
QY 653 GGGAGAGATTAAGGCGCTTCTCAATTTATCAGGCGCTCCCTGCTGCTTCCCGCGCA 712
Db 707 GGGTGAATCAGAGCGCTTCTTAATTTATCGGCGCTCCCTCATGCTCCCTGCTGTA 766
QY 713 GAAAGTTATGATGAAGCTGAACATTTCTCAAAAATTTAAGAGAACCCCTGCCAAA 772
Db 767 GAAAGTTATGAGAGAACTGAATCTTCTCAACAGATATTTGAAGAGAACTCTACAAA 826
QY 773 GATTCGGGATCAGATATCTTCACTTACAGATACGGGACGTTCTGATATGTTGGCA 832
Db 827 GATTCAGTCTCGCT--CTTCAACAGATTAAGTTGTATGAAATATGCTGCA 883
QY 833 CACCAATTTGCGAGCTTGAAGCAAGGATTAACATGAGAGCTGTTGACAGCACTA- 891
Db 884 CACAAATTTGCCAAGATTTGAAGCAAGAAATTAACATGACACACTTGAGAAAGACACAG 943
QY 892 -----AAAATAAGAACGCGCGGAAACTTTTGAACCTTGCAAAATTTGAATTCAA 943
Db 944 TGCATGCGTCAATAAAATGCTGGAGAGAGCTTTTGAACCTTGCAAAATTTGAAGTTCAA 1003
QY 944 TATATTTCACTCTTACAGAGAGAGATTAACATGTTTCCGATGCGGAAAGACTC 1003
Db 1004 TATATTTACTCTTACACAAAAGGATTAACATATCTTTGAGATGCTGGAAGAGATC 1063
QY 1004 GGGTCTCTGAGATGACCTTCTGTGACATGCTCAAGTGAATGATGATGATGATGATG 1063
Db 1064 GGATTTGCTTAATTAATGACATTTGCTCGGATGCTCATGTGGAATTTTACACTTTGGCCTC 1123
QY 1064 CTGCAATGCGTTGAGGCTCAACATTTGATTCAGACTCGGCTTTACCAAGATGCTCA 1123
Db 1124 TTGTATGCAATGAGCCCAAAACATTTGATTCAGACTAGGCTTGCCAAATGTGTCA 1183
QY 1124 TCTTATCAGGTTCTTGAAGCATGTAAGAGTCTTGGCAGACAGTGAAGTGAAGTGAAGT 1183
Db 1184 TCTTATCAGGTTTGAAGCATGTAAGAGTCTTGGCAGACAGTGAAGTGAAGTGAAGTGA 1243
QY 1184 CTTCACAGGCAATTAAGAGATGGATCGTCCGCGATGGAATGCTTCCAGATATAT 1243
Db 1244 CTTCACATCTCAATTAAGAGATGGAATTCATCAGAGATAGAACACCTTCCAGATATAT 1303
QY 1244 GAAAGAGTTCATGATGTTTATCAACCGTAATGAATGCTGATGAGTGGCAGAGAA 1303
Db 1304 GAAATGTGTTCATGATGCTGTGTTGAACGTGAATGATGATGATGATGATGATGATG 1363
QY 1304 GGCTCAAGGCGGAGACAGGCTCAACTATGCAAGACAGGCTTGGAGGCGTGTGATTC 1363

```
Db 1364 GACTCAAGGAGAAACACTCTCAACTATGTTGAAAGGCTTGGAGGCTTATTGATTC 1423
Qy 1364 GTATATGAGAGAACAAAGTGGATGCCACTGGTTATCTGCCACGTTTGAGAGTACTT 1423
Db 1424 ATATATGAGAGAAACAAATGATCTTAATGTTATCTGCCAATGTTGAAGATACCA 1483
Qy 1424 GGAGAACGGGAAAGTTAGCTCTGCTCAATGCCCATGCGCACTGCAACCCATTCTGACGTT 1483
Db 1484 TGAGATGGGAAAGTGAGCTCTGCAATCGCGTAGCAACATTTGCAACCCATCTCACTTT 1543
Qy 1484 GGACATCCCTTTCTCTGATCATCTTCAAGGAAGTTGACTTCCATCGAAGCTCAATGA 1543
Db 1544 GAATGCAATGCTTCTGATTAATCTTGAAGGAATTGATTTCCATCCAGGTTCAATGA 1603
Qy 1544 CTGATATGATCATCTCTCGATTAAAGGTGATACACGGTGTCAAGAGGACAGACAGGCG 1603
Db 1604 TTTGGCATGCTCTTCTTCTCGGCTACGAGGTGACACACGCTGTACAGGCCGATAGGGA 1663
Qy 1604 CCGTGAAGAGAGCTTCTGCTATATCATGTTATATGAAGACAACTCTGATTAAACGGA 1663
Db 1664 TCGTGTGAGAAAGCTTCGTATATCATGTTATATGAAGAACAACTCTGATTCAACCGA 1723
Qy 1664 AGAAGATGCTTGAATCATATCACTTCAATGATCAGGACGCAATCAGAAATTAATTG 1723
Db 1724 AGAAGATGCCCTCAATCATATCAATGCGCATGTCATGACATTAATCAAGAATTAATTG 1783
Qy 1724 GGAGCTTCTAAAGCCAGACACAGTGTTCACATCTTCCAAGAAACGCAATTGACAT 1783
Db 1784 GGAATCTTAAGATCCAACGACATATCCAATGCTGCCAAGAAACATGCTTTGACAT 1843
Qy 1784 AAGCAGATTGGCATCACGGTTACAGATACCGAGATGGCTACAGCTTGGCAACGTTGA 1843
Db 1844 AACAGAGCTCTCCACCATCTCTACATATTCAGATGGCTTTAGTTGCCAACAAAGGA 1903
Qy 1844 AACAAAGATTGGTGTGATGAGAACCGTCAATTGAACCTGTGCTTTGTAACAACACTTCAA 1903
Db 1904 AACAAAAAATTGGTTATGAAACACTCTTGAATCTATGCTTTTAACTAATACCATA 1963
Qy 1904 ATCTACATATTAATCTGAGATGCCCTATGGGTATATAGGGCACA 1950
Db 1964 TCCATTAATTAAGCTCATATGCTAAATTAATTGGCCTTATGACATA 2010
```

RESULT 12
US-09-900-797-29

```
; Sequence 29, Application US/09900797
; Publication No. US20030087406A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20030087406A1, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/900,797
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for windows Version 3.0
; SEQ ID NO 29
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (69)...(1949)
; OTHER INFORMATION: myrcene synthase
; US-09-900-797-29
```

```
Query Match 53.2%; Score 1071.6; DB 10; Length 2196;
Best Local Similarity 75.0%; Pred. No. 1.4e-306;
Matches 1430; Conservative 0; Mismatches 441; Indels 36; Gaps 6;

Qy 68 CAGTTCGCTCAGTCTCTTCATGAGATTAAAGCTCTCCGTAGAACAATCCCACTCT 127
Db 116 CAAGTCGTTGATCAGTTCATTCATGAAACATAAGCCTCCCTATAGAACAATCCCAATCT 175
Qy 128 TGGAACTGCAAGCGCGGGGAAATCCGTCGCCGATTTCCATTAACAATGTTGACAAAGCGT 187
Db 176 TGGAAATGCGTAGGCGAGGGAATCTGTCAAGCCTTCCATGAGCATCAGTTTGGCCACCGC 235
Qy 188 CGCATCTACTGATTCTGTACAGAGACGCGTGGCAACTATCATTTCCAACCTGTGGAGCA 247
Db 236 TGCACCTGATGATGTTGACAAAGACGATAGGTGACTACCAATTCGAATATCTGGAGCA 295
Qy 248 TGATTTATACAGTCTGTATCTCAACGCCCTTATGAGCACTGATTACCGGAACGTGC 307
Db 296 TGATTTATACAGTCTC--TATCAAGCCTTATGAGGAACCTCTTACAGGAACGTGC 352
Qy 308 TGACAGACTTATTGGGAAGTAAGATATATATGTTCAATTTCAAGTCGCTGGAAGATGG 367
Db 353 TGAGAGATTAATTTGTGAGGTAAGAAGATA--TTCAATTCATGTAACCTGATGATGG 409
Qy 368 AGG-----CAATGATCTCCTTCAACGACTTTTCTGCTGCTGATGACGTTGA 412
Db 410 AAGATTATGAGTTCCTTTAATGATCTCATGCAACGCCCTTGGATGATGATGAGCTTGA 469
Qy 413 ACGTTTGGGAATGACAGAGCATTTCAAAAAAGAGATAAAAAAGGCACTCGATTATGTTAA 472
Db 470 ACGTTTGGGATAGCTAGACATTTCAAGAACGAGATTAACATCAGCTCGATTATGTTT 529
Qy 473 CAGTTATTGGAACGAAAAAGCATTTGATGTGGAGGAGAGAGTGTGACTGACCTCAA 532
Db 530 CCGTTACTGGAGAGAAAAAGGCAATGGATGTGGAGAGACAGTATGTTACTGATCTCAA 589
Qy 533 CTCAACGCGCTTGGGCTTGAACCTCTCCGACTACACGGAATCACTGTGCTTCAAGATG 592
Db 590 CTCAACTGCGTTGGGTTTGAACCTCTGATTACACGGGTACATGTATCTCCAGAGGT 649
Qy 593 TTTGAACGTTTTTAAAGACAAAAATGGGCAATTTTCTCCACTGCCAATATTACAGATAGA 652
Db 650 TTTAAAGCTTTTCAAGATCAAAATGAGACAGTTTGTATGCTCCCC--GGTACAGACAGA 706
Qy 653 GGGAGATTTAAGAGCGTCTCAATTTATTCAGAGGCTCCCTGCTGCCCTTCCCGGCGCA 712
Db 707 GGGTGAATCAGAAAGCGTCTTAATCTTATATCGGGCTTCCCTCATTTGCCCTGTGTA 766
Qy 713 GAAAGTTATGATGAAGCTGAACATTTCTCTCAAAAAATATTTAAGAGAAAGCCCTGCAAAA 772
Db 767 GAAAGTTATGAAAGAGAGCTGAATCTTCTCCACAAAGATATTGAAGAAAGCTCTACAAAA 826
Qy 773 GATTCGCGCATCCAGTATACCTTCACTAGAGATACGGGACGTTCTGGAATATGTTGGCA 832
Db 827 GATTCAGTCTCCGCT--CTTCAACAAGAGATAAAGTTTGTATGGAATATGCTGGCA 883
Qy 833 CACCAATTGCGCAGCTTGAAGCAAGAAATTACATGAGACGTCCTTTGGACAGACACTA- 891
Db 884 CACAAATTTGCCAAGATTGGAAGCAAGAAATTACATAGACACACTTGAGAAAGACACAG 943
Qy 892 -----AAATAAGAACGCCGCCGAGAAACTTTTGAACCTTGCAAAATGGAATTCAA 943
Db 944 TGCAATGCTCAATAAAAATGCTGGGAAGAAAGCTTTTGAACCTTGCAAAATGGAATTCAA 1003
Qy 944 TATATTTCACTCTTACAGAGAGAGAGATTAAACATGTTTCCCGATGCTGGAAGACTC 1003
Db 1004 TATATTTAATCTCTTACACAAAGAAAGAAATTACAAATATCTTTTGAAGATGCTGAAAAGACTC 1063
Qy 1004 GGGTTCCTGAGATGACCTTCTGTGACATGTCACAGTGAATACTACGCTTTGGCTTC 1063
Db 1064 GGATTTGCTTAATTTGACATTTGCTGGCATGTCATGTGAATTTCTACACTTTGGGCTTC 1123
```



```
QY 1064 CTGATGCGCTTCGAGCCTCAACATCTTGATTGAGACTCGGCTTACCAAGATGCTCA 1123
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1124 TTGTATGGCATGAGCCAAACATCTCGATTCAGACTAGGCTTCGCCAAATGTGTCA 1183
QY 1124 TCTTATCAGCGTCTTGACGACATGACGACGCTCTTCGGCACAGTAGACGAGCTGGA 1183
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1184 TCTTGTACAGTTTGTGACGATATTACGACACTTTTGGAAACGATTGACGAGCTTGA 1243
QY 1184 CTTACAGCGACATTAAGAGATGGATCCGTCGCCGATGGAATGCTTCCAGATATAT 1243
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1244 CTTACATCTGCAATTAAGAGATGAATTCATCAGAGATAGAACACCTTCCAGATATAT 1303
QY 1244 GAAAGAGTGTACATGATGTTTATCACCCTAAATGAATGAATGGCTGAGTGCGAGAA 1303
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1304 GAAATGTGTACATGCTGCTGTTGAAACTGTAATGAACAGACGAGAGCGGAGAA 1363
QY 1304 GCGTCAAGCCGAGACACGCTCAACTATGCAAGACAGGCTTGGAGCGGTGTTGATTG 1363
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1364 GACTCAAGGAGAAACACTCTCACTATGTTCCGAAAGGCTTGGAGGCTTATTTGATTG 1423
QY 1364 GTATATGCAAGAAAGCAAGTGTATGCGCACTGCTTATCTGCCACGTTTGAGAGTACT 1423
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1424 ATATATGCAAGAAAGCAAAATGATCTCTTAATGTTATCTGCCAATGTTTGAAGAGTAC 1483
QY 1424 GGAGAACGGGAAAGTTAGCTCTGCTATGCGCCATGCGCACTGCAACCCATTCTGACG 1483
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1484 TGAGAAATGGAAAGTGTAGCTCTGATATGCGGTAGCAACATTGCAACCCATCTCACTT 1543
QY 1484 GGACATCCCTTCTCTGATCACAATCCCTGAGGAAGTTGACTTCCATCGAAGCTCAATG 1543
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1544 GAATGCAATGCTCTCTGATTAATCTGAGGGAATTGATTTCCATCCAGGTTCAATGA 1603
QY 1544 CTTGATATGATCATCTCTGATTAAGAGTGTATACAGGCTGTACAGGCAAGAGAGGCG 1603
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1604 TTGGCATGCTCTCTCTGCTGCTACAGAGTGTACACAGCTGTACAGGCGGATAGGA 1663
QY 1604 CCGTGAAGAGAGAGCTTCTGTATATCATGTTATCATGTTATATGAAGACAATCTGGA 1663
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1664 TCGTGTGAAGAGAGCTTCTGTATATCATGTTATATGAAGACAATCTGGAATCAACGA 1723
QY 1664 AGAAGATGCTGTGATCATATCATCTCATGATCAAGGAGCAATCAAGAAATTAATTG 1723
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1724 AGAAGATGCTGTGATCATATCATCTCATGATCAAGGAGCAATCAAGAAATTAATTG 1783
QY 1724 GGAGCTTCTAAAGCCAGACAAGTGTCTCCATCACTTCCAGAGAAACGCAATTTGACAT 1783
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1784 GGAATCTTAAGATCCAAACGACAATATCCAAATGCTGCGCAAGAAACATGCTTTGACAT 1843
QY 1784 AAGCAGATTTGGATCAGGTTACAGATACGAGATGCTACAGCTTTGCAACGTTGA 1843
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1844 AACAGAGCTCTCCACCATCTCTACATATATGAGATGCTTTAGTGTGCAACAAGGA 1903
QY 1844 AACCAAGAGTTTGGTGTAGAGAACCGTCAATGGAACCTGTGCTTTGTAACAACACTTCA 1903
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1904 AACCAAAAAATGTTATGGAACACTCTTGAATCTATGCTTTTAACTATAACCATATA 1963
QY 1904 ATCTACATATTAATGAGATGCGCTATGCGGTGTATATAGGCGACA 1950
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1964 TCCATATATTAAGCTCATATGCTTAATTAATTGGCCTTATGACATATA 2010
```

```
RESULT 13
US-09-893-820-29
; Sequence 29, Application US/09893820
; Publication No. US20040053386A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20040053386A1, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/893,820
```

```
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US/09/398,395A
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for windows Version 3.0
; SEQ ID NO 29
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (69)...(1949)
; OTHER INFORMATION: myrcene synthase
US-09-893-820-29
```

```
Query Match 53.2%; Score 1071.6; DB 13; Length 2196;
Best Local Similarity 75.0%; Pred. No. 1.4e-306;
Matches 1430; Conservative 0; Mismatches 441; Indels 36; Gaps 6;
```

```
QY 68 CAGTCGTGCTCAGTCTCTCTGATGAGATTAAAGGCTCTCCGTGAAACAATCCCACTCT 127
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 116 CAAGTCGTGATCAGTTCAATTCATGACATAGCCCTCCCTATGAAACAATCCCAATCT 175
QY 128 TGAATCTGACGCGCGGGAATCCGTCGCGCATTCCTATAACATGTTGACAAGCGT 187
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 176 TGAATGCGTAGCGGAGGAATCTGTACAGCCCTTCCATGAGCATCAGTTGGCCACCGC 235
QY 188 CGCATCTACTGATCTGTACAGAGACCGGTGGCAACTATCATTCCTCAACCTGTGGACGA 247
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 236 TGCACTGTGATGTTGTACAAAGACGATAGGTGACTACCATTCCAATATCTGGAGCGA 295
QY 248 TGATTTCAATACAGTCTCTGATCTCAAGCCTTATGAGACACCTGATTTACCGGAACTGC 307
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 296 TGATTTCAATACAGTCTCTCTGATCTCAAGCCTTATGAGGAACTCTTACCAAGAACTGC 352
QY 308 TGACAGACTTATTTGGGAAGTAAGATATATGTTCAATTTCAAGTCTGGAAGATG 367
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 353 TGAGAGATTAATTTGTGAGGTAAGAGATA--TTCAATTCATGTAACCTGATGATG 409
QY 368 AGG-----CAATGATCTCTTCAACGACTTTTGTGCTGATGACGTTGA 412
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 410 AAGATTAATGAGTCTCTTATATGATCTCATGCAACGCTTGTGATGATGATGCGTTGA 469
QY 413 ACGTTTGGGAATCGACAGGCAATTCAAAAAGAGATTAACGCACTCGATTATGTTAA 472
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 470 ACGTTTGGGATGCTAGACATTTCAAGAACGAGATTAACATCAGCTCTGATTATGTTT 529
QY 473 CAGTTATTTGAACGAAAAAGGCAATTTGTTGGAGGAGAGAGTGTGACTGACCTCAA 532
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 530 CCGTTACTGGAAGAAAAAGGCAATTTGTTGGAGAGACAGATATTGTTACTGATCTCAA 589
QY 533 CTCAACCGCTTGGGCTTGAAGCTCTCGACTACACGAGATACCTGTGCTTCAGATGT 592
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 590 CTCACTGCGTTGGGTTTGAAGCTCTTGAATTAACAGGAGTACTGTATCTCAGAGGT 649
QY 593 TTGAAGCTTTTAAAGACAAAAAGGCAATTTTCTCCACTGCAATATTTCAGATAGA 652
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 650 TTAAAGCTTTTCAAGATCAAAATGGAACATTTGTATGCTCCGCC--GGTACAGACAGA 706
QY 653 GGAGAGATTAGAGCGTCTCAATTTATTCAGGCGCTCCGCTGCTTCCCGGCGGA 712
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 707 GGGTGAATCAGTAGCGTCTTAATTAATCGGCTTCCCTCATTTGCTTCCCTGTGA 766
QY 713 GAAAGTTATGATGAAGCTGAACATTTCTCTACAAAATATTAAAGAGAGCCCTGCAAAA 772
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 767 GAAAGTTATGAGAGAGCTGAATCTTCTCCACAGATATTGAAGAGAGCTCTACAAAA 826
```

| | | | |
|----|------|---|------|
| QY | 773 | GATTCCGGCATCCAGTATATCTTTCACTAGAGATACCGGACGTTCTGGAATATGGTTGGCA | 832 |
| Db | 827 | GATTCCAGTCTCCGCT---CTTCCAAAGAGATAAAGTTTGTATTGGAATATGGCTGGCA | 883 |
| QY | 833 | CACCAATTTGGCCACGCTTGGGAAGCAAGGAATTACATGACGTCTTGGACAGACACTA- | 891 |
| Db | 884 | CACAAATTTGCCAAGATTGGAAAGCAAGAAATTACATGACACACTTGAGAAAGACACAG | 943 |
| QY | 892 | -----AAATAAAGACGCCGCCGAGAAACTTTTGAAGCTTGCAAAATTGGAATTCAA | 943 |
| Db | 944 | TGCATGGCTCAATAAATAATGCTGGAGAAGACTTTTGAAGCTTGCAAAATTGAGTTCAA | 1003 |
| QY | 944 | TATATTTCACTCCCTTACAAGAGAGAGTTAAAAATGTTCCCGATGGTGAAGAAGCTC | 1003 |
| Db | 1004 | TATATTTAACTCCCTTACACAAAGAAGATTACAATATCTTTGAGATGGTGAAGAAGCTC | 1063 |
| QY | 1004 | GGGTTCCTCGAGATGACCTTCTGTGCATCGTCAAGTGAATACTACGCTTTGGCTTC | 1063 |
| Db | 1064 | GGATTTGCCCTAAATTGACATTTGCTCGGCATCGTCAATGTGGAATTTCAACTTTGGCTTC | 1123 |
| QY | 1064 | CTGCATTGCGTTCGAGCCTCAACATTCTGGATTGAGACTTGGGCTTTACCAAGATGTCTCA | 1123 |
| Db | 1124 | TTGTATTGCCATTGACCCAAACATTCTGCATTGAGACTTGGCTTCGCCAAAATGTCTCA | 1183 |
| QY | 1124 | TCTTATCACGGTTCCTTGAAGACATGTACGACGCTTTCGGCACAAGTAGACGAGCTGGA | 1183 |
| Db | 1184 | TCTTGTACAGTTTGGAGCATATTATTACGACACTTTTGAACGATTGACGAGCTTGA | 1243 |
| QY | 1184 | CTTCACAGCGACAATTAAAGATGGGATCCGTCGGCGAATGGAATGCCTTCCAGAATATAT | 1243 |
| Db | 1244 | CTTCACATCTGCAATTAAGATGGAATTCATCAGAGTAGAACACCTTCCAGAATATAT | 1303 |
| QY | 1244 | GAAAGAGTGTACATGATGGTTTATCACACCGTAAATGAATGGCTCGAGTGACAGAGAA | 1303 |
| Db | 1304 | GAAATGTGTGTACATGTGTGTGTTGAAGCTGTAATGAAGCTGACACGAGAGCGGAGAA | 1363 |
| QY | 1304 | GGCTCAAGGCCGAGACACCGCTCAACTATGCAAGACAGGCTTGGAGGGCGTGTGATTTC | 1363 |
| Db | 1364 | GACTCAAGGGAGAAACACTCTCAACTATGTCGAAAGGCTTGGAGGGCTTATTTGATTTC | 1423 |
| QY | 1364 | GTATATGCAGGAAGCAAAATGGATCGCCACTGGTTATCTGCCCCAGTTGAGGAGTACTT | 1423 |
| Db | 1424 | ATATATGGAAGAGCAAAATGGATCTTAATGGTTATCTGCCAATGTTTGAAGAGTACCA | 1483 |
| QY | 1424 | GGAGAACGGGAAAGTTAGCTCTGCTCATCGCCCATGGCGCACTGCAACCCATTCTGACGTT | 1483 |
| Db | 1484 | TGAGAAATGGGAAAGTGAAGCTTGCATATCGCGTAGCAACATTGCCAACCATTCTCACTTT | 1543 |
| QY | 1484 | GGACATCCCTTCTCTGATTCACATCTCAAGGAAGTTGACTTCCATCGAAGCTCAATGA | 1543 |
| Db | 1544 | GAATGCATGGCTTCTCTGATTCACATCTTGAAGGGAATGATTTCCATCCAGGTTCAATGA | 1603 |
| QY | 1544 | CTTGATATGTATCATCTCTCGATTAAAGAGTGATACAAGGTCTACAAGGCAGACAGGCG | 1603 |
| Db | 1604 | TTTGGCATCGCTCTTCTCTCGGCTACGAGGTGACACACGCTGCTACAAGGCCGATAGGGA | 1663 |
| QY | 1604 | CCGTGAGAGAAGAGCTTCGTCTATATCATGTATATGAAGACAATCCTGGATTAAACGGA | 1663 |
| Db | 1664 | TCGTGTGAAGAAGAGCTTCGTGTATATCATGTTATATGAAGACAATCCTGGATCAACCGA | 1723 |
| QY | 1664 | AGAAGATGCTCTGAATCATATCAACTTCATGATCAGGAGCGCAATCAGAGAAATTAATTG | 1723 |
| Db | 1724 | AGAAGATGCCCTCAATCATATCAATGCCATGGTCAATGACATTAATCAAGAAATTAATTG | 1783 |
| QY | 1724 | GGAGCTTCTAAAGCCAGACAAGTGTTCCTCATCACTTCAAGAAAACGCAATTTGACAT | 1783 |
| Db | 1784 | GGAATCTTAAGATCCAAGACAATATTCCAATGTGGCCAGAAGAAACATGCTTTTGACAT | 1843 |
| QY | 1784 | AAGCAGAGTTTGGCATCAAGGTTACAGATACGAGATGGCTACAGCTTTGCCAAGCTTGA | 1843 |
| Db | 1844 | AAACAAGAGCTCTCACGCACTCTACATATATCGAGATGGCTTTAGTGTGGCCAAACAGGA | 1903 |
| QY | 1844 | AAACAAGAGTTTGGTATGAGAACCGTCATTGGAACCTGTGCCCTTGTAAACAACACTTCAA | 1903 |

Db 1904 AACAAAAAATGGTTATGGAACACTCCTTGAATCTATGCTTTTAACTATAACCAT 1963

QY 1904 ATCTACAATATTAAGTGAAGATGCCCTATGGGTATATATAGGCACA 1950

Db 1964 TCCATAATTAATAGCTCAATATGCTAAATTATTTGGCTTATGACATA 2010

RESULT 14

```

US-10-041-007-25
; Sequence 25, Application US/10041007
; Publication No. US20020164736A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seiichi P.T.
; APPLICANT: Schepmann, Hala G
; TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase
; FILE REFERENCE: P02081US1
; CURRENT APPLICATION NUMBER: US/10/041,007
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259,881
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
;
; LENGTH: 2196
;
; TYPE: DNA
;
; ORGANISM: Abies grandis
US-10-041-007-25

```

| | | | | |
|----------------------------|--------|---------------------|------------|--------------|
| Query Match | 53.2% | Score 1071.6; | DB 14; | Length 2196; |
| Best Local Similarity | 75.0%; | Pred. No. 1.4e-306; | | |
| Matches 1430; Conservative | 0; | Mismatches 441; | Indels 36; | Gaps 6; |

| | | | | |
|----|--|-----|---|-----|
| OY | | 68 | CAGGTCGTGCCTCAGTTCCTTCTCATGAGATTAAAGGCTCTCCGTAGACAATCCCACTCT | 127 |
| Db | | 116 | CAAGCGTTGATCAGTTCAATTCATGAACATTAAGCCTCCCTTATGAAACAATCCCAAATCT | 175 |
| OY | | 128 | TGGAATCTGCAGGCCGGGAAATCCGTCCGCATTCCATAAACATGTGTTTGACAACGCT | 187 |
| Db | | 176 | TGGAATGCGTAGGCGAAGGAAATCTGTCACGCCCTTCATGAGCATCAGTTTGCCACC GC | 235 |
| OY | | 188 | CGCATCTACTGATTCTGTACAGAGACGCGTGGCAACTATCATTC AACCTGTGGAGCA | 247 |
| Db | | 236 | TGCACCTGATGATGGTGTAACAAGA CCGCATAGGTGACTACCATCCAATATCTGGAGCA | 295 |
| OY | | 248 | TGATTTCAATCACAGTCTCTGATCTCAACGCCCTTATGAGCAGCTGATTA CCGGGAACGTGC | 307 |
| Db | | 296 | TGATTTCAATCACAGTCTC--TATCAACGCCCTTATGGGGAACCTCTTAACCAAGGAACGTGC | 352 |
| OY | | 308 | TGACAGACTTATTGGGGAAGTAAAGGATATATGTTCAATTCAAGTCGCTGGAAGATGG | 367 |
| Db | | 353 | TGAGAGATTAA TTGTGGAGGTAAAGAAGATA--TTCAATTCAATGTACCTGGATGATGG | 409 |
| OY | | 368 | AGG-----CAATGATCTCCTTCAACGACTTTTGCTGCTGCATGACGTTGA | 412 |
| Db | | 410 | AAGATTATGAGTTCCTTAAATGATCTCATGCAACGCCCTTGATAGTGCATAGCGTTGA | 469 |
| OY | | 413 | ACGTTTGGGAATCGACAGGCATTTCAAAAAAGAGATAAAAACGGCACTCGATTATGTTAA | 472 |
| Db | | 470 | ACGTTTGGGATAGCTAGACATTTCAAGAACGAGATAACATCAGCTCTGGATTATGTTTT | 529 |
| OY | | 473 | CAGTTATTGGAACGAAAAAGGCATTGGATGTGGGAGGAGAGAGTGTGTGACTGACCTCAA | 532 |
| Db | | 530 | CCGTTACTGGAGAGAAACGGCATTTGATGTGGAGAGACAGTATGTTA CTGATCTCAA | 589 |
| OY | | 533 | CTCAACCGCCTTGGGCTTCGA ACTCTCCGACTACACGATPACA CTGTCTTCAGATGT | 592 |
| Db | | 590 | CTCAACTGCGTTGGGGTTTCGA ACTCTTCGATTACACGGGTACACTGTATCTCCAGAGGT | 649 |
| OY | | 593 | TTTGAACGTTT TTAAGACAAAATGGGCAATTTCTCCACTGSCCAATATTCAGATAGA | 652 |
| Db | | 650 | TTTAAAGCTTTTCAAGATCAAAATGACAGCTTTGTATGCTCCCCC--G GTCAGACAGACA | 706 |

```
QY 653 GGGAGATGTAGAGCGCTTCTCAATTTATTCAGGGCTCCCTCGTCGCTTTCCCGCGA 712
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 707 GGGTGAATCAGAAAGCGTTCTTAATCTATTCGGGCTTCCCTCATTCGCTTCCCTGGTGA 766
QY 713 GAAAGTTATGTAGAGCTGAACATTTCTTCAAAATATTTAAGAGAGCCCTGCAAA 772
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 767 GAAAGTTATGTAGAGAGCTGAATCTTCTCCACAAGATATTTGAAGAGAGCTCTACAAA 826
QY 773 GATTCCGGCATCCAGTATATCTTCACTAGATACGGGACGTTCTGGAAATATGTTGGCA 832
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 827 GATTCCAGTCTCCGCT--CTTCAACAAGATTAAGTTGTTATGGAATATGGCTGGCA 883
QY 833 CACCAATTGGCCACGCTTGGAAAGCAAGAAATTAATGACGCTTTGGAAGACACACTA- 891
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 884 CACAAATTTGCCAAGATTGGAAAGCAAGAAATTAATGACACACTTGAAGAAACACACAG 943
QY 892 -----AAATAAGAACGCCGCGAGAACTTTTGAACCTTGCAAAATTGGAATTCAA 943
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 944 TGCATGGCTCAATAAAATAGCTGGAAAGAGCTTTTGAACCTTGCAAAATTGGAAGTTCAA 1003
QY 944 TATATTTCACTCCTTACAAGAGAGAGTTAAACATGTTCCCGATGGTGAAGAGACTC 1003
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1004 TATATTTAACTCCTTACAACAAAAGAAATTAATATCTTTGAGATGGTGAAGAGAGTC 1063
QY 1004 GGGTCTCTCGAGATGACCTTCTGTCGACATCGTCACGTTGAATATCTAGCGCTTGGCTTC 1063
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1064 GGATTTGCTTAAATTGACATTTGCTCGGCACTGTCATGTGGAATTTTACACTTTGGCCTC 1123
QY 1064 CTGCATTGCGTTGAGCGCTCAACATTTGATTCAGACTCGGCTTTTACCAAGATGTTCTCA 1123
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1124 TTGTATGGCAATTGACCCAAACATTCTGCAATTGACACTAGGCTTCCGCAAAATGTCTCA 1183
QY 1124 TCTTATCAGCGTTCTTGAAGACATGTACGACGTTCTTGGCACAGTAGAGAGCTGGAAC 1183
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1184 TCTTGTACAGTTTGGACGATATTTAGACACTTTTGGAAAGATTTGAGAGCTTGAAC 1243
QY 1184 CTTCAAGCGCAATTAAGAGATGGATCCGCTCGGATGGAATGCCCTTCCAGATATATAT 1243
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1244 CTTCAATCTGCAATTAAGAGATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT 1303
QY 1244 GAAAGAGTTACATGATGTTTATCACACCGTAAATGAATGGCTCGAGTGGCAGAGAA 1303
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1304 GAAATGTGTACATGCTGCTGTGTAAGTGAATGTAATGTAATGTAATGTAATGTAATG 1363
QY 1304 GGGTCAAGGCGGAGACACGCTCAACTATGCAAGACAGGCTTGGAGGCGTGTGATTTC 1363
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1364 GACTCAAGGAGAAACACTCTCACTATGTTCGAAAGGCTTGGAGGCTTATTTGATTTC 1423
QY 1364 GTATATGCAAGAAAGCAAAAGTGTGATCGCCACTGTTATCTGCCACGTTTGAAGAGTACT 1423
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1424 ATATATGAGAAAGCAAAATGATCTCTAAATGTTATCTGCCAATGTTGAAGAGTACCA 1483
QY 1424 GGAGAAAGGAAAGTTAGCTCTGCTCATCGCCCATGCGCACTGCAACCCATCTGACGTT 1483
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1484 TGAGAAATGGGAAAGTGAAGCTCTGATATCGGCTGAGCAACATTTGCAACCCATCTCACT 1543
QY 1484 GGACATCCCTTTCTGATCACATCCCTCAAGGAAGTGAATCCCATGGAAGCTCAATGA 1543
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1544 GAATGCATGGCTTCTGATTAATCATCTTGAAGGAATGATTTTCCATCAAGTTCAATGA 1603
QY 1544 CTTGATATGATCATCTCTTGAATTAAGAGTGAATCAAGGCTTCAAGAGCAAGAGGCG 1603
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1604 TTTGGCATGCTCTTCTTCCGCTACGAGGTGAACACGCTGCTACAAAGGCGGATAGGGA 1663
QY 1604 CCGTGAAGAAAGCTTCTGTATATCATGTTATATGAAGACAACTCTGGAATTAACGGA 1663
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1664 TCGTGTGAAGAGCTTCTGTATATCATGTTATATGAAGACAACTCTGGAATCAACCGA 1723
QY 1664 AGAAGATGCTCTGAATCATATCACTTGAATGAGGAGCGCAATCAAGAAATTAATTTG 1723
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1724 AGAAGATGCTCTCAATCATATCAATGCAATGCTCAATGACATTAATTAATTAATTTG 1783
QY 1724 GGAGCTTCTAAAGCCAGACAAACAGTGTCCCATCACTTCAAGAAACAGCATTTGACAT 1783
```

```
Db 1784 GGAATCTTAAGATTCACACGACCAATATTTCCATGCTGCGCCAAAGAAACATGCTTTGACAT 1843
QY 1784 AAGCAGATTTGGGATCACGGTTACAGATACCGAGATGCTTACAGCTTTGCCAACGTTGA 1843
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1844 AACAGAGCTCTCCACCATCTCTACATATATGAGATGCTTTAGTGTGGCCAAAGAGA 1903
QY 1844 AACAAAGATTTGGTGTATGAGAACCGTCAATGGAACCTGTGCTTTGTAACAACACTTCAA 1903
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1904 AACAAAAAATTTGTTATGGAACACCTCTTGAATCTATGCTTTTAACTATAACCATATA 1963
QY 1904 ATCTACAATTAATGAGATGCGCTATGGGTATATATAGGAGACA 1950
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1964 TCCATAATATAAGCTCATATGCTTAAATTAATTTGGCCTTATGACATA 2010

RESULT 15
US-10-025-145A-1
; Sequence 1, Application US/10025145A
; Publication No. US20030175861A1
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B.
; APPLICANT: Bohlmann, Joeig
; APPLICANT: Steele, Christopher L.
; APPLICANT: Phillips, Michael A.
; TITLE OF INVENTION: Monoterpene Synthases from Grand Fir (Abies Grandis)
; FILE REFERENCE: WSUR118414
; CURRENT APPLICATION NUMBER: US/10/025,145A
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 09/360,545
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: PCT/US98/14528
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: US 60/052,249
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Abies Grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (69)..(1952)
; OTHER INFORMATION:
; US-10-025-145A-1

Query Match 53.2%; Score 1071.6; DB 15; Length 2196;
Best Local Similarity 75.0%; Pred. No. 1.4e-306;
Matches 1430; Conservative 0; Mismatches 441; Indels 36; Gaps 6;

QY 68 CAGTCTGCTCAGTTCTTCTCATGAGATTAAGGCTCTCCGTGAAACAATCCCACTCT 127
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 116 CAACTGTTGATCAGTTCAATTCATGAACATTAAGCCTCCCTATAGAACAAATCCCAATCT 175
QY 128 TGAATCTGCAAGGCGGGGAAATCCGTGCGCATTCATTAACATGTTGTGACAAAGCT 187
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 176 TGAATGCGTAGGCGAGGAAATCTGTCAAGCTTCATGAGCATCAAGTTGGCCACCGC 235
QY 188 CGCATCTAGTATCTGTACAGAGACGCTGGCAACTATCATTCCAACCTGTGGAGCA 247
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 236 TGACACCTGATGATGTTGACAAAGACGATAGTGACTACCATTCATCAATATCTGGAGCA 295
QY 248 TGATTTCAATACAGTCTCTGATCTCAAGCCTTATGAGACACCTGATTAACCGGAACGTGC 307
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 296 TGATTTCAATACAGTCTC--TATCAAGCCTTATGAGGAACCTCTTACAGAAAGTGC 352
QY 308 TGACAGACTTATTTGGGAAGTAAGATATAATGTTCAATTTCAAGTGGCTGGAAGATGG 367
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 353 TGAGAGATTAATTTGTGAGGTAAGAGATATA--TTCAATTTCAATGTAACCTGATGATGG 409
QY 368 AGG-----CAATGATCTCTTCAACGACTTTTGTGCTGATGACGTTGA 412
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```


Db 410 AAGATTAAAGTTCCTTTAATGATCTCATGCAACGCCCTTGGATAGTCGATAGCGTTGA 469
Qy 413 ACCTTTGGGAATCGACAGGCATTTCAAAAAAGAGATAAAAAACGCACTCGATTATGTTAA 472
Db 470 ACCGTTGGGATAGCTAGACATTTCAAGAACGAGATAACATCAGCTTGGAATTATGTTT 529
Qy 473 CAGTTATTGGAACGAAAAAGGCATTTGATGTGGAGGAGAGATGTTGTGACTGACCTCAA 532
Db 530 CCGTTACTGGGAGGAAAAACGCATTTGATGTGGAGAGACAGTATTTGTACTGATCTCAA 589
Qy 533 CTCAACGCCCTTGGGGCTTCGAACCTCCGACTACAGGATACACTGTGCTTCAGATGT 592
Db 590 CTCAACTGGCTTGGGGTTTCGAACCTTCGATTACACGGGTACACTGTATCTCCAGAGGT 649
Qy 593 TTTGAACGTTTTTAAAGACAAAAATGGGCAATTTCTCCCATGCAATATTCAGATAGA 652
Db 650 TTTAAAGCTTTTCAAGATCAAAAATGACAGTTGTATGCTCCCCC--GGTCAGACAGA 706
Qy 653 GGGAGATTAGAGCGCTTCTCAATTTATTCAGGGCCCTCCCTCGTGGCTTTCCCGCGA 712
Db 707 GGGTGAGATCAGAAAGCGTTCTTAATTAATCGGGCTTCCCTCATTTGCCCTTCCCTGTGA 766
Qy 713 GAAAGTTATGATGAGAAGCTGAAACATTTCTCAAAAATATTAAAGAAAGCCCTGCAAAA 772
Db 767 GAAAGTTATGAAAGAAAGCTGAAATCTTCTCCACAAGATATTGAAAGAAAGCTTACAAAA 826
Qy 773 GATTCCGGCATCCAGTATACTTTCACTAGAGATACGGGACGTTCTGGAATATGTGGCA 832
Db 827 GATTCAGTCTCCGCT--CTTTCAGAGAGATAAAGTTGTATGGAATATGGCTGCA 883
Qy 833 CACCAATTTGCCACGCTTGAAGCAAGAAATTAATGACGCTTTGACAGACACTA- 891
Db 884 CACAAATTTGCCAAGATTGGAAGCAAGAAATTAATGACACTGAGAAAGACACCAG 943
Qy 892 -----AAAAATAAGACGCCCCCGAGAACTTTTGAACCTTGCAAAATTGGAATTCAA 943
Db 944 TGCATGGCTCAATAAAAATGCTGGGAAGAGCTTTTGAACCTTGCAAAATTGGAATTCAA 1003
Qy 944 TATATTTCACTCCTTACAGAGAGAGAGTTAAAAATGTTCCCGATGGTGAAGAGACTC 1003
Db 1004 TATATTTAACTCCTTACAAACAAAAGAAATTAATATATCTTTGAGATGGTGAAGAGTTC 1063
Qy 1004 GGGTTCCTGAGATGACCTTCTGTCGATCGTCAAGTGAATACGCTTTGGCTTC 1063
Db 1064 GGATTTGCCCTAAATTGACATTTGCTCGGCATCGTCATGTGAATTTACACTTTGGCTTC 1123
Qy 1064 CTGCATGGCTTCGAGCCTCAACATTTGGAATTCAGACTCGGCTTTAACCAAGATGCTCA 1123
Db 1124 TTGTATGGCATTTGACCCAAACATCTTCGATTCAGACTAGGCTTCGCCAAATGTGCA 1183
Qy 1124 TCTTATCACGCTTCTTGACGACATGTACGACGCTTTCGSCACAGTAGACGAGCTGAACT 1183
Db 1184 TCTTGTACAGTTTTGACGATATTTACGACACTTTTGGAACGATTCGAGCTTGAACCT 1243
Qy 1184 CTTCAAGCGACAATTAAGAGATGGATCCGTCGCGATGGAATGCCCTTCAGAAATATAT 1243
Db 1244 CTTCAATCTGCAATTAAGAGATGGAATTCATCAGAGATAGAACACCTTCCAGAAATATAT 1303
Qy 1244 GAAAGAGTGTACATGATGTTTATCACACCGTAATGAAATGGCTCGAGTGGCAGAGAA 1303
Db 1304 GAAATGTGTACATGTCGTGTTTGAAACTGTAAATGAACTGACACGAGAGCGGAGAA 1363
Qy 1304 GGCCTAAGCCGAGACACGCTCAACTATGCAAGAAGAGGCTTGGAGCGCTGTTTGATTTC 1363
Db 1364 GACTCAAGGGAGAAACACTCTCAACTATGTTGAAAGGCTTGGAGGCTTATTTGATTTC 1423
Qy 1364 GTATATGCAAGCAAAAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1423
Db 1424 ATATATGGAAGAAAGCAAAATGATCTTAATGTTATCTGCAATGTTGAAGAGTACCA 1483
Qy 1424 GGAGAACGGGAAAGTTAGCTCTGCTCATTCGCCCATGCGCACTGCAACCCATTTCTGACGTT 1483
Db 1484 TGAAGATGGGAAAGTGAGCTCTGCATATCGCGTAGCAACATTGCAACCCATCTCACTTTT 1543

Qy 1484 GGACATCCCTTTCCTGATCACAATCCTCAAGGAAGTTGACTTCCCATCGAAGCTCAATGA 1543
Db 1544 GAATGCATGGCTTCCCTGATTAACATCTTGAAGGGAATTGATTTCCATCCAGGTTCAATGA 1603
Qy 1544 CTTGATATGATCATCCTTCGATTAAGAGGTGATACACGGTGTCTACAAGGCAGACAGGC 1603
Db 1604 TTTGGATCGTCTTCTCCCTCGGCTACGAGGTGACACACGCTGTCTACAAGGCCGATAGGA 1663
Qy 1604 CCGTGAGAGAAGAGCTTCGTTATATATCATGTTATATGAAGACAATCCTCGATTAAACGA 1663
Db 1664 TCGTGTGAAGAGAGCTTCGTATATATCATGTTATATGAAGACAATCCTCGATTCAACGA 1723
Qy 1664 AGAAGATGCTCTGAATCATATCACTTCATGATCAGGAGCGCAATCAGAAATTAATTG 1723
Db 1724 AGAAGATGCCCTCAATCATATCAATGCGCATGTCAATGACATTAATCAAAAGATTAAATTG 1783
Qy 1724 GAGCTTCTAAAGCCAGACAAAGTGTTCCTCATCTTCGAGAAACACGCATTTGACAT 1783
Db 1784 GGAATCTTAAGATCCAAACGACAATATTCGAATGCTGGCCAGAAACATGCTTTTGACAT 1843
Qy 1784 AAGCAGATTTGGCATCAGGTTACAGATACCGAGATGGCTACAGCTTTGCCAACGTTGA 1843
Db 1844 AACAGAGCTCTCCACCATCTCTACATATATCAGAGATGGCTTATGTTGCCAACAGGA 1903
Qy 1844 AACAAAGATTTGGTGTAGAGAACCGTCATTTGAACCTGTGCTTTGTAAACAACACTTCAA 1903
Db 1904 AACAAAAAATTGGTTATGAAACACTCCTTGAATCTATGCTTTTAACTATAACCATATA 1963
Qy 1904 ATCTACAATATTAATGAGGATGCCCTATGCGTGTATATAGGCACA 1950
Db 1964 TCCATTAATTAAGCTCATTAATGCTAAATTAATTGCGCTTATGACATA 2010

Search completed: July 26, 2004, 16:33:40
Job time : 3703 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 26, 2004, 09:57:57 ; Search time 7588 Seconds
(without alignments)
11498.356 Million cell updates/sec

Title: US-10-025-145A-64
Perfect score: 2013
Sequence: 1 ttttgacgtgcctcttctatc.....aaaaaaaaaaaaaaaaaaaa 2013

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vl:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
- 20: em_om:*
- 21: em_or:*
- 22: em_ov:*
- 23: em_pat:*
- 24: em_ph:*
- 25: em_pl:*
- 26: em_ro:*
- 27: em_sts:*
- 28: em_un:*
- 29: em_vi:*
- 30: em_htg_hum:*
- 31: em_htg_inv:*
- 32: em_htg_other:*
- 33: em_htg_mus:*
- 34: em_htg_pln:*
- 35: em_htg_rod:*
- 36: em_htg_mam:*
- 37: em_htg_vrt:*
- 38: em_sy:*
- 39: em_htgo_hum:*
- 40: em_htgo_mus:*
- 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|--------|-------------|--------|----|----------|--------------------|
| 1 | 2013 | 100.0 | 2013 | 6 | AR222136 | AR222136 Sequence |
| 2 | 2013 | 100.0 | 2013 | 8 | AGU87910 | U87910 Abies grand |
| 3 | 1306.8 | 64.9 | 2018 | 6 | BD227661 | BD227661 Synthes |
| 4 | 1306.8 | 64.9 | 2018 | 6 | AR222097 | AR222097 Sequence |
| 5 | 1306.8 | 64.9 | 2018 | 6 | AR240696 | AR240696 Sequence |
| 6 | 1306.8 | 64.9 | 2018 | 6 | AR266971 | AR266971 Sequence |
| 7 | 1306.8 | 64.9 | 2018 | 6 | AR316320 | AR316320 Sequence |
| 8 | 1306.8 | 64.9 | 2018 | 6 | AR338463 | AR338463 Sequence |
| 9 | 1306.8 | 64.9 | 2018 | 6 | AR429869 | AR429869 Sequence |
| 10 | 1306.8 | 64.9 | 2018 | 8 | AGU87909 | U87909 Abies grand |
| 11 | 1273.6 | 63.3 | 1958 | 8 | AY237645 | AY237645 Picea slt |
| 12 | 1178.4 | 58.5 | 2082 | 8 | AF543527 | AF543527 Pinus tae |
| 13 | 1155.6 | 57.4 | 2162 | 8 | AF543529 | AF543529 Pinus tae |
| 14 | 1103.2 | 54.8 | 2166 | 8 | AF461460 | AF461460 Picea abi |
| 15 | 1101.4 | 54.7 | 2168 | 8 | AF369918 | AF369918 Picea abi |
| 16 | 1095.4 | 54.4 | 1893 | 8 | AF139206 | AF139206 Abies gra |
| 17 | 1092.4 | 54.3 | 1890 | 6 | AR222146 | AR222146 Sequence |
| 18 | 1085.8 | 53.9 | 2160 | 8 | AF369919 | AF369919 Picea abi |
| 19 | 1072.4 | 53.3 | 2166 | 8 | AR222137 | AR222137 Sequence |
| 20 | 1072.4 | 53.3 | 2166 | 8 | AF139205 | AF139205 Abies gra |
| 21 | 1071.6 | 53.2 | 2196 | 6 | AR222096 | AR222096 Sequence |
| 22 | 1071.6 | 53.2 | 2196 | 6 | AR222096 | AR222096 Sequence |
| 23 | 1071.6 | 53.2 | 2196 | 6 | AR240701 | AR240701 Sequence |
| 24 | 1071.6 | 53.2 | 2196 | 6 | AR266976 | AR266976 Sequence |
| 25 | 1071.6 | 53.2 | 2196 | 6 | AR316325 | AR316325 Sequence |
| 26 | 1071.6 | 53.2 | 2196 | 6 | AR338468 | AR338468 Sequence |
| 27 | 1071.6 | 53.2 | 2196 | 6 | AR429874 | AR429874 Sequence |
| 28 | 1071.6 | 53.2 | 2196 | 8 | AGU87908 | U87908 Abies grand |
| 29 | 1071.6 | 53.2 | 2205 | 6 | AR222116 | AR222116 Sequence |
| 30 | 1040.2 | 51.7 | 2100 | 8 | AF543530 | AF543530 Pinus tae |
| 31 | 971.4 | 48.3 | 1960 | 8 | AF543531 | AF543531 Pinus tae |
| 32 | 929.4 | 46.2 | 2429 | 6 | AR222138 | AR222138 Sequence |
| 33 | 929.4 | 46.2 | 2429 | 6 | AF139207 | AF139207 Abies gra |
| 34 | 925.4 | 46.0 | 2089 | 6 | BD227677 | BD227677 Synthes |
| 35 | 925.4 | 46.0 | 2089 | 6 | AR222098 | AR222098 Sequence |
| 36 | 925.4 | 46.0 | 2089 | 6 | AR240712 | AR240712 Sequence |
| 37 | 925.4 | 46.0 | 2089 | 6 | AR266987 | AR266987 Sequence |
| 38 | 925.4 | 46.0 | 2089 | 6 | AR316336 | AR316336 Sequence |
| 39 | 925.4 | 46.0 | 2089 | 6 | AR338479 | AR338479 Sequence |
| 40 | 925.4 | 46.0 | 2089 | 6 | AR429885 | AR429885 Sequence |
| 41 | 925.4 | 46.0 | 2089 | 8 | AF006193 | AF006193 Abies gra |
| 42 | 889.4 | 44.2 | 2084 | 8 | AF543528 | AF543528 Pinus tae |
| 43 | 807.4 | 40.1 | 1513 | 6 | BD272958 | BD272958 Materials |
| 44 | 805.8 | 40.0 | 1634 | 6 | BD273051 | BD273051 Materials |
| 45 | 623.6 | 31.0 | 1173 | 6 | BD273050 | BD273050 Materials |

ALIGNMENTS

RESULT 1
AR222136
LOCUS AR222136 2013 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 64 from patent US 6429014.
ACCESSION AR222136
VERSION AR222136.1 GI:23329510
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2013)
AUTHORS Steele,C.L., Fohlmann,J. and Croteau,R.B.
TITLE Monoterpene syntheses from grand fir (Abies grandis)
JOURNAL Patent: US 6429014-A 64 06-AUG-2002;
FEATURES Location/Qualifiers

| | | |
|----------------------------|-----|--|
| source | | 1. .2013 |
| | | /organism="unknown" |
| | | /mol_type="genomic DNA" |
| Query Match | | 100.0%; Score 2013; DB 6; Length 2013; |
| Best Local Similarity | | 100.0%; Pred. No. 0; |
| Matches 2013; Conservative | | 0; Mismatches 0; Indels 0; Gaps 0; |
| Qy | 1 | TTTTGACGTGCGCTTCTTATCTGATAGCAAGCTGAATGGCTCTTCTTACTTACTCCGC 60 |
| Db | 1 | TTTTGACGTGCGCTTCTTATCTGATAGCAAGCTGAATGGCTCTTCTTCTAATTAATCTCCGC 60 |
| Qy | 61 | TGGTTCCAGGTGCTGCTCAGTTCCTCTCATAGATTAAAGGCTCTCCGTAGAACAAATCC 120 |
| Db | 61 | TGGTTCCAGGTGCTGCTCAGTTCCTCTCATAGATTAAAGGCTCTCCGTAGAACAAATCC 120 |
| Qy | 121 | CAACTCTTGGAAATCTGCAGGCGGGGAAATCCGTCCGCATTCATTAACATGTGTTGA 180 |
| Db | 121 | CAACTCTTGGAAATCTGCAGGCGGGGAAATCCGTCCGCATTCATTAACATGTGTTGA 180 |
| Qy | 181 | CAAGCGTCGCATCTACTGATTCGTACAGACGCGTGGGCACTATCATTTCCAACCTGT 240 |
| Db | 181 | CAAGCGTCGCATCTACTGATTCGTACAGACGCGTGGGCACTATCATTTCCAACCTGT 240 |
| Qy | 241 | GGGACGATGATTTTCATACAGTCTCTGATCTCAACGCCCTTATGGAGCACCTGATTACCGGG 300 |
| Db | 241 | GGGACGATGATTTTCATACAGTCTCTGATCTCAACGCCCTTATGGAGCACCTGATTACCGGG 300 |
| Qy | 301 | AACGTGCTGACAGACTTATTTGGGGAAGTAAAGGATATATATGTTCAATTTCAAGTCGCTGG 360 |
| Db | 301 | AACGTGCTGACAGACTTATTTGGGGAAGTAAAGGATATATATGTTCAATTTCAAGTCGCTGG 360 |
| Qy | 361 | AAGATGAGGCAATGATCTCCTTCAACGCACTTTTGCTGTCGATGACGTTGAACGTTTGG 420 |
| Db | 361 | AAGATGAGGCAATGATCTCCTTCAACGCACTTTTGCTGTCGATGACGTTGAACGTTTGG 420 |
| Qy | 421 | GAATCGACAGGCATTTCAAAAAAGAGATTAACGCGACTCGATTATGTTAAACAGTTATT 480 |
| Db | 421 | GAATCGACAGGCATTTCAAAAAAGAGATTAACGCGACTCGATTATGTTAAACAGTTATT 480 |
| Qy | 481 | GGAACGAAAAAGGCATTGGATGTGGAGGGAGAGTGTGTGACTGACTCAACTCAACCG 540 |
| Db | 481 | GGAACGAAAAAGGCATTGGATGTGGAGGGAGAGTGTGTGACTGACTCAACTCAACCG 540 |
| Qy | 541 | CCTTGGGGCTTCGAACCTCTCCGACTACGCGATACACTGTGTCTTCAGATGTTTGAACG 600 |
| Db | 541 | CCTTGGGGCTTCGAACCTCTCCGACTACGCGATACACTGTGTCTTCAGATGTTTGAACG 600 |
| Qy | 601 | TTTTTAAAGCAAAAAATGGGCAATTTTCTCTCACTGCCAATATTCAGATAGAGGGAGAGA 660 |
| Db | 601 | TTTTTAAAGCAAAAAATGGGCAATTTTCTCTCACTGCCAATATTCAGATAGAGGGAGAGA 660 |
| Qy | 661 | TTAGAGCGTTCCTCAATTATTCAGGGCCTCCTCGTCCCTTTCCGGCGAGAAAGTTA 720 |
| Db | 661 | TTAGAGCGTTCCTCAATTATTCAGGGCCTCCTCGTCCCTTTCCGGCGAGAAAGTTA 720 |
| Qy | 721 | TGGATGAGCTGAACAATTCTCTACAAAAATATTTAAGAGAAGCCCTGCAAAAAGATTCCGG 780 |
| Db | 721 | TGGATGAGCTGAACAATTCTCTACAAAAATATTTAAGAGAAGCCCTGCAAAAAGATTCCGG 780 |
| Qy | 781 | CATCCAGTATACTTTCAC TAGAGATACGGGACGTTCTGGAATATGTTGGCACACCAATT 840 |
| Db | 781 | CATCCAGTATACTTTCAC TAGAGATACGGGACGTTCTGGAATATGTTGGCACACCAATT 840 |
| Qy | 841 | TGCCACGCTTGGAAAGCAAGGAATTACATGSAAGTCTTTGGACAGCACACTAAAAATTAAGA 900 |
| Db | 841 | TGCCACGCTTGGAAAGCAAGGAATTACATGSAAGTCTTTGGACAGCACACTAAAAATTAAGA 900 |
| Qy | 901 | ACGCCGCCGAGAAACTTTTAGAAGCTTGCAAAATTTGAATTCATATATTTCACTCCTTAC 960 |
| Db | 901 | ACGCCGCCGAGAAACTTTTAGAAGCTTGCAAAATTTGAATTCATATATTTCACTCCTTAC 960 |

| | | |
|----|------|--|
| Qy | 961 | AAGAGAGAGGTTAAAAACATGTTTCCCGATGCTGGGAAAGACTCGGGGTTCTCTGAGATGA 1020 |
| Db | 961 | AAGAGAGAGGTTAAAAACATGTTTCCGATGCTGGGAAAGACTCGGGGTTCTCTGAGATGA 1020 |
| Qy | 1021 | CCTTCGTGACATCGTCAACGTGGAATACTACGCTTTGGCTTCGTGATGCGTTGAGC 1080 |
| Db | 1021 | CCTTCGTGACATCGTCAACGTGGAATACTACGCTTTGGCTTCGTGATGCGTTGAGC 1080 |
| Qy | 1081 | CTCAACATTCGTGATTTCAGACTCGGCTTTACCAAGATGTCTCATCTTATCACGCTTCTTG 1140 |
| Db | 1081 | CTCAACATTCGTGATTTCAGACTCGGCTTTACCAAGATGTCTCATCTTATCACGCTTCTTG 1140 |
| Qy | 1141 | ACGACATGTACGACGCTTCGGGACAGTAGACGAGCTGGAATCTTCACAGCGACAATTA 1200 |
| Db | 1141 | ACGACATGTACGACGCTTCGGGACAGTAGACGAGCTGGAATCTTCACAGCGACAATTA 1200 |
| Qy | 1201 | AGAGATGGGATCCGTCGCGGATGGAATGCCCTTCAGAAATATATGAAGAAGGTACATGA 1260 |
| Db | 1201 | AGAGATGGGATCCGTCGCGGATGGAATGCCCTTCAGAAATATATGAAGAAGGTACATGA 1260 |
| Qy | 1261 | TGGTTATACACCCGTAAATGAATGGCTCGAGTGGCAGAGAGGCTCAAGGCCGAGACA 1320 |
| Db | 1261 | TGGTTATACACCCGTAAATGAATGGCTCGAGTGGCAGAGAGGCTCAAGGCCGAGACA 1320 |
| Qy | 1321 | CGCTCAACTATGCAAGACAGGCTTTGGGAGCGTGTGTTGATTCGTATATGACAGGAACAA 1380 |
| Db | 1321 | CGCTCAACTATGCAAGACAGGCTTTGGGAGCGTGTGTTGATTCGTATATGACAGGAACAA 1380 |
| Qy | 1381 | AGTGAATGCCACTGTTATCTGCCACGTTTGAGAGATGACTTGAGAAACGGGAAAGTTA 1440 |
| Db | 1381 | AGTGAATGCCACTGTTATCTGCCACGTTTGAGAGATGACTTGAGAAACGGGAAAGTTA 1440 |
| Qy | 1441 | GCTGTGCTCATCGCCCATCGCGCACTGCAACCCATTCTGACGTTGACATCCCTTTCCTG 1500 |
| Db | 1441 | GCTGTGCTCATCGCCCATCGCGCACTGCAACCCATTCTGACGTTGACATCCCTTTCCTG 1500 |
| Qy | 1501 | ATCACATCTCAAGGAAGTTGACTTCCCATCGAAGCTCAATGACTTGATATGTATCATCC 1560 |
| Db | 1501 | ATCACATCTCAAGGAAGTTGACTTCCCATCGAAGCTCAATGACTTGATATGTATCATCC 1560 |
| Qy | 1561 | TTGATTAAGAGGTATACACGCTGCTACAAGGCAGACAGGCGCGTGAGAGAAAGCTT 1620 |
| Db | 1561 | TTGATTAAGAGGTATACACGCTGCTACAAGGCAGACAGGCGCGTGAGAGAAAGCTT 1620 |
| Qy | 1621 | CGTCTATATCATGTTATATGAAGAACAATCCTGATTAAACGGAAGAAGTCTCTGAATC 1680 |
| Db | 1621 | CGTCTATATCATGTTATATGAAGAACAATCCTGATTAAACGGAAGAAGTCTCTGAATC 1680 |
| Qy | 1681 | ATATCAACTTCATGATCAGGAGCAATCAGAGAATTAAATGGAGCTTCTAAAGCCAG 1740 |
| Db | 1681 | ATATCAACTTCATGATCAGGAGCAATCAGAGAATTAAATGGAGCTTCTAAAGCCAG 1740 |
| Qy | 1741 | ACAAACGTGTTCCCATCACTTCCAAGAAACACGCAATTTGACATAAGCAGATTGGCATC 1800 |
| Db | 1741 | ACAAACGTGTTCCCATCACTTCCAAGAAACACGCAATTTGACATAAGCAGATTGGCATC 1800 |
| Qy | 1801 | ACGGTACAGATACCGAGATGGCTACAGCTTTGCCAACGTTGAAAACAAAGAGTTGGTGA 1860 |
| Db | 1801 | ACGGTACAGATACCGAGATGGCTACAGCTTTGCCAACGTTGAAAACAAAGAGTTGGTGA 1860 |
| Qy | 1861 | TGAGAACGTCATTGAAACCTGTGCTTTGTAAACAACACTCAAAATCTACAATATTAAC TG 1920 |
| Db | 1861 | TGAGAACGTCATTGAAACCTGTGCTTTGTAAACAACACTCAAAATCTACAATATTAAC TG 1920 |
| Qy | 1921 | AGGATGCCCTATGGGTATATATAGGGCACACAAAAATAAATATGTTGTGTAGTAAAGC 1980 |
| Db | 1921 | AGGATGCCCTATGGGTATATATAGGGCACACAAAAATAAATATGTTGTGTAGTAAAGC 1980 |
| Qy | 1981 | TGTAATTATGAAAAAAAAAAAAAAAAAAAAAA 2013 |
| Db | 1981 | TGTAATTATGAAAAAAAAAAAAAAAAAAAAAA 2013 |

RESULT 2
LOCUS AGU87910 2013 bp mRNA linear PLN 10-AUG-2001
DEFINITION Abies grandis (-)-camphene synthase (AG6.5) mRNA, complete cds.
ACCESSION U87910
VERSION U87910.1 GI:2411484
KEYWORDS Abies grandis
SOURCE Abies grandis
ORGANISM Abies grandis
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.
AUTHORS 1 (bases 1 to 2013)
TITLE Bohlmann, J., Steele, C.L. and Croteau, R.
Monoterpene synthases from grand fir (Abies grandis). cDNA
isolation, characterization, and functional expression of myrcene
synthase, (-)-(4S)-limonene synthase, and (-)-(1S,5S)-pinene
synthase
JOURNAL J. Biol. Chem. 272 (35), 21784-21792 (1997)
MEDLINE 97413772
PubMed 9268308
REFERENCE 2 (bases 1 to 2013)
AUTHORS Bohlmann, J., Phillips, M., Ramachandiran, V., Katoh, S. and Croteau, R.
cDNA cloning, characterization, and functional expression of four
new monoterpene synthase members of the Tpsd gene family from grand
fir (Abies grandis)
JOURNAL Arch. Biochem. Biophys. 368 (2), 232-243 (1999)
MEDLINE 99373092
PubMed 10441373
REFERENCE 3 (bases 1 to 2013)
AUTHORS Bohlmann, J., Steele, C.L. and Croteau, R.
Direct Submission
TITLE Submitted (31-JAN-1997) Institute of Biological Chemistry,
JOURNAL Washington State University, Clark Hall, Pullman, WA 99164-6340,
USA

FEATURES
Source location/Qualifiers
1..2013
/organism="Abies grandis"
/mol_type="mRNA"
/db_xref="taxon:46611"
1..2013
/gene="AG6.5"
36..1892
/gene="AG6.5"
/note="terpene synthase; monoterpene synthase; terpene
cyclase"
/codon_start=1
/product="(-)-camphene synthase"
/protein_id="AAB70707.1"
/db_xref="GI:2411485"

gene
CDS
36..1892
/gene="AG6.5"

ORIGIN
Query Match 100.0%; Score 2013; DB 8; Length 2013;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2013; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 TTTTGACGCTCTTCTATATGATAGCAAGCTGAATGCTCTTCTTCTATTACTCCGC 60
1 TTTTGACGCTCTTCTATATGATAGCAAGCTGAATGCTCTTCTTCTATTACTCCGC 60
61 TGGTTCCAGGCTGCTGCTCAGTCTTCTTCATGAGATTAAAGCTCTCCGTAGAACATCC 120
61 TGGTTCCAGGCTGCTGCTCAGTCTTCTTCATGAGATTAAAGCTCTCCGTAGAACATCC 120

QY 121 CAACCTCTTGAATCTGACGACCGGGGAAATCCGTCGCATTCATTAACATGTGTTGA 180
DB 121 CAACCTCTTGAATCTGACGACCGGGGAAATCCGTCGCATTCATTAACATGTGTTGA 180
QY 181 CAAGCGTCGATCTACTGATCTGTACAGACGCGTGGCAACTATCATCCAACTGT 240
DB 181 CAAGCGTCGATCTACTGATCTGTACAGACGCGTGGCAACTATCATCCAACTGT 240
QY 241 GGGACGATGATTTATACAGTCTCTGATCTCAACGCCCTTATGAGACCTGATTACCGGG 300
DB 241 GGGACGATGATTTATACAGTCTCTGATCTCAACGCCCTTATGAGACCTGATTACCGGG 300
QY 301 AACGTCGTACAGACTTATGGGGAAGTAAAGGATATATGTTCAATTTCAAGTCGCTGG 360
DB 301 AACGTCGTACAGACTTATGGGGAAGTAAAGGATATATGTTCAATTTCAAGTCGCTGG 360
QY 361 AAGATGAGGCAATGATCTCTTCAACGACTTTGCTGTCGATGACGTTGAACGTTGG 420
DB 361 AAGATGAGGCAATGATCTCTTCAACGACTTTGCTGTCGATGACGTTGAACGTTGG 420
QY 421 GAATCGACGCAATTTCAAAAAAGATTA AAAACGGCACTCGATTAATGTTAAACAGTTAT 480
DB 421 GAATCGACGCAATTTCAAAAAAGATTA AAAACGGCACTCGATTAATGTTAAACAGTTAT 480
QY 481 GGAACGAAAAAGCATTTGATGTGGAGGAGAGTGTGTGATGACCTCAACTCAACCG 540
DB 481 GGAACGAAAAAGCATTTGATGTGGAGGAGAGTGTGTGATGACCTCAACTCAACCG 540
QY 541 CCTGGGCTTCGAATCTCTCCGACTACACGGATACACTGTGTCTTCAAGATTTTGAACG 600
DB 541 CCTGGGCTTCGAATCTCTCCGACTACACGGATACACTGTGTCTTCAAGATTTTGAACG 600
QY 601 TTTTAAAGACAATAATGGGCAATTTCTCCACTGCCAATATTCAGATAGAGGAGAGA 660
DB 601 TTTTAAAGACAATAATGGGCAATTTCTCCACTGCCAATATTCAGATAGAGGAGAGA 660
QY 661 TTAGAGGCTTCATTTATTCAGGCTCTCCCTGTCGCTTCCGGCGAGAAAGTTA 720
DB 661 TTAGAGGCTTCATTTATTCAGGCTCTCCCTGTCGCTTCCGGCGAGAAAGTTA 720
QY 721 TGGATGAAGCTGAACATTTCTCAAAATATTTAAGAAAGCCCTGCAAAAGATTCCGG 780
DB 721 TGGATGAAGCTGAACATTTCTCAAAATATTTAAGAAAGCCCTGCAAAAGATTCCGG 780
QY 781 CATCCAGTATCTTCACTAGAGATACGGAGCTTCTGAATATGCTTGGCACACCAATT 840
DB 781 CATCCAGTATCTTCACTAGAGATACGGAGCTTCTGAATATGCTTGGCACACCAATT 840
QY 841 TGCCACGCTTGGAAAGCAAGGAATTACATGACGCTTTGGACAGACACTAAATAAGA 900
DB 841 TGCCACGCTTGGAAAGCAAGGAATTACATGACGCTTTGGACAGACACTAAATAAGA 900
QY 901 ACGCCGCGAGAACTTTAGAACTTGCAAAATTGGAATTCAATATTTCACTCCTTAC 960
DB 901 ACGCCGCGAGAACTTTAGAACTTGCAAAATTGGAATTCAATATTTCACTCCTTAC 960
QY 961 AAGAGAGAGTTAAACATGTTCCGATGCTGGAAGAGACTCGGCTCTCTGAGATGA 1020
DB 961 AAGAGAGAGTTAAACATGTTCCGATGCTGGAAGAGACTCGGCTCTCTGAGATGA 1020
QY 1021 CCTCTGTCGACATCTGTCAGTGAATACTAGCGCTTGGCTTCCGATTCGAGC 1080
DB 1021 CCTCTGTCGACATCTGTCAGTGAATACTAGCGCTTGGCTTCCGATTCGAGC 1080
QY 1081 CTCAACATCTGATTCAGACTCGGCTTACCAAGATGTCTCATCTTATCACGGTCTTG 1140
DB 1081 CTCAACATCTGATTCAGACTCGGCTTACCAAGATGTCTCATCTTATCACGGTCTTG 1140
QY 1141 ACGACATGATACGAGCTCTTGGCACAGTAGACGAGCTGGAATCTTACAGCGACAATTA 1200
DB 1141 ACGACATGATACGAGCTCTTGGCACAGTAGACGAGCTGGAATCTTACAGCGACAATTA 1200

| | | | |
|----|------|---|------|
| QY | 1201 | AGAGATGGATCCGTCGCGATGGAATGCTTCCAGATATATGAAAGAGGTGTACATGA | 1260 |
| Db | 1201 | AGAGATGGATCCGTCGCGATGGAATGCTTCCAGATATATGAAAGAGGTGTACATGA | 1260 |
| QY | 1261 | TGTTTATCAACCCGTAATGAATGGCTCGAGTGGCAGAGAAAGCTCAAGCCGAGACA | 1320 |
| Db | 1261 | TGTTTATCAACCCGTAATGAATGGCTCGAGTGGCAGAGAAAGCTCAAGCCGAGACA | 1320 |
| QY | 1321 | CGCTCAACTATGCAAGACAGAGCTTGGGAGCGTGTGTTGATTCGTATATGCAAGAGCAA | 1380 |
| Db | 1321 | CGCTCAACTATGCAAGACAGAGCTTGGGAGCGTGTGTTGATTCGTATATGCAAGAGCAA | 1380 |
| QY | 1381 | AGTGATCGCACTGTTATCTGCCACGTTTGAGAGTACTTGGAGAACGGGAAGTTA | 1440 |
| Db | 1381 | AGTGATCGCACTGTTATCTGCCACGTTTGAGAGTACTTGGAGAACGGGAAGTTA | 1440 |
| QY | 1441 | GCTCTGCTATCGCCCATGCGCACTGCAACCCATTTCTGACGTTGGACATCCCTTCC | 1500 |
| Db | 1441 | GCTCTGCTATCGCCCATGCGCACTGCAACCCATTTCTGACGTTGGACATCCCTTCC | 1500 |
| QY | 1501 | ATCACATCTCAAGGAAGTTGACTTCCATCGAAGCTCAATGACTTGATATGTCATCC | 1560 |
| Db | 1501 | ATCACATCTCAAGGAAGTTGACTTCCATCGAAGCTCAATGACTTGATATGTCATCC | 1560 |
| QY | 1561 | TTTGATTAAGAGGTGATACACGCTGCTCAAGGCAAGACAGGCGCCGTGGAAGAAGCTT | 1620 |
| Db | 1561 | TTTGATTAAGAGGTGATACACGCTGCTCAAGGCAAGACAGGCGCCGTGGAAGAAGCTT | 1620 |
| QY | 1621 | CGCTATATCATGTTATATGAAAGACAATCCTGATTAACGGAAGATGCTCTGAATC | 1680 |
| Db | 1621 | CGCTATATCATGTTATATGAAAGACAATCCTGATTAACGGAAGATGCTCTGAATC | 1680 |
| QY | 1681 | ATATCAACTTCATGATCAGGAGCGCAATCAGAGAATTAATTGGAGCTTCTAAAGCCAG | 1740 |
| Db | 1681 | ATATCAACTTCATGATCAGGAGCGCAATCAGAGAATTAATTGGAGCTTCTAAAGCCAG | 1740 |
| QY | 1741 | ACAACAGTGTCCCATCACTTCCAAAGAAACGCAATTTGACATTAAGCAGATTGGCATC | 1800 |
| Db | 1741 | ACAACAGTGTCCCATCACTTCCAAAGAAACGCAATTTGACATTAAGCAGATTGGCATC | 1800 |
| QY | 1801 | ACGGTTACAGATACCGAGATGGCTACAGCTTTGCCAAGTTGAACAAGAGTTGGTGA | 1860 |
| Db | 1801 | ACGGTTACAGATACCGAGATGGCTACAGCTTTGCCAAGTTGAACAAGAGTTGGTGA | 1860 |
| QY | 1861 | TGAGAACCGTCATTTGAACCTGTGCTTTGTAACAACACTTCAATCTAATAATTAAC | 1920 |
| Db | 1861 | TGAGAACCGTCATTTGAACCTGTGCTTTGTAACAACACTTCAATCTAATAATTAAC | 1920 |
| QY | 1921 | AGGATGCCCTATGGGTGTATATAGGGCACAAAAATAATATGTTGTGTAGTAAGC | 1980 |
| Db | 1921 | AGGATGCCCTATGGGTGTATATAGGGCACAAAAATAATATGTTGTGTAGTAAGC | 1980 |
| QY | 1981 | TGTAATTTATCAAAAAAAAAAAAAAAAAAAAAA 2013 | |
| Db | 1981 | TGTAATTTATCAAAAAAAAAAAAAAAAAAAAAA 2013 | |

RESULT 3
BD227661
LOCUS BD227661 2018 bp DNA linear PAT 17-JUL-2003
DEFINITION Synthesises.
ACCESSION BD227661 GI:33037431
VERSION BD227661.1
KEYWORDS JP 2002526066-A/13.
SOURCE
ORGANISM Abies grandis
Abies grandis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.
REFERENCE 1 (bases 1 to 2018)
AUTHORS Chappell,J., Manna,K.R., Noel,J.P. and Starks,C.M.
TITLE Synthesises
JOURNAL Patent: JP 2002526066-A 13 20-AUG-2002;
UNIVERSITY OF KENTUCKY RESEARCH DEPARTMENT, THE SALK INSTITUTE FOR

COMMENT BIOLOGICAL STUDIES SECRETARY DEPARTMENT OF HEALTH AND HUMAN SERVICES
OS Abies grandis (giant fir)
PN JP 2002526066-A/13
PD 20-AUG-2002
PF 17-SEP-1999 JP 2000574228
PR 18-SEP-1998 US 60/100993,22-APR-1999 US 60/130628 PR
23-AUG-1999 US 60/150262
PI JOSEPH CHAPPELL, KATHLEEN R MANNA, JOSEPH P NOEL, COURTNEY M PI STARKS
PC C12N15/09,A01H5/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/PC 10,C12N9/12,
PC C12O1/25,G01N33/68//((C12N9/12,C12R1:91),(C12N9/12,C12R1:19),
PC C12N15/00,
PC C12N5/00,C12N5/00
CC pinene synthase
FH key Location/Qualifiers
FT CDS (6)..(1889).
FEATURES
source location/Qualifiers
1..2018
/organism="Abies grandis"
/mol_type="genomic DNA"
/db_xref="taxon:46611"

ORIGIN

Query Match 64.9%; Score 1306.8; DB 6; Length 2018;
Best Local Similarity 81.0%; Pred. No. 0;
Matches 1595; Conservative 0; Mismatches 342; Indels 33; Gaps 5;

| | | | |
|----|-----|---|-----|
| QY | 68 | CAGTCGTCCTCAGTCTCTTCATGAGATTAAAGGCTCTCCGTAGAACAAATCCCACTCT | 127 |
| Db | 53 | CAATCGTTGATCAGTCTTACCATGAGCTTAAAGGCTCTCTCTAGAACAAATCCCACTCT | 112 |
| QY | 128 | TGGAATCTGACGCGCGGAAATCCGTCCGCAATCCATAAATCATGTGTTGACAAAGCGT | 187 |
| Db | 113 | AGGAATGAGTAGGCGAGGAAATCTATCACTCTCCATCAGCATGAGCTTACCACCGT | 172 |
| QY | 188 | CGCATCTACTGATTCTGTACAGACGCGTGGGCAACTATCAATCCAACTGTGGAGCA | 247 |
| Db | 173 | TGTAACGATGATGTTGTAAGAACGCGATGGCGATTTCCATTCCAACTCTGGAGCA | 232 |
| QY | 248 | TGATTTCAATACAGTCTCTGATCTCAACGCTTATGAGACACCTGATTAACGGGAACGTG | 307 |
| Db | 233 | TGATGTATACAGTCT--TTACCAACGCTTATGAGGAAATCGTACCTGAGCGTGC | 289 |
| QY | 308 | TGACAGCTTATTTGGGGAAGTAAGATATATATGTTCAATTTCAAGTCGCTGGAAGATG | 367 |
| Db | 290 | TGAGAACTGATCGGGGAAGTAAG--AACATGTTCAATTCGATGTCAATTAAGAAATGG | 346 |
| QY | 368 | AG-----GCAATGATCTCTCTTCAACGACTTTGCTGTGATGACGTTGA | 412 |
| Db | 347 | AGAGTTAATGAGTCGCGCTCAATGATCTCATTTCAACGCTTTGATGTGACAGCCTTGA | 406 |
| QY | 413 | ACGTTTGGAAATGCACAGGCAATTTCAAAAAAGAGATAAAAAAGCACTGATATGTTAA | 472 |
| Db | 407 | ACGTTTGGGATCCATAGACATTTCAAAAGATGAGATAAAATCGCGCTTGATATGTTTA | 466 |
| QY | 473 | CAGTTATTGCAACGAAAAAGCAATGAGTGTGGAGGAGAGTGTGTGACTGACCTCAA | 532 |
| Db | 467 | CAGTTATTGGGGCGAAAAATGGCATCGGATCGGGAGGAGAGTGTGTACTGATCTGAA | 526 |
| QY | 533 | CTCAACCGCTTGGGCTTGCAACTCCGACTACACGGAATACACTGTGTCTTCAGATGT | 592 |
| Db | 527 | CTCACTGCGTTGGGCTTGCAACTCAGACTACACGGAATACCGGCTCTTCAGATGT | 586 |
| QY | 593 | TTTGAACGTTTAAAGCAAAAAATGGGCAATTTCTCCACTGCCAATATTCAGATAGA | 652 |
| Db | 587 | TTTCAAGCTTTCAAAAGGCCAAAAATGGGCAATTTCTCTGCTGTAATAATATTCAGACAGA | 646 |
| QY | 653 | GGGAGAGTTAGAGGCGTTCTCAATTTATTCAGGGCTCTCCCTGCTTCCGGCGGA | 712 |
| Db | 647 | TGAAGAGATCAGAGCGTTCTGAATTTATTCGGGCTCTCCATTTGCTTCCAGGGGA | 706 |

| | | | |
|----|------|---|------|
| QY | 713 | GAAAGTTATGATGAAGCTGAAACATTTCTCTACAAATAATTAAAGAAAGCCCTGCAAA | 772 |
| Db | 707 | GAAAATTATGATGAGGCTGAAATCTTCTCTACCAAAATATTTAAAGAAAGCCCTGCAAA | 766 |
| QY | 773 | GATTCGGCATCCAGTATACTTCACTAGAGATACGGGCGTCTTGGATATATGTTGGCA | 832 |
| Db | 767 | GATTCGGTCTCCAGT---CTTCCGAGAGATCGGGGACGTTTGGATATATGTTGGCA | 823 |
| QY | 833 | CACCAATTTGCCACGCTTGGAAGCAAGGAATTACATGGAAGTCTTTGGACAGCACACTAA | 892 |
| Db | 824 | CACATATTTGCCCGGATTTGGAAGCAAGGAATTACATCCAGTCTTTGGACAGCACACTGA | 883 |
| QY | 893 | AAATAAGAACGC-----CGCCGAGAAACTTTTGAACCTTGCAAAATTGGAATTCAA | 943 |
| Db | 884 | GAAACAGAACTATATGTGAAGAGCAAAAACTTTAGAACTGCAAAAAATTGGAGTTCAA | 943 |
| QY | 944 | TATATTTCACTCCTTACAGAGAGAGAGATTAAACATGTTTCCGATGTTGAAAGACTC | 1003 |
| Db | 944 | CATCTTCAATCCTTACAAAGAGGAGTTAGAAAGTCTGTCAGATGTTGAAAGAAATC | 1003 |
| QY | 1004 | GGGTTCTCCTGAGATGACCTTCTGTGCACATCGTCAAGTGAATACTACGCTTTGGCTTC | 1063 |
| Db | 1004 | GGGTTTCTCGATGATGACCTTCTGCCGACATCGTCAAGTGAATACTACACTTTGGCTTC | 1063 |
| QY | 1064 | CTGCATTGCGTTCGAGCCTCAACATTTCTGGATTCAAGCTCGGCTTTACCAAGATGTCTCA | 1123 |
| Db | 1064 | CTGCATTGCGTTCGAGCCTCAACATTTCTGGATTCAAGCTCGGCTTTGCCAAGACGTCTCA | 1123 |
| QY | 1124 | TCTTATCACGGTCTTGAAGCATGTACGACGCTTTCGGCACAGTAGACGAGCTGGAAT | 1183 |
| Db | 1124 | TCTTATCACGGTCTTGAAGCATGTGTACGACACCTTCGGCACAGTAGACGAGCTGGAAT | 1183 |
| QY | 1184 | CTTCACAGCGACAATTAAGATGGGATCCGTCGGCGATGGAATGCTTCAGAAATATAT | 1243 |
| Db | 1184 | CTTCACAGCGACAATGAAGATGGGATCCGTCCTGATGATGCTTCAGAAATATAT | 1243 |
| QY | 1244 | GAAAGAGTATACATGATGCTTTATCACACCGTAAATGAATGGCTCGAGTGCGACAGAA | 1303 |
| Db | 1244 | GAAAGAGTATACATAGCGGTTTACGACACCGTAAATGAATGGCTCGAGAGCGACAGGA | 1303 |
| QY | 1304 | GGCTCAAGGCCGAGACACGCTCAACTATGCAAGACAGGCTTGGGAGCGTTTTGATTC | 1363 |
| Db | 1304 | GGCTCAAGGCCGAGATACGCTCACATATGCTCGGGAAGCTTGGGAGGCTTATATTGATTC | 1363 |
| QY | 1364 | GTATATGCAAGGAAGCAAGTGGATCGCCACTGGTTATCTGCCACGTTTGAGGATTA | 1423 |
| Db | 1364 | GTATATGCAAGGAAGCAAGTGGATCGCCACTGGTTATCTGCCCTCTTTGATGAGTACTA | 1423 |
| QY | 1424 | GGAGAACGGGAAAGTTAGCTCTGCTCATCGCCCATGGCGACCTGCAACCCATTTCTGACGTT | 1483 |
| Db | 1424 | CGAGAAATGGAAAGTTAGCTGTGTGTCATCGCATATCGCAATTCGCAACCCATTTCTGACAA | 1483 |
| QY | 1484 | GGACATCCCCCTTCTGTATCAATCTCAAGGAAGTTGACTTCCATCGGAAGCTCAATGA | 1543 |
| Db | 1484 | GGACATCCCCCTTCTGTATCAATCTCAAGGAAGTTGACTTCCATCAAAAGCTTAAAGCA | 1543 |
| QY | 1544 | CTTGATATGTATCATCTTCGATTAAGAGGTGATACACGGTGTCTTCAAGGCGACAGAGGC | 1603 |
| Db | 1544 | CTTGCAATGTGCATCTTCGATTAAGAGGTGATACGCGGTGTCTTCAAGGCGACAGAGGC | 1603 |
| QY | 1604 | CCGTGAGAGAAGCTTCGTCTATATCATGTATATGAAGACAATCCCTGGATTAAAGGA | 1663 |
| Db | 1604 | TCGTGAGAGAAGCTTCCTCTATATCATGTATATGAAGACAATCCCTGGAGTATCAGA | 1663 |
| QY | 1664 | AGAAAGTGTCTCTGAATCATATCAACTTCATGATCAAGGAGCGCAATCAGAGATTTAAATTG | 1723 |
| Db | 1664 | GGAAAGTGTCTCTGAATCATATCAACGCCATGATCAAGTACGTTAATCAAAAGATTTAAATTG | 1723 |
| QY | 1724 | GGAGCTTCTTAAAGCCAGACACAGTGTTCCTCATCACTTCCAGAAACACGCAATTTGACAT | 1783 |
| Db | 1724 | GGAACTTCTCAAAACAGACATCAATGTTCCCATCTCGGCGAAGAAACATGCTTTTGACAT | 1783 |
| QY | 1784 | AAGCAGAGTTTGGCATCACGGTTACAGATACCGAGATGGCTACAGCTTTGCCAACGTTGA | 1843 |

| Db | 1784 | CGCCAGAGCTTCCATTACGCGCTACAATAACGAGACGGCTACAGCGTTGCCAAGCTTGA | 1843 |
|-----------------------|---|---|----------------------------|
| QY | 1844 | AACAAAGAGTTTGTTGATGAGAACCCGTCATTGAACTGTGCCCTTGTAAACAACACTTCAA | 1903 |
| Db | 1844 | AACGAAAGATTGTGTCACGAGAACCCCTCCTTGAATCTGTGCCCTTGTAGCAACAGCTCAA | 1903 |
| QY | 1904 | ATCTACAATATTAAGTGAAGGATGCCCTATGGGTATATAGGGCACACAAAAATTAATAT | 1963 |
| Db | 1904 | ATCTATGCCCTATGCTATGTGCGGTTAAATAATATATGTGAAGGTAGCCGTTGATGTAGA | 1963 |
| QY | 1964 | GGTTGTGTAGTAAAGCTGTATTATGAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAA | 2013 |
| Db | 1964 | GGATAAGTTTGTATTAATTTAATTAAGTTGTAAATTTTAAAAAATTTTAAAAAATTTTAAAAA | 2013 |
| RESULT 4 | | | |
| AR222097 | | 2018 bp | DNA linear PAT 26-SEP-2002 |
| LOCUS | AR222097 | Sequence 3 from patent US 6429014. | |
| DEFINITION | AR222097 | | |
| ACCESSION | AR222097.1 | GI:23329471 | |
| VERSION | | | |
| KEYWORDS | | | |
| SOURCE | Unknown. | | |
| ORGANISM | Unknown. | | |
| REFERENCE | 1 (bases 1 to 2018) | | |
| AUTHORS | Steele,C.L., Bohlmann,J. and Croteau,R.B. | | |
| TITLE | Monoterpene synthases from grand fir (<i>Abies grandis</i>) | | |
| JOURNAL | Patent: US 6429014-A 3 06-AUG-2002; | | |
| FEATURES | Location/Qualifiers | | |
| source | 1..2018 | | |
| ORIGIN | /organism="unknown" | | |
| | /mol_type="genomic DNA" | | |
| Query Match | 54.9%; | Score 1306.8; | DB 6; Length 2018; |
| Best Local Similarity | 31.0%; | Pred. No. 0; | |
| Matches 1595; | Conservative 0; | Mismatches 342; | Indels 33; Gaps 5; |
| QY | 68 | CAGTCGTGCTCAGTCTCTTCTCATGATTAAGGCTCTCCGTAGAAACAATCCCACTCT | 127 |
| Db | 53 | CAATCGTTGATCAGTCTCTACCCATGAGCTTAAGGCTCTCTCTAGAACAAATCCAGCTCT | 112 |
| QY | 128 | TGGAATCTGAGGCCGGGGAATCCGTCCGCAATTCATAAACAATGTTTGAACAACGT | 187 |
| Db | 113 | AGGAATGAGTAGCGCAGGGAATCTATCACTCTCCATCAGCATGAGCTCTACACCGT | 172 |
| QY | 188 | CGCATCTACTGATTTCTGTACAGAGACCGGTGGGCACTATCATTTCCAACCTGTGGACGA | 247 |
| Db | 173 | TGTAACCGATGATGCTGTACGAAGACGCATGGGCGATTTCATTCCAACCTGTGGACGA | 232 |
| QY | 248 | TGATTTCAATACAGTCTCTGATCTCAACGCCCTTATGAGACCACTGATTACCGGGAACGTGC | 307 |
| Db | 233 | TGATGTCAATACGTCT--TTACCAACGGCTTATGAGGAAAAAATCGTACCTGAGCGTGC | 289 |
| QY | 308 | TGACAGACTTAATGGGGGAAGTAAAGGATATAATGTTCAATTTCAAGTGGCTGAGAGATGG | 367 |
| Db | 290 | TGAGAAACTGATCGGGGAAGTAAAG--AACATGTTCAATTGATGTCAATAGAGATGG | 346 |
| QY | 368 | AG-----GCAATGATCTCTTCAACGACTTTTGTGCTGATGACGTTGA | 412 |
| Db | 347 | AGAGTTAATGATTCGCCCTCAATGATCTCATTCACGCGCTTGGATTGTGACAGCGTTGA | 406 |
| QY | 413 | ACGTTTGGGAATCGACAGGCACTTCAAAAAAGATATAAAAAAGCACTCGATTATGTTAA | 472 |
| Db | 407 | ACGTTTGGGATCCATAGACATTTCAAGATGAGATAAATCGCGCTTGATTAATGTTTA | 466 |
| QY | 473 | CAGTTATTTGAAACGAAAAAGGCAATTGATGTGGAGAGAGAGTGTGTGACTGACCTCAA | 532 |
| Db | 467 | CAGTTATTTGGGACGAAAAATGGCATCGGATGCGGAGAGAGAGTGTGTACTGATCTGAA | 526 |
| QY | 533 | CTCAACCGCTTGGGGCTTCGAACCTCTCCGACTACACGGATACACTGTGTCTTCAGATGT | 592 |

Db 527 CTCACTGCGTTGGGGCTTCGAACCCCTACGACTACCGGCTCTTCAGATGT 586
Qy 593 TTTGAACGTTTTTAAGACAAAATGGGCAATTTCTCCACTGCCAATATTCAGATAGA 652
Db 587 TTTCAAAGCTTTCAAAAGGCCAAAATGGGCAATTTCTCGCTCTGAAAATATTCAGACAGA 646
Qy 653 GGGAGAGATTAGAGGCGTCTCAATTTATTCAGGGCCTCCCTCGTCGCTTTCCGGCGA 712
Db 647 TGAAGAGATCAGAGGCGTTCTGAATTTATTCGGGCGCTCCCTCATTGCTTTCCAGGGGA 706
Qy 713 GAAAGTTATGGATGAAGCTGAAACATTCTCTACAAAATATTTAAGAGAAAGCCCTGCAAAA 772
Db 707 GAAAATTTATGGATGAGGCTGAAATCTTCTCTACCAAATATTTAAAGAACCCCTGCAAAA 766
Qy 773 GATTCCGCGATCCAGTATACCTTTCATCTAGAGATACGGACGTTCTGGAATATGTTGCA 832
Db 767 GATTCCGCTCTCCAGT---CTTTCGGAGAGATCGGGACGTTTGGAAATATGTTGGCA 823
Qy 833 CACCAATTTGCCACGCTTGGAGCAAGAAATTCATGAGCGTCTTGGACAGACACTAA 892
Db 824 CACATATTTGCCCGCGATTTGGAAGCAAGAAATTCATCCAAAGTCTTGGACAGGACACTGA 883
Qy 893 AAATAAGAACG-----CGCCGAGAACTTTTAGAACTTGCAAAATTTGAATTCAA 943
Db 884 GAACACGAAATCATATGTGAAGAGCAAAAACCTTTAGAACTCGCAAAATTTGAGTTCAA 943
Qy 944 TATATTCACTCCTTACAGAGAGAGAGTTAAAACATGTTCCCGATGCTGGAAGACTC 1003
Db 944 CATCTTTCATCTTACAAAAGAGGAGTTAGAAAAGTCTGTCAGATGCTGAAAAGATC 1003
Qy 1004 GGGTCTCTGAGATGACCTTCTGTCGATCGTCACGTTGAATACGCTTTGGCTTC 1063
Db 1004 GGGTTTCTGAGATGACCTTCTGCCGACATCGTCACGTTGAATACGCTTTGGCTTC 1063
Qy 1124 TCTTATCAGGTTCTTGACGACATGTACGACGTTCTTGGCAGATGACGAGCTGGA 1183
Db 1124 TCTTATCAGGTTCTTGACGATATGTACGACACCTTCGGCAGATGACGAGCTGGA 1183
Qy 1184 CTTCAAGCGCAATTAAGAGATGGATCGTCCGCGATGGAATGCTTCCAGAATATAT 1243
Db 1184 CTTCAAGCGCAATTAAGAGATGGATCGTCCGCTCTCGATAGATTGCTTCCAGAATATAT 1243
Qy 1244 GAAAGAGTGTACATGATGTTTATCACACCGTAATGAATGGCTCGAGTGGCAGAGAA 1303
Db 1244 GAAAGAGTGTACATGACGGTTTACGACACCGTAATGAATGGCTCGAGAGGCAAGGA 1303
Qy 1304 GGGTCAAGGCGGAGACACGCTCAACTATGCAAGACAGGCTTGGAGGCGTATTGATT 1363
Db 1304 GGGTCAAGGCGGAGATACGCTCACATATGCTCGGAAAGCTTGGAGGCTTATTGATT 1363
Qy 1364 GTATATGCAAGAACAAAGTGATCGCCACTGTTATCTGCCACGTTTGAGAGTACTT 1423
Db 1364 GTATATGCAAGAACAAAGTGATCGCCACTGTTTACCTGCCCTTGTATGAGTACTA 1423
Qy 1424 GGAGAACGGGAAAGTTAGCTCTGCTCATCGCCCATGCGCACTGCAACCATTTGACGTT 1483
Db 1424 CGAAGATGGGAAAGTTAGCTGTGTCTATCGCATATCCGCATTGCAACCATTTGACAA 1483
Qy 1484 GGACATCCCTTCTCTGATCATATCTCAAGGAAGTTGACTTCCATCAAAAGCTTAA 1543
Db 1484 GGACATCCCTTCTCTGATCATATCTCAAGGAAGTTGACTTCCATCAAAAGCTTAA 1543
Qy 1544 CTTGATATGTATCATCTTGTGATTAAAGGTGATACAGGCTGTACAGGCAAGAGG 1603
Db 1544 CTTGGCATGTGCATCTTGTGATTACGAGGTGATACGCGGTGTACAGGCGGAGAG 1603
Qy 1604 CCGTGAGAGAAAGCTTGTCTATATCATGTATATGAAGAACAATCTGGAATTAACGGA 1663
Db 1604 CCGTGAGAGAAAGCTTGTCTATATCATGTATATGAAGAACAATCTGGAATTAACGGA 1663

Db 1604 TCGTGAGAGAAAGCTTCTCTATATCATGTTATATGAAGACAATCTGGAGTATCAGA 1663
Qy 1664 AGAATGCTCTGAATCATATCAACTTCATGATCAGGAGCGCAATCAGAAATTAATTG 1723
Db 1664 GGAAGATGCTCTCGATCATATCAAGCCCATGATCAGTACGATCAATCAAAAGATTAA 1723
Qy 1724 GGAGCTTTAAAGCCAGACAAGTGTCCCATCATCTTCCAAAGAAACACGATTGACAT 1783
Db 1724 GGAATCTTCAAAACAGACATCAATGTCCCATCTCGCGAAGAAACATGCTTTGACAT 1783
Qy 1784 AAGCAGATTTGGCATCACGGTTACAGATACCCGAGATGGCTACAGCTTTGCCAACGTTGA 1843
Db 1784 CGCCAGAGCTTTCATTTACGGCTACAAATACCGAGACGGCTACAGCGTTGCCAACGTTGA 1843
Qy 1844 AACAAAGATTTGGTGTATGAGAACCGTCAATTGAACCTGTGCTTTGTAACAACACTTCAA 1903
Db 1844 AACGAAGATTTGGTGTACAGGAACCTCTTGAATCTGTGCTTTGTAGCAACAGCTCAA 1903
Qy 1904 ATCTAATAATTAATCTGAGATGCGCTATGCGTGTATATAGGCAACAAAAATAATAT 1963
Db 1904 ATCTATGCCCTATGCTATGTGCGGTAAATATATATGTGAAGGTAGCCGTTGATGTAGA 1963
Qy 1964 GGTGTGTAGTAAAGCTGTAAATTTATGAAAAAAAAAAAAAAAAAAAAAA 2013
Db 1964 GGATAGATTGTATATTAATTAAGTTGTGAATTTAAAAAAAAAAAAAAAAAAAA 2013

RESULT 5
AR240696 2018 bp DNA linear PAT 20-DEC-2002
LOCUS AR240696
DEFINITION Sequence 19 from patent US 6468772.
ACCESSION AR240696
VERSION AR240696.1 GI:27285845
KEYWORDS
SOURCE unknown.
ORGANISM unknown.
REFERENCE 1 (bases 1 to 2018)
AUTHORS Chappell,J., Manna,K.R., Noel,J.P. and Starks,C.M.
TITLE Methods of making modified polypeptides
JOURNAL Patent: US 6468772-A 19 22-OCT-2002;
FEATURES
source 1..2018
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 64.9%; Score 1306.8; DB 6; Length 2018;
Best Local Similarity 81.0%; Pred. No. 0;
Matches 1595; Conservative 0; Mismatches 342; Indels 33; Gaps 5;

Qy 68 CAGTCTGCTCAGTCTTCTTCATGAGATTAAAGGCTCTCCGTAGAACAATCCCACTCT 127
Db 53 CAAATCGTTGATCAGTTCTACCCATGAGCTTAAAGGCTCTCTAGAACAATTCAGCTCT 112
Qy 128 TGAATCTGACGCGCGGAAATCCGTGCGCATTTCCATTAACATGTGTTGACAAGCGT 187
Db 113 AGGAATGAGTAGGCGAGGAAATCTATCACTCTTCCATCAGATGAGCTTACACCGT 172
Qy 188 CGCATCTACTGATTCTGTACAGACGCGTGGCAACTATCAATCCAACTGTGGAGCA 247
Db 173 TGTAACCATGATGTGTACGAAGACGATGGCGATTTCATCCAACCTCTGGAGCA 232
Qy 248 TGATTTCAATACAGTCTGTATCTCAACGCCCTTATGAGACACCTGATTAACGGGA 307
Db 233 TGATGTCAATACAGTCT--TTACCAACGGCTTATGAGGAAATACTGTAACCTGAG 289
Qy 308 TGACAGACTTATTTGGGAGATAAAGATATATATGTTCAATTTCAAGTCCCTGGAAG 367
Db 290 TGAGAACTGATCGGGGAAGTAAAG--AACATGTTCAATTTGATGTCAATTAAGAA 346
Qy 368 AG-----GCAATGATCTCTTCAACGACCTTTTGTGCTGATGACGTTGA 412
Db 368 AG-----GCAATGATCTCTTCAACGACCTTTTGTGCTGATGACGTTGA 412

Db 347 AGAGTTAATGAGTCCGCTCAATGATCTCAATCAACGCCCTTGGATTGTCGACAGCCTTGA 406
Qy 413 ACGTTGGGAATCGACAGGCAATTTCAAAAAGAGATAAAACGGCACTCGATTATGTTAA 472
Db 407 ACGTTGGGGATCCATAGACATTTCAAGATGAGATAAAATCGGCCGCTTGATTATGTTTA 466
Qy 473 CAGTTATTTGAAAGAAAAAGGCAATTTGATGTGGAGGAGAGAGTGTGTGACTGACCTCAA 532
Db 467 CAGTTATTTGGGGGCAAAATGGCATCGATGCGGAGGAGAGAGTGTGTGAATCTGATCTGAA 526
Qy 533 CTCAACCGCCTTGGGGCTTGAAGCTCTCCGACTACACGGATACACTGTGCTTCAGATGT 592
Db 527 CTCAACTGCGTTGGGGCTTGAACCTTACGACTACACGGATACCGGCTGCTTCAGATGT 586
Qy 593 TTTGAACGTTTAAAGCAAAAAATGGGCAATTTCTCTCACTGCAATGCAATATTCAGATAGA 652
Db 587 TTTCAAGCTTTCAAAAGGCCAAAATGGGCAATTTCTCTGCTGTAATAATATTCAGACAGA 646
Qy 653 GGGAGAGATTAGAGCGCTTCTCAATTTATCAGGGCCTCCCTCGCTTCCCGGCGA 712
Db 647 TGAAGAGATCAGAGCGCTTCTGAATTTATTCGGGGCCTCCCTCATTTGCCCTTCCAGGGGA 706
Qy 713 GAAAGTTATGATGAAGCTGAAACATTTCTCTACAAATATTTAAGAGAACCCCTGCAAA 772
Db 707 GAAATTTATGATGAGGCTGAAATCTTCTCTACCAATATTTTAAAGAACCCCTGCAAA 766
Qy 773 GATTCGGGCAATCCAGTATCTTCACTAGAGATACGGGACGTTCTGGAATATGTTGGCA 832
Db 767 GATTCGGGCTCTCAGT--CTTCCGAGAGATCGGGGACGTTTGGAAATATGTTGGCA 823
Qy 833 CACCAATTTGCCACGCTTGGAGCAAGGAATACATGAGCGTCTTGGACAGACACTAA 892
Db 824 CACATATTTGCCCGGATTTGGAAGCAAGGAATACATCCAGTCTTGGACAGACACTGA 883
Qy 893 AAATAAGAACGC-----CGCCGAGAACTTTTGAAGCTTGCAAAATTTGAATTCAA 943
Db 884 GAAACAGAGTCATATGTGAAGAGCAAAAACCTTTAGAACTCGCAAAATTTGAGTTCAA 943
Qy 944 TATATTTCACTCCTTACAGAGAGAGAGATTAAACATGTTCCCGATGGTGAAGACTC 1003
Db 944 CATCTTTCAATCCTTACAAAAGAGGAGTTAGAAAGTCTGTGACAGATGGTGAAGAAATC 1003
Qy 1004 GGGTCTCTGAGATGACCTTCTGTGACATCGTCAAGTGAATATCTACGCTTTGGCTTC 1063
Db 1004 GGGTTTCTTGAGATGACCTTCTGCGGACATCGTCAAGTGAATATCTACGCTTTGGCTTC 1063
Qy 1064 CTGCATGCGCTTGAAGCTTCAACATTTCTGAGATTCAGACTCGGCTTGGCAAGACGTGCA 1123
Db 1064 CTGCATGCGCTTGAAGCTTCAACATTTCTGAGATTCAGACTCGGCTTGGCAAGACGTGCA 1123
Qy 1124 TCTTATCAGCGTCTTGAAGCAATGTACGAGTCTTGGCAGACAGTGAAGCTGGAAT 1183
Db 1124 TCTTATCAGCGTCTTGAAGCAATGTACGAGTCTTGGCAGACAGTGAAGCTGGAAT 1183
Qy 1184 CTTCAAGCGCAATTAAGAGATGGATCGCTCGCGATGGAATGCTTCCAGATATAT 1243
Db 1184 CTTCAAGCGCAATTAAGAGATGGATCGCTCGCGATGGAATGCTTCCAGATATAT 1243
Qy 1244 GAAAGAGTGTACATGATGTTATACACCCGTAATGAATGGTTCGAGTGGCAGAGAA 1303
Db 1244 GAAAGAGTGTACATAGCGGTTTACGACACCGTAATGAATGGTTCGAGAGCAGAGGA 1303
Qy 1304 GGGTCAAGGCCGAGATACGCTCACATATGCTCGGGAAGCTTGGGAGGCTTATATTGATT 1363
Db 1304 GGGTCAAGGCCGAGATACGCTCACATATGCTCGGGAAGCTTGGGAGGCTTATATTGATT 1363
Qy 1364 GTATATGCAAGAACCAAGTGGATCGCACTGGTTACTGCTCCCTTGTGATGATGACTA 1423
Db 1364 GTATATGCAAGAACCAAGTGGATCGCACTGGTTACTGCTCCCTTGTGATGATGACTA 1423
Qy 1424 GGAGAACGGGAAAGTTAGCTCTGCTCATCGCCATGCGCACTGCAACCCATTTCTGACGTT 1483
Db 1424 CGAGTAATGGGAAAGTTAGCTGTGTATCGATGATATCCGATTTGCAACCCATTTCTGACMA 1483

Qy 1484 GGACATCCCTTTCTCTGATCACATCTCAAGGAAGTTGACTTCCCATCGAAGCTCAATGA 1543
Db 1484 GGACATCCCTTTCTCTGATCATATCTCAAGGAAGTTGACTTCCCATCAAGCTTAACGA 1543
Qy 1544 CTTGATATGATCATCTCTTCAATTAAGGTGATACACGGTGTCTCAAGGACAGAGGGC 1603
Db 1544 CTTGCAATGTCATCTCTTCAATTAAGGTGATACACGGTGTCTCAAGGACAGAGGGC 1603
Qy 1604 CCGTGAGAGAAAGCTTCTCTATATCATGTTATATGAAGAAATCCTGATTAAACGA 1663
Db 1604 TCGTGAGAGAAAGCTTCTCTATATCATGTTATATGAAGAAATCCTGAGTATCAGA 1663
Qy 1664 AGAAGATGCTCTGATCATATCATATCATATGATCAGGAGCGCAATCAGAAATTAATTG 1723
Db 1664 GGAAGATGCTCTGATCATATCATATCATATGATCAGGAGCGCAATCAGAAATTAATTG 1723
Qy 1724 GAGCTTCTAAAGCCAGACAAAGTGTTCCTCATCTTCCAGAAACACGCAATTTGACAT 1783
Db 1724 GGAATCTTCAACAGACATCAATGTTCCATCTCGCGGAGAAACATGCTTTGACAT 1783
Qy 1784 AAGCAGATTTGGCATCAGGTTACAGATACCGAGATGCTACAGCTTTGCCAAGCTTGA 1843
Db 1784 CGCCAGAGCTTTCATTAACGCTACAAATACCGAGACGCTTACAGGCTTCCCAAGCTTGA 1843
Qy 1844 AACAAAGATTTGCTGATGAGAACCGTCAATGAACTGTGCTTGTAAACAACCTTCAA 1903
Db 1844 AACGAAGATTTGCTGATGAGAACCGTCAATGAACTGTGCTTGTAAACAACCTTCAA 1903
Qy 1904 ATCTACAATATTAAGTGAAGATGCGCTATAGGCTATATAGGCAACAATAATAT 1963
Db 1904 ATCTATGCCCTATGCTATGCTGCTGCTTAAATATATATGGAAGTACCGCTTGATGATA 1963
Qy 1964 GGTGTGTAGTAAAGCTGTAATTTATGAAAAAATTTTAAAAAATTTTAAAAAATTTT 2013
Db 1964 GGATAGTTGTATATTTATTAATTAAGTTGTTAATTTTAAAAAATTTTAAAAAATTTT 2013

RESULT 6
LOCUS AR266971 2018 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 19 from patent US 6495354.
ACCESSION AR266971
VERSION AR266971.1 GI:29696426
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 2018)
AUTHORS Chappell, J., Manna, K.R., Noel, J.P. and Starks, C.M.
TITLE Syntheses
JOURNAL Patent: US 6495354-A 19 17-DEC-2002;
FEATURES
source location/Qualifiers
1..2018
/organism="unknown"
/mol_type="genomic DNA"

Query Match 64.9%; Score 1306.8; DB 6; Length 2018;
Best Local Similarity 81.0%; Pred. No. 0;
Matches 1595; Conservative 0; Mismatches 342; Indels 33; Gaps 5;

Qy 68 CAGGTGCTGCTCAGTCTTCTCATGAGATTAAAGGCTCTCCGTAACAATCCCACTCT 127
Db 53 CAATCGTTGATCAGTCTTACCCATGAGCTTAAAGGCTCTCTTGAACAATCCAGCTCT 112
Qy 128 TGAATCTGCAAGCGGGAATCCGTCGCGCATTCATTAACATGTGTTGACAAAGCGT 187
Db 113 AGAATGATAGGCGAGGAAATCTTACTCTTCCATCAGATGAGCTCTACCAACCGT 172
Qy 188 CGCATCTACTGATTTCTGTACAGAGACGCTGGGCAACTATATCCAACTGTGGAGCA 247
Db 173 TGTAAACGATGATGTGTACGAAGACGATGGCGATTTCCATTCAACTCTGGAGCA 232

| | |
|----------|--------------------------------------|
| JOURNAL | Patent: US 6569656-A 19 27-MAY-2003; |
| FEATURES | Location/Qualifiers |
| source | 1. 2018 |

ORIGIN

| | | | | |
|----------------------------|--------|-----------------|------------|--------------|
| Query Match | 64.9% | Score 1306.8; | DB 6; | Length 2018; |
| Best Local Similarity | 81.0%; | Pred. No. 0; | | |
| Matches 1595; Conservative | 0; | Mismatches 342; | Indels 33; | Gaps 5; |

| | | | |
|----|-----|---|------|
| QY | 68 | CAGGTCGTCCCTCAGTTCTTCTCATGAGATTAAAGCTCTCCGTAGAACAAATCCCACTCT | 127 |
| Db | 53 | CAAAATCGTTGATCAGTTCTAACCCATGAGCTTAAAGCTCTCTTAGAACAAATTCAGCTCT | 112 |
| QY | 128 | TGGAATCTGACGCGCGGGAATCCGTCCGCATTCCATAAACATGTGTTGACAACCGT | 187 |
| Db | 113 | AGGAATGAGTAGCGCAGGGAATCTATCACTCCTTCATCAGCATGAGCTCTACACCGT | 172 |
| QY | 188 | CGCATCTACTGATTCTGTACAGACGCGTGGCAACTATCAATCCAACCTGTGGACGA | 247 |
| Db | 173 | TGTAACCGATGATGGTGTACAGACGCGATGGCGATTTCATTCCAAACCTGTGGACGA | 232 |
| QY | 248 | TGATTTTCATACAGTCTCTGATCTCAACGCTTATGAGACACCTGATTACCGGAACGTG | 307 |
| Db | 233 | TGATGTCATACAGTCT--TTACCAACGCGCTTATGAGAAATACTGTAACCTGAGCGTGC | 289 |
| QY | 308 | TGACAGACTTATTGGGGAAGTAAGATATATATGTTCAATTTCAGTCCGCTGGAAGATGG | 367 |
| Db | 290 | TGAGAAACTGATCGGGGAAGTAAG--AACATGTTCAATTGCATGTCAATTAGAAGATGG | 346 |
| QY | 368 | AG-----GCATGATCTCTCTTCAACGACTTTGCTGCTGATGACGTTGA | 412 |
| Db | 347 | AGAGTTAATGAGTCCGCTCAATGATCTCATTTCAACGCTTTGGATTGTGCACAGCCTTGA | 406 |
| QY | 413 | ACGTTTGGGAATCGACAGGCAATTTCAAAAAAGAGATAAAAAAGCACTCGATTATGTTAA | 472 |
| Db | 407 | ACGTTTGGGATCCATAGACATTTCAAAAGATGAGATAAAATCGCGCTTGATTATGTTTA | 466 |
| QY | 473 | CAGTTATTGGAACGAAAAAGCATTTGATGTGGAGGAGAGAGTGTGTGACTGACCTCAA | 532 |
| Db | 467 | CAGTTATTGGGCGAAAAATGCATCGATGCGGAGGAGAGAGTGTGTACTGATCTGAA | 526 |
| QY | 533 | CTCAACCGCCTTGGGCTTCGAACTCTCCGACTACACGAGTACACTGTCTTCAGATGT | 592 |
| Db | 527 | CTCACTGCGTTGGGCTTCGAACCTCAGACTACACGGAATACCGGTCTTCAGATGT | 586 |
| QY | 593 | TTTGAACGTTTTTAAAGCAAAAAATGGCAATTTCTCTCACTGCCAATATTCCAGATAGA | 652 |
| Db | 587 | TTTCAAGCTTTCAAAAGCCAAATGGGCAATTTCTCTGCTCTGAATAATTCCAGACAGA | 646 |
| QY | 653 | GGGAGAGATTAGAGCGCTTCAATTTATTCAGGGCCTCCCTGCTCGCCTTCCCGGCGA | 712 |
| Db | 647 | TGAAGAGATCAGAGCGCTTCTGAATTTATTCGGGCTCCCTCATTTGCCCTTCCAGGGGA | 706 |
| QY | 713 | GAAAGTTATGATGAGAGCTGAAACATTTCTCTACAAATATTTAAGAGAAGCCCTGCAAAA | 772 |
| Db | 707 | GAAAATTTATGATGAGGCTGAAATCTTCTCTACCAATATTTAAGAAAGCCCTGCAAAA | 766 |
| QY | 773 | GATTCGGGCATCCAGTATATCTTCACTAGAGATACGGGACGTTCTGGAATATGTTGGCA | 832 |
| Db | 767 | GATTCGGTCTCCAGT--CTTTGCGAGAGATCGGGGACGTTTGGAAATATGTTGGCA | 823 |
| QY | 833 | CACCAATTTGGCCACGCTTGAAGCAAGGAATTACATGAGCGCTTTGGACAGCACACTAA | 892 |
| Db | 824 | CACATATTTCGCGGATGGAAGCAAGGAATTACATCCAACTTTTGGACAGCACACTGA | 883 |
| QY | 893 | AAATAGAAGCGC-----CGCCGAGAAACTTTAGAACTTGCAAAATTGGAATTCAA | 943 |
| Db | 884 | GAAACAGAAATCATATGTGAAGACAAAAAACTTTAGAACTCGCAAAATTTGAGTTCAA | 943 |
| QY | 944 | TATATTTCACTCCTTACAAGAGAGAGTTAAAAACATGTTTCCCGATGTTGAAAGACTC | 1003 |

| | | | |
|----|------|---|------|
| Db | 944 | CATCTTCAATCCTTACAAAAGAGGAGTTAGAAAAGTCTGTCAGATGGTGGAAAAGATC | 1003 |
| Qy | 1004 | GGGTCTCTGTAGATGACCTTCTGTGCACATCGTCACGTGAATACTACGCTTTGGCTTC | 1063 |
| Db | 1004 | GGGTTTCTGTAGATGACCTTCTGCGACATCGTCACGTGAATACTACCTTTGGCTTC | 1063 |
| Qy | 1064 | CTGCATTGCGTTCGAGCCTCAACATCTTGATTAGACTCGGCTTTACCAAGATGCTCA | 1123 |
| Db | 1064 | CTGCATTGCGTTCGAGCCTCAACATCTTGATTAGACTCGGCTTTGCAAGAGCTGTCA | 1123 |
| Qy | 1124 | TCTTATCACGGTCTTGAACGACATGTACGACGTCCTTCGGACAGTAGACGAGCTGAACT | 1183 |
| Db | 1124 | TCTTATCACGGTCTTGAACGATATGTACGACACCTTCGGACAGTAGACGAGCTGAACT | 1183 |
| Qy | 1184 | CTTCACAGCGACATTAAGAGATGGATTCGCTCCGCGATGGAAATGCCCTTCCAGAAATATAT | 1243 |
| Db | 1184 | CTTCACAGCGACATGAAGAGATGGATTCGCTCCGCTCGATAGATTGCCCTTCCAGAAATATAT | 1243 |
| Qy | 1244 | GAAAGAGTGTACATGATGCTGTTATCACACCGTAAATGAATGGCTCGAGTGGCAGAGAA | 1303 |
| Db | 1244 | GAAAGAGTGTACATAGCGGTTTACGACACCGTAAATGAATGGCTCGAGAGCAGAGGA | 1303 |
| Qy | 1304 | GGCTCAAGGCCGAGACACGCTCAACTAATGCAAGACAGGCTTGGAGCGCTTTGATTTC | 1363 |
| Db | 1304 | GGCTCAAGGCCGAGATACGCTCACATATGCTCGGAAAGCTTGGAGGCTTATATTGATTTC | 1363 |
| Qy | 1364 | GTATATGACGAAGCAAGTGATGCGCATGCTGTTATCTGCCACGTTTGAGAGTACTT | 1423 |
| Db | 1364 | GTATATGACGAAGCAAGTGATGCGCATGCTGTTATCTGCCCTCTTGATGAGTACTA | 1423 |
| Qy | 1424 | GGAGAACGGGAAGTTAGCTCTGCTCATCGCCCATGCGCACTGCACCCCATTTGACGTT | 1483 |
| Db | 1424 | CGAAGATGGGAAGTTAGCTGTGTCATCGCATATCCGCATTGCACCCCATTTGACAAAT | 1483 |
| Qy | 1484 | GGACATCCCCCTTCTGTATCATATCCTCAAGGAAGTTGACTTCCCATCAAGCTTAAACGA | 1543 |
| Db | 1484 | GGACATCCCCCTTCTGTATCATATCCTCAAGGAAGTTGACTTCCCATCAAGCTTAAACGA | 1543 |
| Qy | 1544 | CTTGATATGTATCATCTTGCATTAAAGAGTGATACACGGTCTACAAAGGCAGACAGGC | 1603 |
| Db | 1544 | CTTGCAATGTGCCATCTTGCATTAAAGAGTGATACACGGTCTACAAAGGCAGACAGGC | 1603 |
| Qy | 1604 | CCGTGAGAAAGAGCTCGTCTATATCATGTTATGAAAAGCAATCTTGATTAAACGA | 1663 |
| Db | 1604 | TCGTGAGAAAGAGCTCTCTATATCATGTTATGAAAAGCAATCTTGATTATCAGA | 1663 |
| Qy | 1664 | AGAAGATGCTTGAATCATATCAACTTCATGATCAGGAGCGCAATCAGAGAAATTAATTG | 1723 |
| Db | 1664 | GGAAGATGCTCTGCATCATATCAACGCCATGATCAGTGAACGTAAATCAAGAAATTAATTG | 1723 |
| Qy | 1724 | GGAGCTTCTAAAGCCAGACAACAGTGTCCCATCACTTCCAAAGAAACGCAATTGACAT | 1783 |
| Db | 1724 | GGAATCTCTCAAAACAGACATCAATGTTCCCATCTCGCGGAAGAAACATGCTTTGACAT | 1783 |
| Qy | 1784 | AAGCAGAGTTGGCATCACGGTTACAGATACCGAGATGGCTACAGCTTTGCCAACGTTGA | 1843 |
| Db | 1784 | CGCCAGAGCTTCCATTACGGCTACAAATACCGAGACGGCTACAGCGTTGCCAACGTTGA | 1843 |
| Qy | 1844 | AACAAAGAGTTTGGTATGAGAACCGTCATTGAACCTGTGCCCTTTGTAACACACTTCAA | 1903 |
| Db | 1844 | AACGAAGAGTTTGGTACAGAGAACCTCTTGAAATCTGTGCTTTGTAGCAACAGCTCAA | 1903 |
| Qy | 1904 | ATCTACAATATTAATGAGGATGCCCTATGGGTATATAGGGCACACAAAATAATAT | 1963 |
| Db | 1904 | ATCTATGCCCTATGCTATGTGCGGTAAATAATATGTGAAGGTAGCCGTTGATGTAGA | 1963 |
| Qy | 1964 | GGTTGTGTTAGTAAAGCTGTAATTTATGAATAAAAAAAAAAAAAAAAAAAAAA 2013 | |
| Db | 1964 | GGATAAGTTTGTATTAATTTAATAAAGTTGTAATTTAAAAAAAAAAAAAAAAAAAA 2013 | |

| | | | | | |
|-----------------------|--|---|------------|--------------|-----------------|
| LOCUS | AR429869 | 2018 bp | DNA | Linear | PAT 18-DEC-2003 |
| DEFINITION | Sequence 19 from patent US 6645762. | | | | |
| ACCESSION | AR429869 | | | | |
| VERSION | AR429869.1 | GI:40190267 | | | |
| KEYWORDS | Unknown. | | | | |
| SOURCE | Unknown. | | | | |
| ORGANISM | Unclassified. | | | | |
| REFERENCE | 1 (bases 1 to 2018) | | | | |
| AUTHORS | Chappell,J., Manna,K.R., Noel,J.P. and Starks,C.M. | | | | |
| TITLE | Syntheses | | | | |
| JOURNAL | Patent: US 6645762-A 19 11-NOV-2003; | | | | |
| FEATURES | Location/Qualifiers | | | | |
| Source | 1. 2018 | | | | |
| | /organism="unknown" | | | | |
| | /mol_type="genomic DNA" | | | | |
| ORIGIN | | | | | |
| Query Match | 64.9%; | Score 1306.8; | DB 6; | Length 2018; | |
| Best Local Similarity | 81.0%; | Pred. No. 0; | | | |
| Matches 1595; | Conservative 0; | Mismatches 342; | Indels 33; | Gaps 5; | |
| Qy | 68 | CAGTCCGCTCACTTCTCTCATGAGATTAAAGCTCTCCGTAGACAATCCCACTCT | 127 | | |
| Db | 53 | CAAAATCGTTGATCAGTCTACCCATGAGCTTAAAGCTCTCTTAGAACAATCCAGCTCT | 112 | | |
| Qy | 128 | TGGAATCTGCAGCCCGGAAATCCGTGCGCATTCATTAACATGTGTTGACAACGCT | 187 | | |
| Db | 113 | AGGAATGATGAGCGAGGAAATCTATCACTCTTCATCAGCATGAGCTCTACCACTCT | 172 | | |
| Qy | 188 | CGCATCTAATGATTTCTGTACAGAGACGCGTGGCAACTATCATTCCAACTGTGGACGA | 247 | | |
| Db | 173 | TGTAACCGATGATGTGTACGAAGACGATGGCGATTCATTCCAACTCTGGGACGA | 232 | | |
| Qy | 248 | TGATTTCAATACAGTCTCTGATCTCAACGCTTATGAGACACCTGATTAACGGGACGTG | 307 | | |
| Db | 233 | TGATGTCTATACAGTCT--TTACCAACGGCTTATGAGAAATCGTACCTGAGCGTGC | 289 | | |
| Qy | 308 | TGACAGACTTATGGGGAGTAAGATATATCTTCAATTTCAAGTCGCTGGAAGATGG | 367 | | |
| Db | 290 | TGAGAAACTGATCGGGGAAGTAAAG---AACATGTTCATTCGATGTCAATTAAGAATGG | 346 | | |
| Qy | 368 | AG-----GCAATGATCTCTTCAACGACTTTTGTGCTGATGACGTGA | 412 | | |
| Db | 347 | AGAGTTAATGAGTCCGCTCAATGATCTCAATTCACGCTTTGATGTGACAGCCTTGA | 406 | | |
| Qy | 413 | ACGTTGGGAATCGACAGGCAATTCAAAAAGAGATAAAAAAGGCACTCGATTATGTTAA | 472 | | |
| Db | 407 | ACGTTGGGATCCATAGACATTTCAAGATGAGATAAATCGGCGCTGATTATGTTTA | 466 | | |
| Qy | 473 | CAGTTATGGAACGAAAAAGCATTTGATGTGGAGAGAGAGTGTGTAAGTGAAGCTCAA | 532 | | |
| Db | 467 | CAGTTATGGGGCGAAAAATGCGATCGGATGGGAGAGAGAGTGTGTAAGTGAAGCTCAA | 526 | | |
| Qy | 533 | CTCAACGCTTGGGGCTTGAACCTCTCGACTACACGATACATGCTCTTCAGATGT | 592 | | |
| Db | 527 | CTCAACGCTTGGGGCTTGAACCTCTCGACTACACGATACCGGCTCTTCAGATGT | 586 | | |
| Qy | 593 | TTTGAACGTTTTTAAAGCAAAATGGGCAATTTCTCCACTGCAATATTCAGATAGA | 652 | | |
| Db | 587 | TTTCAAGCTTTCAAAAGCCAAATGGGCAATTTCTCTGCTCTGAATAATTCAGACAGA | 646 | | |
| Qy | 653 | GGGAGATTAAGAGCGCTTCTCAATTTATTCAGGGCTCCCTCGTCCCTTTCCGGCGA | 712 | | |
| Db | 647 | TGAAGAGATCAGAGCGCTTCTGAATTTATTCGGGGCTCCCTCATTTGCTTTCCAGGGGA | 706 | | |
| Qy | 713 | GAAAGTTATGATGAAGCTGAACATTTCTACAAATATTTAAGAGAGCCCTGCAGAAA | 772 | | |
| Db | 707 | GAAATTTATGATGAGGCTGAATCTTCTCTACCAATATTTAAAGAGCCCTGCAGAAA | 766 | | |
| Qy | 773 | GATTCGGGATCCAGTATACCTTTCATGAGATACGGGACGTTCTGGAATATGTTGCA | 832 | | |
| Db | 767 | GATTCGGGATCCAGT---CTTTCGCGAGAGATCGGGACGTTTGTGAATATGTTGCA | 823 | | |

| | | | | | |
|----|------|--|------|--|--|
| Qy | 833 | CACCAATTTGCCACGCTTGGAGCAAGAAATTACATGACGCTTTTGGACACACACTAA | 892 | | |
| Db | 824 | CACATATTTGCCCGATTGGAGCAAGAAATTACATCCAAAGTCTTTGGACACACACTGA | 883 | | |
| Qy | 893 | AAATTAAGACGC-----CGCCGAGAACTTTTAGAAGCTTGAAGAAATTGGAATCAA | 943 | | |
| Db | 884 | GAAACAGAGTATATGTGAAGAGCAAAAACTTTAGAACTCGCAAAATTTGAGTTCAA | 943 | | |
| Qy | 944 | TATATTTCACTCCTTACAGAGAGAGTTAAACATGTTTCCGATGTGTGAAGAACTC | 1003 | | |
| Db | 944 | CATCTTCAATCCTTACAAAAAGAGGAGTTAGAAAGTCTGGTCAATGTGTGAAGAAATC | 1003 | | |
| Qy | 1004 | GGTTCTCTGAGATGACCTTCTGTGACATCGTCAAGTGAATTAACGCTTTGGCTTC | 1063 | | |
| Db | 1004 | GGTTTCTCTGAGATGACCTTCTGTGACATCGTCAAGTGAATTAACGCTTTGGCTTC | 1063 | | |
| Qy | 1064 | CTGCATTCGCTTCAAGCTTCAACATTTCTGATTCAGACTCGGCTTTGCCAAGACGTCTCA | 1123 | | |
| Db | 1064 | CTGCATTCGCTTCAAGCTTCAACATTTCTGATTCAGACTCGGCTTTGCCAAGACGTCTCA | 1123 | | |
| Qy | 1124 | TCTTATCAGGTTCTTGACGACATGTACGAGCTTCTCGGACACAGTACGAGCTGAACT | 1183 | | |
| Db | 1124 | TCTTATCAGGTTCTTGACGATATGTACGACACTTCGGACAGTACGAGCTGAACT | 1183 | | |
| Qy | 1184 | CTTCAAGCGACATTTAAGAGATGGATCCGTCGCGATGAATGCTTCCAGATATAT | 1243 | | |
| Db | 1184 | CTTCAAGCGACATGAAGAGATGGATCCGTCGATAGATGCTTCCAGATATAT | 1243 | | |
| Qy | 1244 | GAAAGAGTGTACATGATGTTTATCAACCGTAAATGAATGGCTCGAGTGGCAGAGAA | 1303 | | |
| Db | 1244 | GAAAGAGTGTACATAGCGGTTTACGACACCGTAATGAATGGCTCGAGAGCAGAGAA | 1303 | | |
| Qy | 1304 | GGCTCAAGCCGAGACACGCTCAACTATGCAAGACAGGCTTGGAGGCGCTTTGATTC | 1363 | | |
| Db | 1304 | GGCTCAAGCCGAGATACGCTCAACTATGCTCGGGAAGCTTGGAGGCTTATTTGATTC | 1363 | | |
| Qy | 1364 | GTATATGAGGAAGCAAGTGATCGGCACTGTTATCTGCCACGTTTGAAGAGTACTT | 1423 | | |
| Db | 1364 | GTATATGAGGAAGCAAGTGATCGGCACTGTTATCTGCCACGTTTGAAGAGTACTT | 1423 | | |
| Qy | 1424 | GGAGAACGGGAAAGTTAGCTCTGCTCATCGCCATGCGCACTGCAACCACTTGCAGCTT | 1483 | | |
| Db | 1424 | CGAGATGGGAAAGTTAGCTGTGTGTCATCGCATATCCGATTCGAACCACTTGCAGCAAT | 1483 | | |
| Qy | 1484 | GGACATCCCTTCTCTGATCAATCTCAAGAAAGTTGACTTCCATCGAAAGCTCAATGA | 1543 | | |
| Db | 1484 | GGACATCCCTTCTCTGATCAATCTCAAGAAAGTTGACTTCCATCGAAAGCTTAAAGA | 1543 | | |
| Qy | 1544 | CTTGATATGATCATCTCTGATTAAGAGTGATACACGCTGTCAAGGACAGACAGGCG | 1603 | | |
| Db | 1544 | CTTGCAATGCTCCATCTTCAATTAAGAGTGATACACGCTGTCAAGGACAGACAGGCG | 1603 | | |
| Qy | 1604 | CCGTGAGAGAAAGCTTCTGTATATCATGTTATATGAAGACAAATCCTGGATTAAACGA | 1663 | | |
| Db | 1604 | TCGTGAGAGAAAGCTTCTGTATATCATGTTATATGAAGACAAATCCTGGAGTACAGA | 1663 | | |
| Qy | 1664 | AGAAGATGCTCTGAATCATATCAACTTCATGATCAGGAGCGCAATCAGAGATTAAATTG | 1723 | | |
| Db | 1664 | GGAAGATGCTCTGATCATATCAAGCCATGATCAGTACGCTAATCAAGAGATTAAATTG | 1723 | | |
| Qy | 1724 | GGAGCTTCTAAAGCCAGACAAAGTGTCCCATCACTTCCAAGAAACAGCATTTGACAT | 1783 | | |
| Db | 1724 | GGAATTTCTCAACACAGACATCAATGTCCCATCTCGGCAAGAAACATGCTTTGACAT | 1783 | | |
| Qy | 1784 | AAGCAGATTTGGCATCACGCTTACAGATACCGAGATGCTACGCTTGGCCAACGTTGA | 1843 | | |
| Db | 1784 | CGCCAGAGCTTCCATTAAGGCTCAAAATACCGAGACGCTACGCTTGGCCAACGTTGA | 1843 | | |
| Qy | 1844 | AACAAGATTTGGTATGAGAACGCTCATTTGAACCTGTGCTTTGTAAACAACACTTCAA | 1903 | | |
| Db | 1844 | AACGAAGATTTGGTACGAGAACCTCTTGAATCTGTGCTTTGTAGCAACAGCTCAA | 1903 | | |

[illegible]

| | | | |
|----|------|---|------|
| Db | 113 | AGGAATGAGTAGCGGAGGAAATCTATCACTCCTTCCATCAGCATGAGCTCTACCACCGT | 172 |
| QY | 188 | CGCATCTACTGATTCCTGTACAGAGACGCGTGGCAACTATTCATCCAACTGTGGACGA | 247 |
| Db | 173 | TGTAACCGATGATGGGTGTACGAAGACGCATGGCGGATTTCCATTCCAACCTCTGGACGA | 232 |
| QY | 248 | TGATTTCAATACAGTCTCTGATCTCAACGCCCTTA TGGAGCACTGATTTACCGGGAACGTGC | 307 |
| Db | 233 | TGATGTCAATACAGTCTCTTACCAACGGCTTA TGAAGAAAAATCGTACCCTGAGCGCTGC | 289 |
| QY | 308 | TGACAGACTTATTGGGGAAGTAAAGATATATATGTTCAATTTCAGTCGCTGGAAGATGG | 367 |
| Db | 290 | TGAGAAACTGATCGGGGAAGTAAAG--AACATGTTCAATTGATGTCAATAGGAATGG | 346 |
| QY | 368 | AG-----GCAATGATCTCTTCAACGACTTTGCTGCTGATGACGTTGA | 412 |
| Db | 347 | AGAGTTAATGAGTCCGCTCAATGATCTCATTCACGCGCTTGGATGTGACAGCGCTTGA | 406 |
| QY | 413 | ACGTTTGGGAATCGACAGCGATTTCAAAAAAGAGATAAAACGGCACTCGATTATGTTAA | 472 |
| Db | 407 | ACGTTTGGGATCCATGACATTTCAAGATGAGATAAATCGCGCTTGATTATGTTTA | 466 |
| QY | 473 | CAGTTATTGGAA CGAAAAAGCCATTGGATGTGGGAGGAGAGTGTGTGACTGACCTCAA | 532 |
| Db | 467 | CAGTTATTGGGGCGAAAAATGGCATCGGATCGGGAGGAGAGTGTGTACTGATCTGAA | 526 |
| QY | 533 | CTCAACCGCCTTGGGGCTTGGAACTCTCCGACTACACGGATACACTGTGTCTTCAGATGT | 592 |
| Db | 527 | CTCAACTGCGTTGGGGCTTGGAA CCGTACGACTACCGGATACCCGGTGTCTTCAGATGT | 586 |
| QY | 593 | TTTGAACGTTTTTAAAGCAAAAAATGGGCAATTTCTTCACTGCGCAATATTTCAGATAGA | 652 |
| Db | 587 | TTTCAAGCTTTCAAGGCCAAAAATGGGCAATTTCTTCTGTGAAAAATATTTCAGACAGA | 646 |
| QY | 653 | GGGAGAGATTAGAGCGCTTCTCAATTTATTACAGGCGCTCCCTGCTGCGCTTTCCCGGCGA | 712 |
| Db | 647 | TGAAGAGATCAGAGCGCTTCTGAATTTATTCCGGCGCTCCCTCATTCGCTTTCCAGGGGA | 706 |
| QY | 713 | GAAAGTTATGATGAAGCTGAACATTTCTTACAAAAATTTAAGAGAAGCCCTGCAAAA | 772 |
| Db | 707 | GAAATTTATGATGAGCGCTGAATCTTCTTACCAAAATTTAAGAGAAGCCCTGCAAAA | 766 |
| QY | 773 | GATTCGGGATCCAGTATTACTTTCACTAGAGATACGGGACGTTCTGGAATATGTTGGCA | 832 |
| Db | 767 | GATTCGGGCTCCAGT---CTTTCGGAGAGATCCGGGACGTTTGGAAATATGTTGGCA | 823 |
| QY | 833 | CACCAATTTGGCCACGCTTGGAAAGCAAGGAATTACATGAGCGTCTTTGGACAGCACACTAA | 892 |
| Db | 824 | CACATATTTGCCCGCGATTGGAAAGCAAGGAATTACATCCAGTCTTTGGACAGGACACTGA | 883 |
| QY | 893 | AAATTAAGAACGC-----CGCCGAGAAACTTTTGAACCTTGCAAAAATTGGAATTCAA | 943 |
| Db | 884 | GAAACAGAAATCATATGTGAAGAGCAAAAAA CTTTGAACCTTGCAAAAATTGGAATTCAA | 943 |
| QY | 944 | TATATTTCACTCCTTACAGAGAGAGAGATTAAAAACATGTTCCCGATGTTGGAAGAATC | 1003 |
| Db | 944 | CATCTTTCAATCCTTACAAAAAGAGGAGTTAGAAAGTCTGGTCAAGATGTTGGAAGAATC | 1003 |
| QY | 1004 | GGGTTCTCTGAGATGACTCTTGTGACATCGTCAAGTGAATACTACGCTTTGGCTTC | 1063 |
| Db | 1004 | GGGTTTCTGAGATGACTCTTGTCCGACATCGTCAAGTGAATACTACACTTTGGCTTC | 1063 |
| QY | 1064 | CTGCATTGGCTGAGCGCTCAACATTTCTGGAATTCAGACTCGGCTTTACCAAGATGTCTCA | 1123 |
| Db | 1064 | CTGCATTGGCTGAGCGCTCAACATTTCTGGAATTCAGACTCGGCTTTGCCAAGACGTGTCA | 1123 |
| QY | 1124 | TCTTATCAGCGGTTCTTGAAGACATGTACGACGCTTTGGGACAGTAGACGAGCTGGAATCT | 1184 |
| Db | 1124 | TCTTATCAGCGGTTCTTGAAGATATGTACGACACCTTCGGCACAGTAGACGAGCTGGAATCT | 1184 |
| QY | 1184 | CTTCAAGCGACAAATTAAGATGGGATCCGTCGGCGATGGAATGCTTCCAGAAATATAT | 1244 |

| | | | |
|----|------|--|------|
| QY | 518 | TGTGACTGACCTCAACTCAACCGCCTTGGGGCTTCGAACCTCCGACTACACGGATACAC | 577 |
| Db | 581 | TGTTGCTGATCTGAACCTCAACTGCTTGGGGTTTCGAACCTTCGACTACACGGATACGC | 640 |
| QY | 578 | TGTGCTCTCAGATGTTTGAACGTTTTTAAAGACAAAAATGGGCAATTTTCTCCACTGC | 637 |
| Db | 641 | TGTGCTGCGCAGACGTTTGAATCTTTCAAAAGACAAAATGGGCAATTTCATGCTTCC | 700 |
| QY | 638 | CAATATTCAGATAGAGGGAGAGATTAGAGCGCTTCTCAATTTATTAGGGCTCCCTCGT | 697 |
| Db | 701 | ---GAGTCAGACAGAGAAAGATCAGAAAGCGTACTCAATTTATATCGGGCTTCCCTCAT | 757 |
| QY | 698 | CGCCTTTCCCGGAGAAAGTTATGATGAAGCTGAACATTTCTTACAATAATTTAAG | 757 |
| Db | 758 | CGCCTTTCCCGGAGAAAGTTATGGAAGAGCGCTGAATCTTCTCGCCAATATTTGGA | 817 |
| QY | 758 | AGAAAGCCCTGCAAAAGATTCGCGCATCCAGTATATCTTCACTAGAGATACGGGACGTTCT | 817 |
| Db | 818 | AGAAATCCCTGCAAAAGATTTAGTCTCCAGT--CTTTCACAGAGATACGGGACGTTCT | 874 |
| QY | 818 | GGAATATGTTGGCACACCAATTTGCCACGCTTGAAGCAAGAAATTACATGAGCGTCTT | 877 |
| Db | 875 | GGAATATGTTGGCACACATATTTGCCACGAATGAAGCAAGAAATCACATGACGCTTT | 934 |
| QY | 878 | TGGAAGACACACTAAAAATAGAACGC-----CGCCGAAAACTTTTAGAACTTGC | 928 |
| Db | 935 | TGGAAGAGACACTAGAAATTCAAAGTCATGTATATAATACAGAAAACTTTGGAACCTTC | 994 |
| QY | 929 | AAAATTGGAATTCATATATTTCACTCCTTACAAGAGAGAGATTAAACATGTTCCCG | 988 |
| Db | 995 | AAAATTGAGTTCAACATCTTCACTCCTTACAAAAGAGAGATTAGAATATCTCGTAG | 1054 |
| QY | 989 | ATGCTGAAAAGACTCGGGTCTCTGAGATGACCTTCTGTGCACATCGTCACGTGGAATTA | 1048 |
| Db | 1055 | ATGCTGAAAAGATTCAAGTTTCACTCAATGACCTTTGTGCACATCGTCACGTGGAATTA | 1114 |
| QY | 1049 | CTACGCTTTGGCTTCTCTGCATTTGCGTTTCGAGCCTCAACATTTCTGATTTCAGACTCGGCTT | 1108 |
| Db | 1115 | CTACACTTTGGCTTCTGCAATTTGCGTTTTCGAGCCTCAACATTTCTGATTTCAGACTCGGCTT | 1174 |
| QY | 1109 | TACCAAGATGCTCATCTTATTCACGGTTCCTGACGACATGTACGACGTCTTCGGCACAGT | 1168 |
| Db | 1175 | TGCCAAAGCGTGCATATTTATTCACGATTCTCGACGATATTTACGACACCTTTGGAACAGT | 1234 |
| QY | 1169 | AGACGAGCTGGAACCTTTCACAGCGCAATTTAAGAGATGGGATCCGTCGCGATGGAATG | 1228 |
| Db | 1235 | TGACGAGCTCGAACTCTTCACAGCGGCAATGAAGAGATGGGATCCGTCGCGATGATG | 1294 |
| QY | 1229 | CCTTCCAGATATATGAAAGAGTGTACATGATGGTTTATCACACCGTAATGAATGCG | 1288 |
| Db | 1295 | CCTTCCAGATATATGAAGAGGTGTACTCTGATACCTTTCGACACCGTAATGAACGTC | 1354 |
| QY | 1289 | TTCGAGTGGCAGAGAGGCTCAAGCGCCGAGACACGCTCAACTATGCAAGACAGGCTTGGGA | 1348 |
| Db | 1355 | TTCGAGAGGCGAGAGAGGCTCAAGAGAGACACGCTCGACTATGCTCGACGGGCTTGGGA | 1414 |
| QY | 1349 | GCGCTGTTTGTATTCGTATATGCAAGGAAGCAAAAGTGATCGCCACTGTTATCTGCCAC | 1408 |
| Db | 1415 | CGATTAATCTGATTCGTATATGCAAGGAAGCAAAAGTGATCGCCACTGTTATCTGCCAC | 1474 |
| QY | 1409 | GTTTGAGGAGTACTTTGAGAACGGGAAAGTTAGCTCTGCTCATCGCCATGCGCACTGCA | 1468 |
| Db | 1475 | GTTTGCGGAGTACTACGAGACGGGAAAGTTAGCTCTGCTCATCGCACTGCGCACTGCA | 1534 |
| QY | 1469 | ACCCATTTCTGACGTTGGAACATCCCTTCTCTGATCACATCCTCAAGGAAGTTGACTTCC | 1528 |
| Db | 1535 | ACCCATTTCTGACGATGGAACATCCCTTCTCTCTCACATCCTCAAGGAAGTTGACTTCC | 1594 |
| QY | 1529 | ATCGAAGCTCAATGACTTGTATGTATCATCTCTTCGATTAAAGGTGATACACGGTGTCTA | 1588 |
| Db | 1595 | ATCGAAGCTCAATGACTTGTGCACTTCCCATCTTCGACTACGAGGTGATACCGGGTGTCTA | 1654 |
| QY | 1589 | CAAGGCAGACAGGGCCCGTGGAGAAAGACTTCGTCTATATCATGTTATATGAAGACAA | 1648 |

| | | | |
|----|------|--|------|
| Db | 1655 | CAAGCGGACAGAGCCCGTGAGAGAAGAGCTTCTAGTATATCTTGTATATGAAGACAA | 1714 |
| QY | 1649 | TCCTGATTAACGGAAGAAGATGCTCTGAATCATATCAACTTCATGATCAGGACGCAAT | 1708 |
| Db | 1715 | TCCTGGAGCAACAGAGGAAGATGCTCTCGACCATATCAACGCCATGATCAGTGAAGTAAT | 1774 |
| QY | 1709 | CAGAGAATTAAATTGGAGCTTCTAAAGCCAGACAACAGTGTCCCATCACTTCCAAGAA | 1768 |
| Db | 1775 | CAGAGATTAAATTGGAGCTTCTCAACCCAAACAGCAGTGTCCCATATCTTCCAAGAA | 1834 |
| QY | 1769 | ACACGCATTTGCATATAAGCAGAGTTTGGCATCAACGGTTACAGATACCGAGATGGCTACAG | 1828 |
| Db | 1835 | ACATGTTTTTGACATTAAGCAGAGCTTCCATTTACGGGTACAATAATCGAGATGGCTACAG | 1894 |
| QY | 1829 | CTTTGCCAACGTTGAAACAAAGAGTTTGGTGAATGAGAACCGTCATTGAACCTGTGCCTTT | 1888 |
| Db | 1895 | CGTTGCCAACATGAAACAAAGAGTTTGGTGAAGAGAACCGTGATTGATCCTGTGACTTT | 1954 |
| QY | 1889 | GTAAT 1892 | |
| Db | 1955 | GTAAT 1958 | |

| | | | | | |
|------------|---|---------|------|--------|-----------------|
| RESULT 12 | AF543527 | 2082 bp | mRNA | linear | PLN 10-MAR-2003 |
| LOCUS | AF543527 | | | | |
| DEFINITION | Pinus taeda (-)-alpha-pinene synthase mRNA, complete cds. | | | | |
| ACCESSION | AF543527 | | | | |
| VERSION | AF543527.1 | | | | |
| KEYWORDS | | | | | |
| SOURCE | Pinus taeda (loblolly pine) | | | | |

REFERENCE
AUTHORS
1 (bases 1 to 2082)
Phillips, M.A., Wildung, M.R., Williams, D.C., Hyatt, D.C. and

TITLE CDNA isolation, functional expression, and characterization of (+)-alpha-pinene synthase and (-)-alpha-pinene synthase from loblolly pine (*Pinus taeda*): Stereocontrol in pinene biosynthesis

JOURNAL Arch. Biochem. Biophys. 411 (2), 267-276 (2003)

REFERENCE
2 (Vases 1 to 2002),
AUTHORS Phillips, M.A., Wildung, M.R., Williams, D.C. and Croteau, R.B
TITLE Direct Submission
JOURNAL Submitted (09-SEP-2002) Institute of Biological Chemistry,

JOURNAL Submitted (09-SEP-2002) Institute of Biological Chemistry,
Washington State University, PO Box 646340, Pullman, WA 99164-6340,
USA

| FEATURES | Location/Qualifiers |
|----------|---------------------|
| source | 1. .2082 |

CDS

```

/NOTE="monoterpene synthase"
/codon_start=1
/product="(-)-alpha-pinene synthase"
/protein_id="AAO61225.1"
/db_xref="GI:28894482"
/translation="MSPVSVISLPSDLCLPTSFIDRSRELPLHITIPNVAMRROGK
LMTRASMSMIRTAVSDDAVIRRRGDTFSNLWDDDLIQSLSPYGEPSYREARERLIG
EVKNSFNSMNEDESITPLDDLQRLMWYDSVERLIGIDRHFKELKSALDHVRYWS
EKGIGCGRESVTDLNSTALGLRTLRLHGVDVSADVLNHPKNOGQPACTLKQTEDOI
RTVLNLYRASLIAFPEGKVMDEAESFAKYLKEALQKIPVSSFREIADVLEYGWHTY
LPRLEARNYIDVEGYQDTEKNSYMKTEKLELAKLEFNI FHALQKRELEVLVRWKGYS
GSPQMTFCRHRYVEYYTLASCIAPFQSGFRLGPAKACHIITVLDDMYDTFGTLDEL
ELFTSAIKRMEPSATECLPEYMKGVMYIYNTVNMESQEADKAOGRDTLNYCRQAWEE
YIDAYMQEAKMTASGEVPTFEEYYENGRYSSGHRVSAIQPLITLTDIPBEHVLKEVDI
PSQLNDIASALRLRGDTRCYQADRARGEASCSICYMKDNPGETEADLANHLNAMIS
DVIKGLNWEELLKRNSSVPISAKHAFDISRAFHCGKYKRDGYSVANIEFKSLVKRTVI
DPVTL"

```


(+)-alpha-pinene synthase and (-)-alpha-pinene synthase from
loblolly pine (*Pinus taeda*): Stereocontrol in pinene biosynthesis
Arch. Biochem. Biophys. 411 (2), 267-276 (2003)
JOURNAL
MEDLINE
22510022
PUBMED
12623076
REFERENCE
2 (bases 1 to 2162)
AUTHORS
Phillips, M.A., Wildung, M.R., Williams, D.C. and Croteau, R.B.
TITLE
Direct Submision
JOURNAL
Submitted (09-SEP-2002) Institute of Biological Chemistry,
Washington State University, PO Box 646340, Pullman, WA 99164-6340,
USA

FEATURES
source
Location/Qualifiers
1. 2162
/organism="Pinus taeda"
/mol_type="mRNA"
/db_xref="taxon:3352"
59.1942
/note="monoterpene synthase; P110"
/codon_start=1
/product="alpha-terpineol synthase"
/protein_id="AA061227.1"
/db_xref="GI:28894486"
/translation="MDLISVLPASAKSCVCLHKPLSSSTHKLKPFCKTIRILVMBRW
EFARPSMSLSTVASEDDIQRTGYSLSNLMNDVIOFLSTPYGELAYRERARLIDEV
RDISSMSLEDGFSDLIORLWVNDVERLIGIDRHFKNEIKSALDYVSYWSEKIGC
GTSIIITNLNSTALGFRTLRHGVPSADVLKHFNRQIGFVSCPSETEEDIRLWNL
YRASLIAPVAFPEKMEBESFSEKYLKETLQKIPDSLSREIGDVLBHGHTNLP
RUEARNYIDVFQDITKMEPNRKTLELAKLEFNIFQSIQKTBLESLRWNDGS
POITFTRHVEYTLASCLAFEPQHSFRLGFAKACHILVLDMDYDLFGTVDLKL
FTAIAIKRWDPSATDCLPQYKGIYMWVYNTVNEMSAEQAKQGRDITLYARQAWEDCL
DSHMQEAKIATGFLPTFEEXLENGKVSASHRVSLQPMILMDIPEPHILKEVDPS
NINDLACAMRLRGDTRCYQADRARGEETSCISCYMKDNGATEDALNHLNVMISGV
IKELMWELLKPNSVPISSKXINFDITRAFHGYKYRDSVSVSVETKSLVMRTLEP
VPL"

ORIGIN

Query Match 57.4%; Score 1155.6; DB 8; Length 2162;
Best Local Similarity 79.0%; Pred. No. 3.6e-308;
Matches 1464; Conservative 0; Mismatches 354; Indels 36; Gaps 6;

QY 81 AGTCTCTCATGAGATTAAAGGCTCTCCGTAGAACAAATCCCAACTCTTGAATCTGCAGG 140
DB 125 AGTTCTACTATAAATTAAAGCTTTCTGCAAAAACAATCCGATCTTGTAATGCCGAGG 184
QY 141 CCGGGAAATCCGTCGCGCATTCATTAACATGTTGTGACAAGCGTCGATCTACTGAT 200
DB 185 CGATGGGAATTGCGACGCGCTCCATGA-----GTCTGAGTACCGTTGCATCTGAAGAT 238
QY 201 TCTGTACAGACGCGTGGCAACTATTCACCACTGTGGAGCATGATTTCATACAG 260
DB 239 GATATACAAAGACGACGCGGCTTATCTTCCAACCTGTGAACGATGATGATACAG 298
QY 261 TCTCTGATCTCAACGCGCTTATGAGCACTGATTACCGGGAACGTGCTGACAGACTTAT 320
DB 299 TTTCTG---TCAACGCGCTTATGGGGAACCTTACCGTGAACGTGCTGACGCACTGATT 355
QY 321 GGGGAAGTAAAGATATAATGTTCAATTCAAGTCGCTGGAAGATGAGGCAATGATCTC 380
DB 356 GATGAAGTAAAGGACATATTCAATTGATGATTCATTGGAAGATGAGAAATTCAAGTATCTC 415
QY 381 CTTCAACGACTTTTGCTGCTGATGAGCACTGGAACGTTGGGAATCGACGCAATTTCAA 440
DB 416 ATTCAACGCTTTTGATGCTGATTAACGTTGAACGTTGGGATCGAATGCGCAATTTCAA 475
QY 441 AAAGAGATAAAACGCGCACTGATTAATGTTAAAGATTATGGAACGAAAGGCAATTTGA 500
DB 476 AATGAGATCAAAATCAGCGCTGATTAATGTTAAAGATTACTGAGCGAAAGGCAATTTGA 535
QY 501 TGTGGAGGAGAGTGTGTGACTGACCTCAACTCAACGCGCTTGCGGCTTGAAGTCTC 560
DB 536 TGTGGAGCAAAAGTATTACTAATCTCAATCAACTGCGCTTGCGGCTTTCGAAGTCTT 595
QY 561 CGACTACAGGATACACTGTGTCTTCAAGTCTTTGAACGTTTAAAGCAAAATGCGG 620

DB 596 CGATTACACGATACCCTGTTTCTGCAGACGTTTGAACAATTTCAGAAACCAAAATTTGGG 655
QY 621 CAATTTCTCTCCACTGCAATATTCAGATAGAGGAGAGATTAGAGCGCTTCTCAATTTA 680
DB 656 CAGTTTGATCATGTCC--TAGTAGACAGAGAGAGACATAAGAAATCATGTCAATTTA 712
QY 681 TTCAGGCGCTCCCT-----CGTCGCTTCCCGCGAGAAAGTTATGATGA 728
DB 713 TATCGGCTTCCCTCATGCTTCCCGTTCGCTTCCCGGTGAGAAAGTTATGAGAG 772
QY 729 GCTGAAACATTTCTTACAAATATTTAAGAGAGCCCTGCAAAAGATTCCGGCATCCAGT 788
DB 773 GCAGAAAGCTTCTCAGAGAAATATTTAAAGGAAACTCTGCAAAAGATTCCGGACTGCAGT 832
QY 789 ATACTTTCACTAGAGATACGGGACGTTCTGGAATATGTTGGCACACCAATTTGCCACGC 848
DB 833 ---CTTCAAGAGATAGGGGACGTTTGGAAACATGGTTGGCACACAAATTTGCCGCA 889
QY 849 TTGGAAGCAAGAAATTACATGACGCTTTTGGACAGACACTAAATAATAGAACGC--- 904
DB 890 TTAGAAGCAAGAAATTACATGACGCTTTCGACAAAGACACTAAGAAATATGAGCCAAAT 949
QY 905 -----CGCCGAGAACTTTTAAAGCTTGCAAAATTTGAAATTCATATATTTCACTCCTTA 959
DB 950 AGGAAGACGGAAGAACTGTGAAGACTTGCGAAACTGAGTTCAACATCTTCAATCCATA 1009
QY 960 CAAGAGAGAGAGTTAAACAATGTTCCCGATGCTGGAAGACTCGGGTCTCCTGAGATG 1019
DB 1010 CAGAAGACAGAGTTAGAGTCCCTCTTGAGATGTTGGAATGATTCAGGTTCCGCTCAGATT 1069
QY 1020 ACCTTCTGTGACATCGTCACGTTGGAATTACTACGCTTTGGCTTCTGCAATGCGTTCCAG 1079
DB 1070 ACCTTCACTGACATCGCCACGTGAGTACTACACTTTGGCTTCTGCAATGCGTTTGAG 1129
QY 1080 CTTCAACATTTGATTCAGACTCGGCTTTTACCAAGATGCTCATCTTATCAGCGTTCTT 1139
DB 1130 CCTCAACATTTGATTCAGACTCGGCTTTTGCMAAGCTTGTCATATTTCTACGTGTTCTC 1189
QY 1140 GAGCAGATGTACGACGCTTTCGGAACAGTAGACGAGCTGGAATCTTTCACAGCGCAAT 1199
DB 1190 GAGCATATGTACGACCTCTTCGGAACAGTTGACGAGCTCAAACTTTTCACAGCGCAATT 1249
QY 1200 AAGAGATGGGATCCGTCGCGATGGAATGCTTCCAGAAATATGAAAGAGTGTACATG 1259
DB 1250 AAGAGATGGGATCCGTCGCGCACAGATGCTTCCACAAATATGAAAGATTTACATG 1309
QY 1260 ATGTTTATCAACACCGTAATGAATGCTCGAGTGGCAGAGAGGCTCAAGCGCGAGAC 1319
DB 1310 ATGTTTATCAACACCGTAATGAATGCTCGAGTGGCAGAGAGGCTCAAGCGCGAGAC 1369
QY 1320 ACGTTCAATATGCAAGACAGGCTTGGGAGGCGTGTGTTGATTCGTATATGACGAGAGCA 1379
DB 1370 ACTTCAACTATGCTGCACAGGCTTGGAGGATGTGTTGATTCACATATGCAAGAGCA 1429
QY 1380 AAGTGAATGCCCACTGTTATCTGCCCAAGTTGAGAGATCTTGGAAGACGGGAAAGTT 1439
DB 1430 AAGTGAATGCCCACTGTTTCTGCCCAACATTCGAGGAATCTTGGAAGACGGGAAAGTT 1489
QY 1440 AGCTCTCTCATCGCCCATGCGCACTGCAACCCCAATTCGACGTTGGAACATCCCTTTCT 1499
DB 1490 AGCTCTCTCATCGCGTATCGGCAATGCAACCCCATGCTGACGATGGAATCCCTTCCCT 1549
QY 1500 GATCAATCCTCAAGGAAGTTGACTTCCCATGGAAGCTCAATGACTGATATGATCATC 1559
DB 1550 CCTCAATCCTCAAGGAAGTTGACTTCCCATCCAACTCAATGACTTGGCATGTGCCATG 1609
QY 1560 CTTGATTAAGAGGTGATACAGGCTCTACAAGGCAAGACAGGCGCGTGAGAGAAAGCT 1619
DB 1610 CTTGATTAAGAGGTGATACAGGCTCTACAAGGCAAGACAGGCGCTGTGAGAGAAAGCC 1669
QY 1620 TCGTATATATCATGTTATATGAAGCAATCTGATTAACGGAAGAAAGATGCTGAAAT 1679

Db 1670 TCCTGATATCTTGTATATGAAGAACAACCTCGAGCAACAGAGAGATGCTTAAAT 1729
QY 1680 CATATCAACTTCATGATCAGGACGCAATCAGAAATTAATTGGAGCTTCTAAAGCCA 1739
Db 1730 CATCTCAACGTCATGATCAGTGCGCTAATTAAGAATTAATTGGAGCTTCTCAAAACC 1789
QY 1740 GACACAGAGTGTCCCATCACTTCCAGAAACACGCAATTTGACATAGCAGATTGGCAT 1799
Db 1790 AACAGCAGTGTGCCATTTCTTCCAGAAATAATTAATTTGACATTACGAGCTTTCCAT 1849
QY 1800 CACGGTTACAGATACCGAGATGCGTACAGCTTTGCCAACGTTGAACAAAGATTGGTG 1859
Db 1850 TACGGTTACAAATACCGAGATGCGTACAGCGTTTCCAGCGTTGAACAAAGATTGGTG 1909
QY 1860 ATGAGAACCGTCATTTGAACCTGTGCTTTGTAAACAACACTTCAATCTACAATA 1913
Db 1910 ATGAGAACCCCTCCTTGAACCTGTGCTTTGTAAACAATCTAGAAATTACAAGA 1963

RESULT 14
AF461460 2186 bp mRNA linear PLN 27-MAR-2003
LOCUS AF461460
DEFINITION Picea abies (+)-3-carene synthase (JF67) mRNA, complete cds.
ACCESSION AF461460
VERSION AF461460.1 GI:29293033
KEYWORDS Picea abies (Norway spruce)
SOURCE Picea abies
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
REFERENCE 1 (bases 1 to 2186)
AUTHORS Faeldt, J., Martin, D., Miller, B., Rawat, S. and Bohlmann, J.
TITLE Traumatic resin defense in Norway spruce (Picea abies): methyl
jasmonate-induced terpene synthase gene expression, and cDNA
cloning and functional characterization of (+)-3-carene synthase
JOURNAL Plant Mol. Biol. 51 (1), 119-133 (2003)
MEDLINE 22490501
PUBMED 12602896
REFERENCE 2 (bases 1 to 2186)
AUTHORS Faeldt, J. and Bohlmann, J.
TITLE Direct Submission
JOURNAL Submitted (20-DEC-2001) Biotechnology Laboratory, University of
British Columbia, 237-6174 University Blvd, Vancouver, BC V6T1Z4,
Canada

FEATURES
source location/Qualifiers
1. 2186
/organism="Picea abies"
/mol_type="mRNA"
/db_xref="taxon:3329"
1. 2186
/gene="JF67"
/note="PAJF67"
1. 42
/gene="JF67"
43. 1926
/gene="JF67"
/function="catalyzes the cyclization of geranyl
diphosphate to (+)-3-carene"
/product="(+) -3-carene synthase"
/protein_id="AA073863.1"
/db_xref="GI:29293034"
/translation="MSVISILPLASKSCLYKSLMSSTHELKALCRPIATLGMCRGKS
VMASKSTSLTAVSDGVORRIGDHSNLMNDNFISLSPYGAASSYGERAERLIGEV
KEIFNSLSRTDDELVSHVDLLOHLSMVDNVERLIGIDRHQTEIKVSLDYVSYWSEK
GIGSGRDIVCTDLNTALGFRILRLHGYTVFPDVEHFHFKOMGRICASDNHTRQISS
ILNLFASRLIAFGEKMEAEIISATYLKEALQTIPIVSSLSQEIQYLYRWHSNLP
RLAARTYIDILQENTKNQMDLVNTKVLKLEAKLEFNI FHSIQONELKSVSRWKEGSR
PDNFIIRHRAVEFYTLVSGIDMEPKHCTFRLSFVKMCHLITVLDMDYDTFGTIDELRL
FTAAVKRWDVSTTECLPEYMKGYTVLYETVNEMAEAGSOGSDTLSTYRQALEAYI
GAYHKEAEWISSGYLPTFDEYFENGKVSNGHRIATLOPTMLDI PPHHVLQEI DFP
KENDFACSLRLRGDTRCYQADBARAGEASCI SYMKDNPGSTQEDALNHINMIET
IKKLWELLKPDNNVPISSKGAFDINRGLHFFYNYRDGYVASNETKNLVIKTVLEP

3' UTR VPM 1927. 2186
ORIGIN /gene="JF67"

Query Match 54.8%; Score 1103.2; DB 8; Length 2186;
Best Local Similarity 76.1%; Pred. No. 1.1e-293;
Matches 1434; Conservative 0; Mismatches 420; Indels 30; Gaps 5;

QY 64 TTTCAGGTCGCTCAGTCTTCTCTGAGATTAAGGCTCTCCGTAGAACATCCCA 123
Db 86 TTACACAGTCGTTGATGAGTCTTACTCATGAGCTTAAGCTCTCTGTAGACCAATCGCA 145
QY 124 CTCTGGAATCTGCAAGCGCCGGGAATCCGTCGCCATTTCCATTAACATGTGTTGACA 183
Db 146 CACTTGGAATGTGAGCGGAGGAATCTGTATGGCTTCCAGAGCAGAGTTGACCA 205
QY 184 GCGTCGATCTACTGATTTCTGTACAGACGCGTGGCAACTATCATTTCCAACCTGTGG 243
Db 206 CTGCTGATCTGATGATGTGTACAAAGACGATAGCGGATCATCATTTCCAACCTGTGG 265
QY 244 ACGATGATTCATACAGTCTCTGATCTCAACGCTTATGAGACACTGATTAACCGGAAC 303
Db 266 ACGATAATTCATACATCTC---TCTCATCACTTATGGGCACTTCGTATGTGAAC 322
QY 304 GTGCTGACAGCTTATTGGGGAAGTAAGATATATGTTCAATTTCAAGTCGCTGGAAG 363
Db 323 GTGCTGAGAGCTCATTTGGGGAAGTAAGATATTTCAACTCACTTTCGAGACAGATG 382
QY 364 ATGA-----GGCAATGATCTCTTCAACGACTTTGCTGCTGATGACGTTG 411
Db 383 GAGAATTAGTACGTCACGTCGATGATCTCTTCAACACCTCTCGATGCTGATTAACGTTG 442
QY 412 AACGTTGGGAATGACAGGCACTTCAAAAAGATTAATAAAGCGCACTGATATGTTA 471
Db 443 AACGATTGGGATCGACAGACATTTCCAACTGAGATAAAGTTTCCCTTGATTATGTT 502
QY 472 ACAGTTATTGGAACGAAAAAGGCATGATGTGGAGGAGAGATGTTGTAAGTCACTGAC 531
Db 503 ACAGTTACTGAGCGAAAAAGGCATGATCTGGAGAGATATGTTGTAAGTCACTGAC 562
QY 532 ACTCAACCGCTTGGGCTTGAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 591
Db 563 ACAGACTGCGCTGGGCTTGAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 622
QY 592 TTTGAAGCTTTTAAAGCAAAATGGCAATTTCTCCACACTGCCAATATTCAGATAG 651
Db 623 TGTGTAACATTTCAAGACCAAGATGGCCGATTTGCT--GTTCCGACATCATACAG 679
QY 652 AGGAGAGATTAAGAGCGCTTCTCAATTTATTCAGGGCTCCCTCGCTTCCCGGCG 711
Db 680 AGAGGACAGATCAAGCGCATTTCTGAATTTATTTAGGGCTTCTCTCATGCTTTCCCG 739
QY 712 AGAAGTTATGATGAAGCTGAACATTTCTTCAAAAATATTTAAGAGAGCCCTGCAAA 771
Db 740 AAAAAGTTATGGAACAGGCTGAATATTTCTGCTACATATTTAAGAGAGCCCTACAAA 799
QY 772 AGATTCGGCATCCGTATATCTTCACTAGAGATACGGGACGTTCTGGAATATGTTGGC 831
Db 800 CGATTCAGTCTCAGT--CTTTCGAAGAGATACAGTACGTTCTCCAATATCGCTGGC 856
QY 832 ACACCAATTTGCCACGCTTGAAGCAAGAAATTAACATGACGCTTTGGAACAGACACTA 891
Db 857 ACTCAAAATTTGCCCTGATTTGAAGCAAGAAATTAACATGACGCTTTGGAACAGACTA 916
QY 892 AAAATAGA-----ACGCGCGAGAAACTTTTGAACCTTGAACCTTGAATTTCA 942
Db 917 AAAATCAAAATGCTAGATGTGAACCAAGAAAGTTTGAACCTTGAACCTTGAATTTCA 976
QY 943 ATATATTTCACTCTTCAAGAGAGAGAGTAAACATGTTTCCGATGCTGGAAGACT 1002
Db 977 ATATCTTCACTCTTCAACAGAGAGAGTAAATATCTGTTTCAAGATGCTGGAAGAAAT 1036

| | | | |
|----|------|---|------|
| Qy | 1003 | CGGTTCTCTGAGATGACCTTCTGTCGATCGTCACGCTGGAATACTACGCTTGGCTT | 1062 |
| Db | 1037 | CAGTTTCCCTGATCTAAACTTCATTCCGCGATCGTCACGCTGGAATTCTACACTTGGTCT | 1096 |
| Qy | 1063 | CCTGCAATTGCGTTGAGCCTCAACATTCTGGATTGAGACTCGGCTTTACCAAGATGTC | 1122 |
| Db | 1097 | CTGGCAATTGACATGAGCCCTAAACATTGTACATTTAGACTGAGCTTTGTGAAATGTGTC | 1156 |
| Qy | 1123 | ATCTTATCACGGTTCTTGACGACATGTACGACGTCTTCGGCACAGTAGACGAGCTGGAAC | 1182 |
| Db | 1157 | ACCTTATCACGGTTCTTGATGATATGTACACACTTTCGGAACAATAGACGAACTCCGAC | 1216 |
| Qy | 1183 | TCTTCACAGCGACATTAAGAGATGGATCCGTCGCGATGGAATGCCCTTCCAGATATA | 1242 |
| Db | 1217 | TCTTCACAGCTGCAGTTAAGAGATGGATCCGTCACCTAACCTACAGAGTGTCTTCCAGATATA | 1276 |
| Qy | 1243 | TGAAGAGAGTGTACATGATGTTTATCACACCGTAATGAATGGCTCGAGTGCAGAGA | 1302 |
| Db | 1277 | TGAAGAGAGTGTACACAGTCTTTATGAAACCGTAATGAATGGCCGCAAGAGGCACAAA | 1336 |
| Qy | 1303 | AGGCTCAAGCCGAGACACAGCTCAACTATGCAAGCAGGCTTGGAGGCGTGTGATT | 1362 |
| Db | 1337 | AGTCAAGAGCCGAGACACAGCTCAGCTATGTTCGACAGCTTTGGAGGCTTATATTGTTG | 1396 |
| Qy | 1363 | CGTATATGCAAGAACAAAGTGAATCGCCACTGTTATCTGCCACGTTTGAGAGTACT | 1422 |
| Db | 1397 | CATACCATTAAGAAAGCAGAGTGGATCTCCAGCGGTATCTACCAACGTTTGATGAGTACT | 1456 |
| Qy | 1423 | TGGAGAACGGGAAAAGTTAGCTCTGCTCATCGCCCATGCGCACTGCACCATTCTGACGT | 1482 |
| Db | 1457 | TTGAGAAATGGGAAAAGTTAGTTAGGTCAATCGCATAGCGACATTGCAACCCACATTCAATGT | 1516 |
| Qy | 1483 | TGGACATCCCTTTCTCTGATCACATCCTTCAAGGAAGTTGACTTCCCATCGAAGCTCAATG | 1542 |
| Db | 1517 | TGACATTCCTCTTCTCTCATCAGCTCTCGAGGAATGACTTTCATTCGAAGTTCAATG | 1576 |
| Qy | 1543 | ACTTGATATGTATCATCCTTCGATTAAAGGTGATACACGGTGCTACAGGCGACAGAGGG | 1602 |
| Db | 1577 | ACTTGCATGTTCATCCTTCGATTACGAGGTGACACACAGGTGTTACCAAGGCGACAGAGG | 1636 |
| Qy | 1603 | CCCGTGAGAGAAGAGCTTCTCTATATCATGTTATGAAAGACAAATCCTGATTAAACGG | 1662 |
| Db | 1637 | CTCGTGAGAGAAGAGCTTCTGTATATCATGCTATATGAAGATTAATCCCGATCCACAC | 1696 |
| Qy | 1663 | AAGAAGATGCTTGAATCATATCAACTTCATGATCAGGAGCGCAATCAGAGAATTAAAT | 1722 |
| Db | 1697 | AGGAAGATGCTCTCATCATATCAACAATGATTGAAGAAACAATCAAAAATTAAT | 1756 |
| Qy | 1723 | GGAGCTTCTAAAGCCAGACACAGTGTCCCATCACTTCCCAAGAAACACGATTTGACA | 1782 |
| Db | 1757 | GGGAGCTTCTGAAACCTGACAAACAACGTTCCAATCTCTTCCAAAGAAACATGCTTTGACA | 1816 |
| Qy | 1783 | TAAGCAGAGTTTGGCATCACGGTTACAGATACCGAGATGGCTTACAGCTTTGCCAACGTTG | 1842 |
| Db | 1817 | TAAACAGAGTTTGGCATCACTTCTACAAATTAATGAGATGGCTTACAGCTTTGCCAACATG | 1876 |
| Qy | 1843 | AAACAAAGAGTTTGGTGATGAGAACCGTCATGAAACCTGTGCTTTGTAACAACACTTCA | 1902 |
| Db | 1877 | AAACAAAGAGTTTGGTGATAAAAACCGTCTTGAACCTGTGCTTATGTAAACCGCGTATCA | 1936 |
| Qy | 1903 | AATCTACAATATTAATGAGATG | 1926 |
| Db | 1937 | ACATATCAGATGTAATTAAGTTG | 1960 |

RESULT 15
AF369918
LOCUS AF369918 2198 bp mRNA linear PLN 04-JUN-2002
DEFINITION Picea abies beta-phellandrene synthase-like protein mRNA, complete cds.
ACCESSION AF369918
VERSION AF369918.2 GI:21322149
KEYWORDS

| | | | |
|----------------------------|---|--|--------------------|
| SOURCE | Picea abies (Norway spruce) | | |
| ORGANISM | Picea abies | | |
| REFERENCE | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea. | | |
| AUTHORS | Morency,M.J., Nicole,M.C. and Seguin,A. | | |
| TITLE | 1 (bases 1 to 2198) | | |
| JOURNAL | Terpene synthase from Norway spruce, cDNA isolation and characterization of beta-phellandrene synthase-like gene Unpublished | | |
| REFERENCE | 2 (bases 1 to 2198) | | |
| AUTHORS | Morency,M.J., Nicole,M.C. and Seguin,A. | | |
| TITLE | Direct Submission | | |
| JOURNAL | Submitted (11-APR-2001) Laurentian Forestry Centre, Natural Resources Canada, 1055 du P.E.P.S. P.O. Box 3800, Sainte-Foy, Quebec G1V 4C7, Canada | | |
| REFERENCE | 3 (bases 1 to 2198) | | |
| AUTHORS | Morency,M.J., Nicole,M.C. and Seguin,A. | | |
| TITLE | Direct Submission | | |
| JOURNAL | Submitted (04-JUN-2002) Laurentian Forestry Centre, Natural Resources Canada, 1055 du P.E.P.S. P.O. Box 3800, Sainte-Foy, Quebec G1V 4C7, Canada | | |
| REMARK | Sequence update by submitter | | |
| COMMENT | On Jun 4, 2002 this sequence version replaced gi:13775100. | | |
| FEATURES | location/Qualifiers | | |
| source | 1..2198 | | |
| | /organism="Picea abies" | | |
| | /mol_type="mRNA" | | |
| | /db_xref="taxon:3329" | | |
| | /clone="Terp12c-1" | | |
| | 69..1973 | | |
| | /note="monoterpene synthase" | | |
| | /codon_start=1 | | |
| | /product="beta-phellandrene synthase-like protein" | | |
| | /protein_id="AAK39127.2" | | |
| | /db_xref="GI:21322150" | | |
| | /translation="MSPVSVIPLAYKCLPRSLMSSREVKPLHITIPNLGMCRRGKS MAPASTSMILTAAVSDDRRVQRGRNYSNLWDDFIQSLSTPYGERSYRBAETLKG EIKMFRSISKDDELITPLNDLIQRLMVDSEVLGIDRFKNEIKSLDYVSYWN EKGIGGRDSVADLNSTALGFRTLRLHGYTVSSEVLKFEDONGQFACSPKTEGEI RSNLNLVRASLIAFPGEKVMDDAEIIFSSRYLKEAVOKIPDCSLOEIAVALEYGMHTN MRLLEARNYMDVFGHPSSPWLKKNKTQYMDGEKLELAKLEFNI FHSLOQEBLOYISR WKDGLPKLAFSRHRYEYTLGSCIATDPKRAFRIGFVKTHLNTVLDDIYDFEG TMDEIELFTEAVRRWDPSSETESLPDYMKGVMVLYEALTEMAQEAQKTQGRDILNVAR KAMEIYLDYSYIOEAKNIATGYLPTFQRYFENGKISSAYRAAALTPILTLDVPLPEYIL KGIDPSPRFNDLASSFLRLRGDTRCYKADRARGEASCISSYMKDNPGSTGEDALNHI NSMINEI IKELNWEELRPDSNIPMPARKHAFDITRALHLLYKYRDERSVATKETKSLV SRMVLPEVPVL" | | |
| ORIGIN | | | |
| Query Match | 54.7%; | Score 1101.4; | DB 8; Length 2198; |
| Best Local Similarity | 77.3%; | Pred. No. 3.6e-293; | |
| Matches 1461; Conservative | 0; | Mismatches 371; | Indels 57; Gaps 8; |
| Qy | 67 | CCAGTGTGCTCCTCAGTTCCTTCATGAGATTAAAGGCTCTCCGTAGAACAAATCCCACTC | 126 |
| Db | 115 | CCAGATCGTTGATGAGTTCTAGTCGTGAGGTTAAGCCTCTCCATATAACAATCCCAATC | 174 |
| Qy | 127 | TTGGAATCTGAGCGCGGGAATCCGTCGCGC--ATTCCATAAACATGTGTTGACAA | 183 |
| Db | 175 | TTGGAATGTGACAGCGGAGGAATCAATGGCACACGACTTCCACGACATGATTTGACCG | 234 |
| Qy | 184 | GCGTGCATCTACTGAT--TCTGTACAGAGACGCGGTGGCAACTATCATTCCAACCTGT | 240 |
| Db | 235 | CCGCCGTCTCTGATGATGACCCGTGTACAAAGACGACAGAGGCAATTATCACTCGAACCTCT | 294 |
| Qy | 241 | GGGACGATGATTTCATACAGTCTCTGATCTCAACGCCCTTATGAGACCACTGATTACCGG | 300 |
| Db | 295 | GGGACGATGATTTCATACAGTCTC--TTTCAACGCCCTTATGGGGAACCTTCTTATCGGG | 351 |
| Qy | 301 | AACGTGCTGACAGACTTATTGGGGAAGTAAAGATATAATGTTCAATTCAAGTCGCTGG | 360 |
| Db | 352 | AACGTGCTGAGACACTGAAAGGGGAAATAAAG--AAGATGTTCAAGATCAATCTCAAAAG | 408 |

QY 361 AAGATGAG-----GCAATGATCTCTTCAACGACTTTGCTGTCGATG 405
 DB 409 ACGATGAGAAATTAATACACCCCTCAATGATCTCATTCACGACTTGGATGTCGATA 468
 QY 406 ACGTTGAACGTTTGGGAATCGACAGGCAATTCAAAAAGAGATAAAAACGCACTCGATT 465
 DB 469 GCGTTGAACGTTTGGGGATCGATAGACATTTCAAAAATGAGATAAATACGCGCTGATT 528
 QY 466 ATGTTAACAGTTATTGGAACGAAAAAGGCATTTGATGTGGAGGGAGAGTGTGTACTG 525
 DB 529 ATGTTACAGTTATTGGAATGAAAAAGGCATTTGATGTGGAGAGATAGTGTGTGCTG 588
 QY 526 ACCCTCACTCAACCGCTTGGGGCTTCGAATCTCCGACTACACGATACATGTGTCTT 585
 DB 589 ATCTCAATTCACCTGCTTGGGGTTTCAACTCTGCGCTGCACGGGTACACGCTGTCTT 648
 QY 586 CAGATGTTTGAACGTTTAAAGACAAAAATGGGCAATTTCTCCACTGCCAATATTC 645
 DB 649 CAGAGGTTTGAAGTTTGAAGACCAAAACGACAGTTTGCATGCTCTCCCACTA--- 705
 QY 646 AGATAGAGGAGAGATTTAGAGGCGTCTCAATTTATTCAGGGCCTCCCTGCTGCTTTC 705
 DB 706 AAACAGAAAGGAGATTCAGAGCGCTCTTAATTTATTCGGGCTTCCCTCATTTGCCCTTC 765
 QY 706 CCGCGAGAAAGTTATGATGAAGCTGAACATTTCTACAAAATATTTAAGAGAAAGCCC 765
 DB 766 CTGGGGAGAAAGTTATGAGCAGCGCTGAATCTTCTTCAGATATTTGAAGAAAGCCG 825
 QY 766 TGCAAAAGATTCGGGCATCCAGTATCTTCACTAGAGATACGGGACGTTCTGGAATATG 825
 DB 826 TGCAAAAGATTCGGGCATCCGAGTCACT---CTTCAAGAGATAGCCTATGCTTGGAAATATG 882
 QY 826 GTTGGCACACCAATTTGCCACGCTTGAAGCAAGAAATTACATGACGCTTTGGAC--- 882
 DB 883 GTTGGCACACCAATATGCAAGATTTGAAGCAAGAAATTACATGACGATTTGGACATC 942
 QY 883 -----AGCACATTAATAAGAAAGCGCGCGAGAACTTTAG 921
 DB 943 CTAGTAGCCCATGGCTCAAGAAAGATTAAGCAATATATGACGGCGAGAACTTTAG 1002
 QY 922 AACTTGCAAAATTTGAATTCATATATTTCACTCTTACAGAGAGAGAGTTAAACATG 981
 DB 1003 AACTAGCAAAATTTGAAGTTCAATATCTTTCACTCTTGAACAGAGAGAGTTCAATATA 1062
 QY 982 TTTCCCGATGCTGGAAGACTCGGGTCTCTGAGATGACCTTCTGTGACATCGTCACG 1041
 DB 1063 TCTCCAGATGCTGGAAGAAATTCGGGTTGCTTAACTGGCCTTCAATCGGCATCGTCACG 1122
 QY 1042 TGAATATCAAGCTTTGGCTTCTGATTCGCTTGCAGCTTCAACATTTCTGATTCAAGAC 1101
 DB 1123 TGAATATCAAGCTTTGGGCTTCTGATTCGACTGACCCCAACATCGTGCATTCAGAC 1182
 QY 1102 TCGCTTTTCAAGATGCTCATCTTATCAAGGTTCTTGAAGCAATGACGCTTTCG 1161
 DB 1183 TCGCTTTTCAAGATGCTCATCTTATCAAGGTTCTGAGCATATCTACGACATTCG 1242
 QY 1162 GCACAGTAGAGAGCTGGAAGCTTTCACAGCGACAATTAAGAGATGGATCCGTCGCGA 1221
 DB 1243 GAACGATGAGAGAAATCGAAGCTTTCACAGAGCAAGTCAAGAGATGGATCCGTCGCGA 1302
 QY 1222 TGAATGCTTCCAGATATATGAAGAGCTTACATGATGTTATACACCGTAATG 1281
 DB 1303 CAGAGAGCTTCCAGACTATATGAAGAGAGTGTACATGTTACTTACGAAAGCCCTAATG 1362
 QY 1282 AAATGCTTCAAGTGGCAGAGAGGCTCAAGCGCGAGACACGCTCAACTATGCAAGACAG 1341
 DB 1363 AAATGCTTCAAGAGGCGCAGAAAAACAAAGCGCGAGACACGCTCAACTATGCTGAAAGG 1422
 QY 1342 CTTGGAGAGGCGTGTGTTGATTCGATATGAGAGAAAGCAAGTGGATCGCACTGGTTATC 1401
 DB 1423 CTTGGAGATTTATCTTGAATTCGATATTCAGAAAGCAAGTGGATCGCACTGGTTATC 1482
 QY 1402 TGCCACGTTTGAAGAGTACTTGAGAAAGGAAAGTTAGCTCTGCTCATCGCCCATGCG 1461

DB 1483 TGCCACATTTCAAGAGTACTTTGAGAAAGGAAATTAAGCTCTGCTTATCGCGACGG 1542
 QY 1462 CACTGCAACCATTTCTGACGTTGACATCCCTTCTGATACATCTCAAGAAAGTTG 1521
 DB 1543 CATTCACACCATCTTCAATTTGACGTAACGCTTCTGATATACATCTGAAAGGAATTG 1602
 QY 1522 ACTTCCCATGGAAGCTCAATGACTTGAATATGATCATCTTGCATTAAGAGGTGATAC 1581
 DB 1603 ATTTTCAATGAGATTTCAATGATTTGGCATCTTCTTCTGACTACGAGGTGACACAC 1662
 QY 1582 GGTCTACAGGCAAGACAGAGGCGCGTGAGAGAAAGCTTCGTATATCATGTTATATGA 1641
 DB 1663 GCTGCTACAGGCGGATAGGGCCCGTGAGAGAAAGCTTCGTATATCTTGTATATGA 1722
 QY 1642 AAGACAATCTGGAATTAACGGAAGAGATGCTCTGAATCATATCAACTCATGATCAGG 1701
 DB 1723 AAGACAATCTGGAATTAACGGAAGAGATGCTCTGAATCATATCAACTCATGATCAATG 1782
 QY 1702 ACGCAATCAGAAATTAATTTGGAGCTTCTAAAGCCAGACAAAGTGTCCCATCACTT 1761
 DB 1783 AAATATCAAGAAATTAATTTGGAAATTAAGACCTGATAGCAATATTCATGCTG 1842
 QY 1762 CCAAGAAACGCAATTTGACATTAAGAGATTTGGCATCACGCTTACAGATACCGAGATG 1821
 DB 1843 CGAGAAACATGCTTTGACATTAACGAGCTCTCCACCACTCTATTAATAACGAGATG 1902
 QY 1822 GCTACAGCTTGGCCACGTTGAACAAAGATTTGGTATGAGAACGCTCATTTGAACCTG 1881
 DB 1903 GGTTCAGCGTGGCCACTAAGGAAACGAAAGTCTGTCAGCAGAAATGCTTGAACCTG 1962
 QY 1882 TGCTTTGTAAACAAGACTTCAATCTTACA 1910
 DB 1963 TGCTTTGTAAACAAGCTTATCTTTTACA 1991

Search completed: July 26, 2004, 12:26:24
 Job time : 7598 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 26, 2004, 09:57:53 ; Search time 762 Seconds
(without alignments)
11222.602 Million cell updates/sec

Title: US-10-025-145A-64
Perfect score: 2013
Sequence: 1 tttagcgtgcctcttctatc.....aaaaaaaaaaaaaaaa 2013

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|------------|--------------------|
| 1 | 2013 | 100.0 | 2013 | 4 AAF73411 | Aaf73411 Grand fir |
| 2 | 1306.8 | 64.9 | 2018 | 2 AAX08644 | Aax08644 Pinene sy |
| 3 | 1306.8 | 64.9 | 2018 | 3 AAA38922 | Aaa38922 Grand fir |
| 4 | 1306.8 | 64.9 | 2018 | 4 AAF73372 | Aaf73372 Grand fir |
| 5 | 1092.4 | 54.3 | 1890 | 4 AAF73421 | Aaf73421 Grand fir |
| 6 | 1072.4 | 53.3 | 2186 | 4 AAF73412 | Aaf73412 Grand fir |
| 7 | 1071.6 | 53.2 | 2196 | 2 AAX08643 | Aax08643 Myrcene s |
| 8 | 1071.6 | 53.2 | 2196 | 3 AAA38927 | Aaa38927 Grand fir |
| 9 | 1071.6 | 53.2 | 2196 | 4 AAF73371 | Aaf73371 Grand fir |
| 10 | 1071.6 | 53.2 | 2205 | 2 AAX08663 | Aax08663 Grand fir |
| 11 | 1071.6 | 53.2 | 2205 | 4 AAF73391 | Aaf73391 Grand fir |
| 12 | 929.4 | 46.2 | 2429 | 4 AAF73413 | Aaf73413 Grand fir |
| 13 | 925.4 | 46.0 | 2089 | 2 AAX08645 | Aax08645 Limonene |
| 14 | 925.4 | 46.0 | 2089 | 3 AAA38938 | Aaa38938 Limonene |
| 15 | 925.4 | 46.0 | 2089 | 4 AAF73373 | Aaf73373 Grand fir |
| 16 | 807.4 | 40.1 | 1513 | 3 AAA69551 | Aaa69551 Pinus rad |
| 17 | 805.8 | 40.0 | 1634 | 3 AAA69644 | Aaa69644 Pinus rad |
| 18 | 623.6 | 31.0 | 1173 | 3 AAA69643 | Aaa69643 Pinus rad |
| 19 | 471 | 23.4 | 696 | 4 AAF73414 | Aaf73414 Grand fir |
| 20 | 448.6 | 22.3 | 1885 | 2 AAX87534 | Aax87534 Delta-sel |
| 21 | 445.8 | 22.1 | 1865 | 3 AAA38933 | Aaa38933 Grand fir |
| 22 | 445.8 | 22.1 | 1885 | 2 AAX87533 | Aax87533 Delta-sel |
| 23 | 445.8 | 22.1 | 1888 | 2 AAX87505 | Aax87505 Grand fir |

| | | | | | |
|----|-------|------|------|------------|--------------------|
| 24 | 444.2 | 22.1 | 1885 | 2 AAX87532 | Aax87532 Delta-sel |
| 25 | 429.6 | 21.3 | 1967 | 2 AAX87513 | Aax87513 Grand fir |
| 26 | 429.6 | 21.3 | 1967 | 2 AAX08655 | Aax08655 Grand fir |
| 27 | 429.6 | 21.3 | 1967 | 4 AAF73383 | Aaf73383 Grand fir |
| 28 | 427 | 21.2 | 2700 | 2 AAT97447 | Aat97447 Pacific y |
| 29 | 427 | 21.2 | 2700 | 3 AAA38931 | Aaa38931 Yew taxad |
| 30 | 391.6 | 19.5 | 1977 | 2 AAX87506 | Aax87506 Grand fir |
| 31 | 391.6 | 19.5 | 2424 | 2 AAX08654 | Aax08654 Grand fir |
| 32 | 391.6 | 19.5 | 2424 | 3 AAA38932 | Aaa38932 Grand fir |
| 33 | 391.6 | 19.5 | 2424 | 4 AAF73382 | Aaf73382 Grand fir |
| 34 | 391.6 | 19.5 | 2528 | 2 AAX87529 | Aax87529 Grand fir |
| 35 | 391.6 | 19.5 | 2528 | 2 AAX87531 | Aax87531 E-alpha-b |
| 36 | 391.6 | 19.5 | 2571 | 2 AAX87504 | Aax87504 Gamma-hum |
| 37 | 390.2 | 19.4 | 1785 | 2 AAX87536 | Aax87536 Gamma-hum |
| 38 | 390.2 | 19.4 | 1785 | 2 AAX87537 | Aax87537 Gamma-hum |
| 39 | 390.2 | 19.4 | 1785 | 2 AAX87535 | Aax87535 Gamma-hum |
| 40 | 390.2 | 19.4 | 1785 | 3 AAA38934 | Aaa38934 Grand fir |
| 41 | 388.6 | 19.3 | 779 | 2 AAX87530 | Aax87530 Pinus rad |
| 42 | 387.8 | 19.3 | 2525 | 2 AAX87537 | Aax87537 Gamma-hum |
| 43 | 333.6 | 16.6 | 2861 | 3 AAA38937 | Aaa38937 Grand fir |
| 44 | 285.8 | 14.2 | 462 | 3 AAA69611 | Aaa69611 Pinus rad |
| 45 | 267.2 | 13.3 | 1416 | 2 AAX08656 | Aax08656 Grand fir |

ALIGNMENTS

| | |
|-----------|---|
| RESULT 1 | |
| ID | AAAF73411 |
| AAAF73411 | standard; cDNA; 2013 BP. |
| AC | AAAF73411; |
| DT | 30-APR-2001 (first entry) |
| DE | Grand fir monoterpene synthase coding sequence fragment SEQ ID NO: 64. |
| KW | Monoterpene synthase; grand fir; cancer; (-)-camphene synthase; |
| KW | myrcene synthase; (-)-limonene synthase; (-)-pinene synthase; |
| KW | terpinolene synthase; insect resistance; nutrition; ss. |
| OS | Abies grandis. |
| PN | WO200107565-A2. |
| PD | 01-FEB-2001. |
| PF | 24-JUL-2000; 2000WO-US020264. |
| PR | 26-JUL-1999; 99US-00360545. |
| PA | (UNIW) UNIV WASHINGTON STATE RES FOUND. |
| PI | Steele CL, Bohlmann J, Croteau RB, Phillips MA; |
| DR | WPI; 2001-182782/18. |
| DR | P-PSDB; AAB69390. |
| PT | New nucleic acid encoding monoterpene synthases, for increasing terpene |
| PT | synthesis in plants, e.g. for increasing resistance to pests or for |
| PT | treatment of cancer. |
| PS | Claim 8; Page 147-149; 175pp; English. |
| CC | The present invention provides the protein and coding sequences of |
| CC | monoterpene synthases from the grand fir. These include (-)-camphene |
| CC | synthase, (-)-beta-phenylandrene synthase, terpinolene synthase, (-)- |
| CC | limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase |
| CC | and pinene synthase. The sequences can be used to produce transgenic |
| CC | plants expressing high levels of the enzymes, resulting in levels which |
| CC | are useful in protecting against and treating cancers, and to confer |
| CC | insect resistance on plants |

| | | |
|----|---|--|
| SQ | Sequence 2013 BP; 591 A; 432 C; 464 G; 526 T; 0 U; 0 Other; | |
| | Query Match | 100.0%; Score 2013; DB 4; Length 2013; |
| | Best Local Similarity | 100.0%; Pred. No. 0; |
| | Matches 2013; Conservative | 0; Mismatches 0; Indels 0; Gaps 0; |
| QY | 1 TTTTGAGCGCCTTCTTATCTGATAGCAAGCTGAATGGCTCTTCTTCTATTA | 60 |
| DB | 1 TTTTGACGTGCCCTTCTTATCTGATAGCAAGCTGAATGGCTCTTCTTCTATTA | 60 |
| QY | 61 TGGTTTCCAGAGTCGTGCGCTCAGTTCTTCTCATGAGATTAAAGGCTCTCCGTAGA | 120 |
| DB | 61 TGGTTTCCAGAGTCGTGCGCTCAGTTCTTCTCATGAGATTAAAGGCTCTCCGTAGA | 120 |
| QY | 121 CAACTCTTGGAATCTGCAGGCGCGGGAATCCGTCGCGCATTCATTAACATGTGTTGA | 180 |
| DB | 121 CAACTCTTGGAATCTGCAGGCGCGGGAATCCGTCGCGCATTCATTAACATGTGTTGA | 180 |
| QY | 181 CAAGCGTCGATCTACTGATTTCTGTACAGACGCGTGGGCAACTATCTCAACCTGT | 240 |
| DB | 181 CAAGCGTCGATCTACTGATTTCTGTACAGACGCGTGGGCAACTATCTCAACCTGT | 240 |
| QY | 241 GGGACGATGATTTTCATACAGTCTCTGATCTCAACGCGCTTATGGAGCACTGATTA | 300 |
| DB | 241 GGGACGATGATTTTCATACAGTCTCTGATCTCAACGCGCTTATGGAGCACTGATTA | 300 |
| QY | 301 AACGTGCTGACAGACTTATTTGGGGAATAAAGGATATATGTTCAATTTCAAGTC | 360 |
| DB | 301 AACGTGCTGACAGACTTATTTGGGGAATAAAGGATATATGTTCAATTTCAAGTC | 360 |
| QY | 361 AAGATGGAGGCAATGATCTCCTTCAACGACTTTTGCTGCTGATGACGTTGAACG | 420 |
| DB | 361 AAGATGGAGGCAATGATCTCCTTCAACGACTTTTGCTGCTGATGACGTTGAACG | 420 |
| QY | 421 GAATCGACAGGCAATTTCAAAAAAGATAAAAACGGCACTCGATTATGTTAA | 480 |
| DB | 421 GAATCGACAGGCAATTTCAAAAAAGATAAAAACGGCACTCGATTATGTTAA | 480 |
| QY | 481 GGAACGAAAAAGGCAATTTGATGTGGAGGAGAGTGTGTTGACTGACCTCAACT | 540 |
| DB | 481 GGAACGAAAAAGGCAATTTGATGTGGAGGAGAGTGTGTTGACTGACCTCAACT | 540 |
| QY | 541 CCTGGGCTTCCAACTCTCCGACTACGAGATACACTGTGCTTCAGATGTTTGA | 600 |
| DB | 541 CCTGGGCTTCCAACTCTCCGACTACGAGATACACTGTGCTTCAGATGTTTGA | 600 |
| QY | 601 TTTTAAAGCAAAAAATGGGCAATTTCTCCACTGCGCAATATTCAGATAGAGG | 660 |
| DB | 601 TTTTAAAGCAAAAAATGGGCAATTTCTCCACTGCGCAATATTCAGATAGAGG | 660 |
| QY | 661 TTAGAGGCGTCTCAATTTATTCAGGCGCTCCCTGCTGCGCTTTCCGGCGAG | 720 |
| DB | 661 TTAGAGGCGTCTCAATTTATTCAGGCGCTCCCTGCTGCGCTTTCCGGCGAG | 720 |
| QY | 721 TGGATGAGCTGAACATTCTCTACAAATATTTAAGAGAAAGCCCTGCAAAAG | 780 |
| DB | 721 TGGATGAGCTGAACATTCTCTACAAATATTTAAGAGAAAGCCCTGCAAAAG | 780 |
| QY | 781 CATCCAGTATACTTTCACTAGAGATACGGGAGTCTTGAATATGTTGGCACAC | 840 |
| DB | 781 CATCCAGTATACTTTCACTAGAGATACGGGAGTCTTGAATATGTTGGCACAC | 840 |
| QY | 841 TGGCAGCGTTTGAAGCAAGGAATTACATGACGTTTGGACAGCACACTAA | 900 |
| DB | 841 TGGCAGCGTTTGAAGCAAGGAATTACATGACGTTTGGACAGCACACTAA | 900 |
| QY | 901 ACGCCGCCGAGAACTTTTGAACCTTGCAAAATTTGGAATTCATATATTTCA | 960 |
| DB | 901 ACGCCGCCGAGAACTTTTGAACCTTGCAAAATTTGGAATTCATATATTTCA | 960 |
| QY | 961 AAGAGAGAGAGTTAAAAATGTTTCCCGATGGTGGAAAGACTCGGCTTCTC | 1020 |
| DB | 961 AAGAGAGAGAGTTAAAAATGTTTCCCGATGGTGGAAAGACTCGGCTTCTC | 1020 |

| | | |
|----|--|------|
| QY | 1021 CCTTCTGTCGACATCGTCAACGTCGAATACTACGCTTTGGCTTCTGCA | 1080 |
| DB | 1021 CCTTCTGTCGACATCGTCAACGTCGAATACTACGCTTTGGCTTCTGCA | 1080 |
| QY | 1081 CTCAACATTTCTGATTGAGACTCGGCTTTACCAAGATGTCTCATCTTAT | 1140 |
| DB | 1081 CTCAACATTTCTGATTGAGACTCGGCTTTACCAAGATGTCTCATCTTAT | 1140 |
| QY | 1141 ACGACATGTACGACGTCCTTCCGACAGTAGACGAGCTGGAATCTTCA | 1200 |
| DB | 1141 ACGACATGTACGACGTCCTTCCGACAGTAGACGAGCTGGAATCTTCA | 1200 |
| QY | 1201 AGAGATGGGATCCGTCGCGAGTCGAATGCCCTTCCAGAAATATGA | 1260 |
| DB | 1201 AGAGATGGGATCCGTCGCGAGTCGAATGCCCTTCCAGAAATATGA | 1260 |
| QY | 1261 TGGTTTATCACACCGTAAATGAATGGCTCGAGTGGCAGAGAAAGCT | 1320 |
| DB | 1261 TGGTTTATCACACCGTAAATGAATGGCTCGAGTGGCAGAGAAAGCT | 1320 |
| QY | 1321 CGCTCAACTATGCAAGACAGGCTTTGGAGGCGGTGTTTGATTCGTAT | 1380 |
| DB | 1321 CGCTCAACTATGCAAGACAGGCTTTGGAGGCGGTGTTTGATTCGTAT | 1380 |
| QY | 1381 AGTGAATGCCACTGTTATCTGCCCCAGTTTGAGAGTACTTGGAGAA | 1440 |
| DB | 1381 AGTGAATGCCACTGTTATCTGCCCCAGTTTGAGAGTACTTGGAGAA | 1440 |
| QY | 1441 GCTCTGCTCATCGCCCATGCGCATGCAACCCATTCTGACGTTGA | 1500 |
| DB | 1441 GCTCTGCTCATCGCCCATGCGCATGCAACCCATTCTGACGTTGA | 1500 |
| QY | 1501 ATCACAATCCTCAAGAAAGTTGACTTCCCATCGAAGCTCAATGACT | 1560 |
| DB | 1501 ATCACAATCCTCAAGAAAGTTGACTTCCCATCGAAGCTCAATGACT | 1560 |
| QY | 1561 TTGGAATTAAGAGTGATACACGGTGTCTACAAGGACAGAGGCGCT | 1620 |
| DB | 1561 TTGGAATTAAGAGTGATACACGGTGTCTACAAGGACAGAGGCGCT | 1620 |
| QY | 1621 CGTCTATATCATGTTATATGAAGACAATCCTGGATTAAACGGA | 1680 |
| DB | 1621 CGTCTATATCATGTTATATGAAGACAATCCTGGATTAAACGGA | 1680 |
| QY | 1681 ATATCACTTCATGATCAGGAGCGCAATCAGAAATTAATTTGGAG | 1740 |
| DB | 1681 ATATCACTTCATGATCAGGAGCGCAATCAGAAATTAATTTGGAG | 1740 |
| QY | 1741 ACAACAGTGTCCCATCACTTCCAGAAACACGCAATTTGACATA | 1800 |
| DB | 1741 ACAACAGTGTCCCATCACTTCCAGAAACACGCAATTTGACATA | 1800 |
| QY | 1801 ACGGTTACAGATACCGAGATGGCTTACAGCTTTGCCAACGTTGA | 1860 |
| DB | 1801 ACGGTTACAGATACCGAGATGGCTTACAGCTTTGCCAACGTTGA | 1860 |
| QY | 1861 TGAGAACCGTCATTGAACTGTGCTTGTACACACACTTCAATCTA | 1920 |
| DB | 1861 TGAGAACCGTCATTGAACTGTGCTTGTACACACACTTCAATCTA | 1920 |
| QY | 1921 AGGATGCCCTATGGGTGTATATAGGGCACACAAAATTAATATG | 1980 |
| DB | 1921 AGGATGCCCTATGGGTGTATATAGGGCACACAAAATTAATATG | 1980 |
| QY | 1981 TGTAAATTTATGAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAA | 2040 |
| DB | 1981 TGTAAATTTATGAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAA | 2040 |

RESULT 2
AAK08644
ID AAK08644 standard; cDNA; 2018 BP.

| Query Match | Best Local Similarity | Score | Length | DB | Matches | Conservative | 0 | Mismatches | 342 | Indels | 33 | Gaps | 5 |
|-------------|--|-------|--------|------|---------|--------------|---|------------|-----|--------|----|------|---|
| 68 | CAGTCGTCGCTCAGTCTCTTCATGAGATTAAAGGCTCTCCGTAGACAAATCCCACTCT | 64.9% | 1306.8 | DB 2 | 127 | 81.0% | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 53 | CAATCGTTGATCAGTCTTACCCATGAGCTTAAGGCTCTCTAGAACAAATCCAGCTCT | 64.9% | 1306.8 | DB 2 | 112 | 81.0% | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 128 | TGGAATCTGCAGCGCGGGAATCCGTCGCCCATTCCTAATAACATGTGTTGACAAGCGT | 64.9% | 1306.8 | DB 2 | 187 | 81.0% | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 113 | AGGAATGAGTAGGCGGAGGAATCTATCACTCTTCATCAAGCATGAGCTCTAACACCGT | 64.9% | 1306.8 | DB 2 | 172 | 81.0% | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 188 | CGCATCTACTGATTTCTGTACAGAGCGGTGGGCAACTATCATTCACACTGTGGGACGA | 64.9% | 1306.8 | DB 2 | 247 | 81.0% | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 173 | TGTAAACGATGATGTGTACGAAGCGCATGGGCGATTTCATTCCACTCTGGGACGA | 64.9% | 1306.8 | DB 2 | 232 | 81.0% | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 248 | TGATTTTCATACAGTCTCTGATCTCAACGCTTATGAGACACCTGATTAACGGGAACGTGC | 64.9% | 1306.8 | DB 2 | 307 | 81.0% | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 233 | TGATGTCTACACAGTCT--TTACCAACGCGCTTATGAGAAAAATCGTACCTGGAACGTGC | 64.9% | 1306.8 | DB 2 | 289 | 81.0% | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 308 | TGACAGACTTATTTGGGAAGTAAGATATAATGTTCATTTCAAGTCGCTGGAAGATGG | 64.9% | 1306.8 | DB 2 | 367 | 81.0% | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

| | | | | | | | |
|----|------|--------------------------------|---------------------------------|----------------|--------------------|------|------|
| Db | 290 | TGAGAAACTGATCGGGAGATAAG--- | AACATGTTCAATTCGATGTCATTAGAAATGG | 346 | | | |
| Qy | 368 | AG-----GCAATGATCTCCTTCAACGAC | CTTTTGTCTGTGATGACGTTGA | 412 | | | |
| Db | 347 | AGAGTTAATGAGTCCGCTCAATGATCTCAT | TCAACGCCCTTTGGATTGTGACAGACCTTGA | 406 | | | |
| Qy | 413 | ACGTTTGGGAATCGACAGGCATTTCAAAAA | AGATATAAAA | CGGCAC | TCGATTATGTTAA | 472 | |
| Db | 407 | ACGTTTGGGATCCATAGACATTTCAAAAG | TAGATATAAA | TCGGCGCT | TGATTATGTTTA | 466 | |
| Qy | 473 | CAGTTATTGGAACGAAAAAGCAATTG | ATGTGGAGGGAGAGTGTGTGACTGAC | CTTC | CA | 532 | |
| Db | 467 | CAGTTATTGGGGCGAAAAATGGCAT | TCGGATCGGGAGGGAGAGTGTGT | ACTGATCTGAA | | 526 | |
| Qy | 533 | CTCAACCGCTTGGGGCTTCGAAC | CTCCGACTACACGGATACACTGTG | CTTCAGATGT | | 592 | |
| Db | 527 | CTCACTGCGTTGGGCTTCGAAC | CCCTACGACTACACGGATACCCGGT | GTCCTTCAATGT | | 586 | |
| Qy | 593 | TTTGAACGTTTAAAGACAAAAATGG | CGCAATTTTCTCCCACTGCCAATAT | TCAGATAGA | | 652 | |
| Db | 587 | TTTCAAGCTTTGAAAGGCCAAAA | TGGGCAGTTTCTCTGCTCTGAAAA | TATTCAGACAGA | | 646 | |
| Qy | 653 | GGGAGAGATTAGAGCGTCTCAAT | TATTTACAGGGCCCTCCCTGTC | CTTCCGGCGA | | 712 | |
| Db | 647 | TGAAGAGATCAGAGCGCTCTGA | ATTATTTCCGGGCTCCCTCAT | TGCTTCCAGGGGA | | 706 | |
| Qy | 713 | GAAAGTTATGATGAAGCTGAAC | ATCTCTCACAAAATATTTAAG | AGAAGCCCTGCAAA | | 772 | |
| Db | 707 | GAAATTTATGATGAGAGCTGA | AAATCTTCTACCAAAATATTTAA | AGAAGCCCTGCAAA | | 766 | |
| Qy | 773 | GATCCGGCATCCAGTATAC | TTTCACTAGAGATACGGGAGCTT | CGAATATGTTGCA | | 832 | |
| Db | 767 | GATCCGGCTCCAGT---CTT | CGAGAGAGATCGGGAGCTTTG | GAATATGTTGCA | | 823 | |
| Qy | 833 | CACCAATTTGCCACCGCTTGA | AGCAAGAAATTACATGACGCT | CTTTGGA | CAGCACTTAA | 892 | |
| Db | 824 | CACATATTTGCCCGCATTTGA | AGCAAGAAATTACATCCAG | GTCTTTGGA | CAGCACTGA | 883 | |
| Qy | 893 | AAATAAGACGC-----CG | CGGAGAACTTTAGAACTTGC | AAAAATTGGA | ATTCAA | 943 | |
| Db | 884 | GAAACAGAGTCATATGTGA | AGACAAAAAACTTTAGAACT | CGCAAAATTG | GAGTTCAA | 943 | |
| Qy | 944 | TATATTTCACTCCTTACA | AGAGAGAGTTAAAA | CATGTTTCCG | ATGTTGAAGACTC | 1003 | |
| Db | 944 | CATCTTCAATCCTTACA | AAAAAGGAGTTAGAAAG | CTGTGATGTTGA | AAAGATC | 1003 | |
| Qy | 1004 | GGGTTCTCTGAGATGAC | CTTCTGACATCGTCA | CGTGAATACTAC | GCTTTGCTTC | 1063 | |
| Db | 1004 | GGGTTTCTCGAGATGAC | CTTCTGCCGACATCGT | CA | CGTGAATACTACACTTTG | CTTC | 1063 |
| Qy | 1064 | CTGCAATTCGCTTCGAG | CCCTCAACATTTCTGATTC | AGACTCGGCTTTAC | CAAGATGTCTCA | 1123 | |
| Db | 1064 | CTGCAATTCGCTTCGAG | CCCTCAACATTTCTGATTC | AGACTCGGCTTTG | CCAAGACGTCTCA | 1123 | |
| Qy | 1124 | TCTTATCACGGTCTTGA | CGACATGTACGCGTCTT | CGGCACAGTAG | ACGAGCTGAACT | 1183 | |
| Db | 1124 | TCTTATCACGGTCTTGA | CGATATGTACGACAC | CTTCCGACAGTAG | ACGAGCTGAACT | 1183 | |
| Qy | 1184 | CTTACAGCGCAATTAA | GATGGATCCGTC | CGGATGGAATGCC | CTTCAGAAATATAT | 1243 | |
| Db | 1184 | CTTACAGCGCAATGA | AGATGGATCCGTC | CGGATGGAATGCC | CTTCAGAAATATAT | 1243 | |
| Qy | 1244 | GAAAGAGTGTACATG | ATGTTTATCACACCGTAA | ATGAATGGCTCG | AGTGGCAGAGAA | 1303 | |
| Db | 1244 | GAAAGAGTGTACATG | ATGTTTATCACACCGTAA | ATGAATGGCTCG | AGAGAGCAGAGGA | 1303 | |
| Qy | 1304 | GGCTCAAGGCCAG | ACATACGCTCACATATG | CTCGGAAGCTTGA | AGGCTTATATGATTC | 1363 | |
| Db | 1304 | GGCTCAAGGCCAG | ACATACGCTCACATATG | CTCGGAAGCTTGA | AGGCTTATATGATTC | 1363 | |
| Qy | 1364 | GTATATGACGAA | AGCAAGTGAATCG | CACTGTTATCTG | CCCACTTTGAGAGTACTT | 1423 | |
| Db | 1364 | GTATATGACGAA | AGCAAGTGAATCG | CACTGTTATCTG | CCCTTTGATGAGTACTA | 1423 | |

QY 1424 GGAGAACGGAAAGTTAGCTCTGCTCATCGCCCATGCGCACTGCAACCCATTCTGACGTT 1483
DB 1424 CGAGAAATGGAAAGTTAGCTGTGGTCAATCCGATATCCGATTGCAACCCATTCTGACAAAT 1483
QY 1484 GGACATCCCTTCTTCTGATCATCATCCTCAAGGAAGTTGACTTCCCATCGAAGCTCAATGA 1543
DB 1484 GGACATCCCTTCTTCTGATCATCATCCTCAAGGAAGTTGACTTCCCATCGAAGCTCAATGA 1543
QY 1544 CTTGATATGATCATCCTTCGATTAAAGGTGATACACGGTGTCTTACAAAGGCAGACAGGGC 1603
DB 1544 CTTGGCATGTGCCATCCTTCGATTACGAGGTGATACGCGGTGTCTTACAAAGGCAGACAGGGC 1603
QY 1604 CCGTGAGAGAAAGCTTCGTCTATATCATGTATATGAAGACAATCCTGGATTAAACGGA 1663
DB 1604 TCGTGAGAGAAAGCTTCCTCTATATCAATGTATATGAAGACAATCCTGGATTACAGA 1663
QY 1664 AGAAGATGCTCTGAATCATATCAACTTCATGATCAGGAGCAATCAGAAATTAATTTG 1723
DB 1664 GGAAGATGCTCTGATCATATCAACGCCATGATCAGTACGTAATCAAGATTAATTTG 1723
QY 1724 GGAGCTTCTAAAGCCAGACACAGTGTCCCATCACTTCCAAAGAAACACGCAATTGACAT 1783
DB 1724 GGAATCTTCAAAACCAACACATCAATGTTCCTTCGCGGCAAGAAACATGCTTTGACAT 1783
QY 1784 AAGCAGATTGGCATCAGCGTTACAGATACCGAGATGGCTACAGCTTTGCCAACGTTGA 1843
DB 1784 CGCCAGAGCTTTCATTACCGCTACAAATACCGAGACGGCTACAGCGTTGCCAACGTTGA 1843
QY 1844 AACAAAGATTGGTGATGAGAACCGTCATGAACTGTGCTTTGTAACAACACTTCAA 1903
DB 1844 AACGAAGATTGGTGACGAGAACCTTCCTTGAATCTGTGCTTTGTAACAACACTTCAA 1903
QY 1904 ATCTACAATTAATCTGAGATGCCCTTATGGGTGTATATAGGCAACAATAATATAT 1963
DB 1904 ATCTATGCCCTATGCTATGTCGGGTAAATATATATGTGAAGGTAGCGCTTGATGTAGA 1963
QY 1964 GGTGTGTAGTAAAGCTGTAATTTATGAAAAA 2013
DB 1964 GGATAAGTTGTATATTAATTAAGTTGTAATTTAAAAA 2013

RESULT 3
AAA38922 standard; DNA; 2018 BP.
AC AAA38922;
XX 25-AUG-2000 (first entry)
DT
XX Grand fir pinene synthase DNA sequence SEQ ID NO:19.
DE
XX Synthase; protein co-ordinate data; active site; modification; terpenoid;
KW 3-dimensional coordinate; alpha carbon atom; plant; terpene synthase;
KW isoprenoid; breeding programme; fragrance; flavour; pheromone;
KW defensive agent; pigment; antitumour; steroid hormone;
KW signal transduction pathway; bile acid; affinity purification;
KW photoreceptor; enzymatic synthesis; nutrient supplement;
KW immunological reagent; ds.
XX
OS Abies grandis.
XX
PN WO200017327-A2.
XX
PD 30-MAR-2000.
XX
PF 17-SEP-1999; 99WO-US021419.
XX
PR 18-SEP-1998; 98US-0100993P.
PR 22-APR-1999; 99US-0130628P.
PR 23-AUG-1999; 99US-0150262P.
XX
PA (KENT) UNIV KENTUCKY RES DEPT.

PA (SALK) SALK INST BIOLOGICAL STUDIES.
XX
PI Chappell J, Manna KR, Noel JP, Starks CM,
XX
DR WPI; 2000-292839/25.
DR P-PSDB; AAY90837.
XX
PT Novel terpene synthase enzymes, useful for producing terpene
PT hydrocarbons, e.g. fragrances or antitumor agents, are derived from known
PT enzymes by specific amino acid alterations.
XX
PS Disclosure; Page 363-366; 450pp; English.

CC The present invention describes an isolated terpene synthase (I)
CC comprising a region with at least 20% identity to region 265-535 of a 548
CC amino acid (aa) sequence (Ia), given in AAY90831. (I) contains nine alpha
CC -carbon atoms (alphaC) that have interatomic distances, between each
CC other, within tabulated ranges, have a centre point (within a sphere of
CC radius 2.3 Angstrom) within tabulated ranges, and have an ordered
CC arrangement of R groups (defining aa side chains), excluding specific
CC tabulated arrangements (tables given in the specification). (I), and
CC related enzymes, are used to produce a wide range of terpenoids (e.g.
CC cyclic, acyclic, optionally hydroxylated), useful e.g. as fragrances,
CC flavours, pheromones, defensive agents, pigments, antitumour agents,
CC components of signal transduction pathways, precursors of steroid
CC hormones and bile acids, as photoreceptors and as co-factor side chains.
CC Some synthases with little or no catalytic activity (and nucleic acids
CC encoding them) are used as controls in the analysis of products formed by
CC enzymatic synthesis; as nutrient supplements; for affinity purification
CC of isoprenoids; or to develop immunological reagents or nucleic acids for
CC monitoring expression of terpene synthase or inheritance of the gene in
CC plant breeding programs. The new synthases may produce novel terpene
CC products. AAA38910 to AAA38938 and AAY90831 to AAY90859 represent
CC sequences used in the exemplification of the present invention

XX Sequence 2018 BP; 583 A; 431 C; 479 G; 525 T; 0 U; 0 Other;

Query Match 64.9%; Score 1306.8; DB 3; Length 2018;
Best Local Similarity 81.0%; Pred. No. 0;
Matches 1595; Conservative 0; Mismatches 342; Indels 33; Gaps 5;

QY 68 CAGTGTGCTCAGTCTTCTCATGAGATTAAAGGCTCTCCGTAGAACAAATCCCACTCT 127
DB 53 CAAATCGTTGATCAGTCTTACCAATGAGCTTAAGGCTCTCTAGAACAAATCCCACTCT 112
QY 128 TGAATCTGCAGGCGCGGGAATCCGTCGGCATTCCTCAATAACATGTGTTGACAAGCGT 187
DB 113 AGGAATGAGTAAGCGAGGGAATCTTATCACTCTTCCATCAGCATGAGCTCTACACCGT 172
QY 188 CGCATCTACTGATTTGTACAGAGACGCGTGCGCAACTATCATTTCCAACCTGTGGACGA 247
DB 173 TGTAAACGATGATGTGTACGAGACGATGGCGATTTCATTTCCAACCTGTGGACGA 232
QY 248 TGATTTCATACAGTCTCTGATCTCAACGCTTATGAGACACCTGATTAACGGGAACGTGC 307
DB 233 TGATGTATACAGTCT--TTACCAACGGCTTATGAGAAAAATCTGTAACCTGAGCGTGC 289
QY 308 TGACAGACTTATTGGGAAGTAAGATATATGTTCAATTTCAGTCTGCTGAAGATGG 367
DB 290 TGAGAACTGATCGGGGAAGTAAG--AACATGTTCAATTGATGCTATTAGAAGATGG 346
QY 368 AG-----GCAATGATCTCCTTCAACGACTTTTGCTGTGATGACGTTGA 412
DB 347 AGAGTTAATGAGTCCGCTCAATGATCTCATTCACGCGCTTGATGTGACAGACCTTGA 406
QY 413 ACGTTGGGAATCGACAGGCAATTCAAAAAAGAGATAAAACGCACTCGATTATGTTAA 472
DB 407 ACGTTGGGGAATCCATAGACATTTCAAAAGATGAGATAAAATCGCGCTTGATTATGTTTA 466
QY 473 CAGTTATTTGAAACGAAAAAGGCATTTGATGTGGAGGAGAGAGTGTGTAAGTCACTCAA 532
DB 467 CAGTTATTTGGGCGGAAAAATGCGATCGATGCGGAGGAGAGAGTGTGTTACTGATCTGAA 526

| | | | | |
|----|------|--|-------------------|-------|
| Qy | 533 | CTCAACCGCCTTGGGGCTTCGAACCTCTCCGACTACACGGATACA | CTGTGTCCTTCAGATGT | 592 |
| Db | 527 | CTCAACTGCGTTGGGGCTTCGAACCTCTACGACTACACGGATACC | CGGTGTCCTTCAGATGT | 586 |
| Qy | 593 | TTTGAACGTTTTTAAAGCAAAAAATGGCAATTTTCTCCACTGCCAATATT | CAGATAGA | 652 |
| Db | 587 | TTTCAAAAGCTTTCAAAGGCCAAAAATGGGACGTTTTCTGCTCTGAAAAATATT | CAGACAGA | 646 |
| Qy | 653 | GGGAGAGATTAGAGGCGTCTCAATTTATTACAGGCGCTCCCTCGTCGCCCTT | TCCGGCGA | 712 |
| Db | 647 | TGAAGAGATCAGAGGCGTCTGAATTTATTTCCGGGCGCTCCCTCATTTGCCCTT | TCCAGGGGA | 706 |
| Qy | 713 | GAAAGTTATGATGTAAGCTGAAACATTTCTCTACMAATATTTAAGAAAGCCCTG | CAAAA | 772 |
| Db | 707 | GAAATTTATGATGAGGCTGAAATCTTCTCTACCAATATTTAAGAAAGCCCTG | CAAAA | 766 |
| Qy | 773 | GATTCCGGCATCCAGTATATTCTTCACTAGAGATACGGGACGTTCTGGAATATG | TTGGCA | 832 |
| Db | 767 | GATTCCGGTCTCCAGT---CTTTCCGAGAGATCGGGACGTTTGGAAATATG | TTGGCA | 823 |
| Qy | 833 | CACCAATTTGGCCACGCTTGGAGCAAGGAATTACATGAGCTCTTGGACAGACA | CTAA | 892 |
| Db | 824 | CACATATTTGCCCGGATTTGGAGCAAGGAATTACATCCAAGTCTTGGACAGACA | CTGA | 883 |
| Qy | 893 | AAATAAGAACGC-----CGCCGAGAACTTTTAGAATTCGCAAAATTGGAAT | TCAA | 943 |
| Db | 884 | GAAACAGAAATCATATGTGAAGACCAAAAACTTTTAGAATTCGCAAAATTG | GAGTTCAA | 943 |
| Qy | 944 | TATATTTCACTCCTTTACAGAGAGAGAGTTAAACATGTTCCCGATGCTG | GAAGACTC | 10033 |
| Db | 944 | CATCTTTCATCTTTACAAAAGAGGAGTTAGAAAGTCTGCTCAGATGCTG | GAAGAAATC | 10033 |
| Qy | 1004 | GGGTTCTCTGAGATGACCTTCTGTGACATCGTCACTGGAATTA | CTACGCTTTGGCTTC | 10633 |
| Db | 1004 | GGGTTTCTGAGATGACCTTCTGCCACATCGTCACTGGAATTA | CTACACTTTGGCTTC | 10633 |
| Qy | 1064 | CTGCATTGCGTTTCGAGCCTCAACATTTCTGATTCAAGCTCGGCTTTG | CCAAGACGTGCA | 11233 |
| Db | 1064 | CTGCATTGCGTTTCGAGCCTCAACATTTCTGATTCAAGCTCGGCTTTG | CCAAGACGTGCA | 11233 |
| Qy | 1124 | TCTTATCAGGTTCTTGACGACATGTACGAGCTTTGGGACAGTAGACGAG | CTGGAAT | 11833 |
| Db | 1124 | TCTTATCAGGTTCTTGACGATATGTACGACACCTTCGGCACAGTAGACG | AGCTGGAAT | 11833 |
| Qy | 1184 | CTTCACAGCGACAATTAAAGATGGGATCCGTCGCCGATGGAATGCC | TTCCAGAATATAT | 12433 |
| Db | 1184 | CTTCACAGCGACAATGAAGAGATGGGATCCGTCCTCGATAGATTGCC | TTCCAGAATATAT | 12433 |
| Qy | 1244 | GAAAGAGTGTACATGATGGTTTATCACACCGTAAATGAATGGCTCGAG | TGGCAGAGAA | 13033 |
| Db | 1244 | GAAAGAGTGTACATAGCGGTTTACGACACCGTAAATGAATGGCTCGAG | TGGCAGAGAA | 13033 |
| Qy | 1304 | GGCTCAAGGCCGAGACACGCTCAACTATGCAAGACAGGCTTGGAGGCG | TGTTTGATTC | 13633 |
| Db | 1304 | GGCTCAAGGCCGAGATACGCTCACATATGCTCGGAAAGCTTGGGAGG | CTTATATTGATTC | 13633 |
| Qy | 1364 | GTATATGCAAGCAAGTGAATCGCCACTGGTTATCTGCCCACTTTGAGAG | TAATCTT | 14233 |
| Db | 1364 | GTATATGCAAGCAAGTGAATCGCCACTGGTTATCTGCCCTCTTTGATG | AGTACTTA | 14233 |
| Qy | 1424 | GGAGAACGGGAAAGTTAGCTCTGCTCATCGCCCATGGCACTGCAAC | CCATTCTGACGTT | 14833 |
| Db | 1424 | CGAGAAATGGGAAAGTTAGCTGTGTCATCGCATATCCGCATTGCAAC | CCATTCTGACAAAT | 14833 |
| Qy | 1484 | GGACATCCCCCTTCTGTATCATATCTCTCAAGGAAGTTGACTTCCCAT | CAAAAGCTTAAACGA | 15433 |
| Db | 1484 | GGACATCCCCCTTCTGTATCATATCTCTCAAGGAAGTTGACTTCCCAT | CAAAAGCTTAAACGA | 15433 |
| Qy | 1544 | CTTGATATGTATCATCTCTTCGATTAAAGAGGTGATACACGGTGTCTA | CAAGGCAGACAGGCG | 16033 |
| Db | 1544 | CTTGGCATGTGCATCTTTCGATTACGAGGTGATACGCGGTGTCTA | CAAGGCAGACAGGCG | 16033 |
| Qy | 1604 | CCGTGAGAGAAAGCTTCGTATATCATGTATATGAAAGCAATCCTGATTA | ACGGA | 16633 |

| | | | |
|----|------|---|------|
| Db | 1604 | TCGTGAGAAAGACTTCCCTCATATCATGTATAAGAACAATCCTGGAGTATCAGA | 1663 |
| QY | 1664 | AGAAGATGCTCTGCATCATATCAACTTCATGATCAGGACGCAATCAGAGAATTAAATTG | 1723 |
| Db | 1664 | GGAAGATGCTCTGCATCATATCAACGCCATGATCAGTGACGTAATCAAAGATTAAATTG | 1723 |
| QY | 1724 | GGAGCTTTCTAAGCCAGACACAAGTGTTCCTCACTTCCAAGAACACGCAATTTGACAT | 1783 |
| Db | 1724 | GGAACCTTCTCAAAACCAGACATCAATGTTCCTCATCTCGGCGAAGAAACATGCTTTTGACAT | 1783 |
| QY | 1784 | AAGCAGAGTTTGGCATCACCGTTACAGATACCGAGATGGCTACAGCTTTGCCAACGTTGA | 1843 |
| Db | 1784 | CGCCAGAGCTTCCCATTTACGGCTACAAATACCGACGCGTACAGCGTTGCCAACGTTGA | 1843 |
| QY | 1844 | AACAAAGAGTTTGGTGATGAGAACCGTCATTGAACTGTGCCCTTTGTACACACACTTCAA | 1903 |
| Db | 1844 | AACGAAAGATTGGTCACGAGAACCCCTCCTTGAACTGTGCCCTTTGTAGCACACAGCTCAA | 1903 |
| QY | 1904 | ATCTACAATATTACTGAGGATGCCCTATGGGTGTATATAGGGCACACAAAATAATATAT | 1963 |
| Db | 1904 | ATCTATGCCCTAAGCTATATGTCGGGTAAATAATATATGTGGAAGGTAGCCGTTGGATGTAGA | 1963 |
| QY | 1964 | GGTTGTATTAGTAAAGCTGTAAATTATGAAAAAATTTTTTTTTTTTTTTTTTTTTTTT | 2013 |
| Db | 1964 | GGATAAGTTTGTATTAAATTTAATAAAGTTGTAAATTAAAAAATTTTTTTTTTTTTTTTTTTTTTTT | 2013 |

RESULT 4
AAAF73372
ID AAF73372 standard; cDNA, 2018 BP.
XX
AC AAF73372;
XX
DT 30-APR-2001 (first entry)
XX
DE Grand fir (-)-pinene synthase coding sequence SEQ ID NO: 3.
XX
KM Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;
KW myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;
KM terpinolene synthase; insect resistance; nutrition; ss.
XX
OS Abies grandis.
XX
PN WO200107565-A2.
XX
PD 01-FEB-2001.
XX
PF 24-JUL-2000; 2000WO-US020264.
XX
PR 26-JUL-1999; 99US-00360545.
XX
PA (UNIV) UNIV WASHINGTON STATE RES FOUND.
XX
PI Steele Cl, Bohlmann J, Croteau RB, Phillips MA;
XX
DR WPI: 2001-182782/18.
XX
PT P-PSDB; AAB69371.
XX
PT New nucleic acid encoding monoterpene synthases, for increasing terpene
PT synthesis in plants, e.g. for increasing resistance to pests or for
PT treatment of cancer.
XX
PS Claim 38; Page 108-110; 175bp; English.
XX
XX The present invention provides the protein and coding sequences of
CC monoterpene synthases from the grand fir. These include (-)-camphene
CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-
CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase
CC and pinene synthase. The sequences can be used to produce transgenic
CC plants expressing high levels of the enzymes, resulting in levels which
CC are useful in protecting against and treating cancers, and to confer
CC insect resistance on plants

XX Sequence 2018 BP; 583 A; 431 C; 479 G; 525 T; 0 U; 0 Other;

Query Match 64.9%; Score 1306.8; DB 4; Length 2018;
Best Local Similarity 81.0%; Pred. No. 0;
Matches 1595; Conservative 0; Mismatches 342; Indels 33; Gaps 5;

```
QY 68 CAGTCGTGCTCAGTCTTCTCTAGAGATTAAAGCTCTCCGTAGAACAACTCCACTCT 127
Db 53 CAAATCGTTGATCAGTTCTACCCCACTGAGCTTAAAGCTCTCTCTAGAACAACTCCAGCTCT 112
QY 128 TGGAACTGCAGCGCCGGGAAATCCGTCCGCATTCATTAACATGTGTTGACAAGCGT 187
Db 113 AGGAATGAGTAGCGAGGAAATCTATCACTCTTCATCAGCATGAGCTCTACCAACCGT 172
QY 188 CGCATCTACTGATTCTGTACAGAGACGCGTGCGCACTATCATTCCAACCTGTGGACGA 247
Db 173 TGTAAACGATGATGTTGTACGAAGACGATGGCGGATTTCCATTCCAACCTGTGGACGA 232
QY 248 TGATTTCATACAGTCTCTGATCTCAACGCCCTTATGAGCACCTGATTACCGGGAACGTGC 307
Db 233 TGATGTCATACAGTCT--TTACCAACGCCCTTATGAGGAAAAATCGTACCTGGAACGTGC 289
QY 308 TGACAGACTTATTTGGGGAAGTAAGATATAATGTTCATTTCAAGTCCGCTGGAAGATGG 367
Db 290 TGAGAAACTGATCGGGGAAGTAAG--AACATGTTCAATTGATGTCATTAGAAAGATGG 346
QY 368 AG-----GCAATGATCTCTCTCAACGACTTTTGTGCTGATGACGTTGA 412
Db 347 AGAGTTAATGAGTCCGCTCAATGATCTCATCAACGCCCTTGGATTGTGACAGCCCTTGA 406
QY 413 ACGTTTGGGAATCGACAGGCATTTCAAAAAAGAGATAAAAAAGGCACTCGATTATGTTAA 472
Db 407 ACGTTTGGGATCCATAGACATTTCAAGATGAGATAAATCGCGCTTGATTATGTTTA 466
QY 473 CAGTTATTGGAACGAAAAAGGCATTTGATGTGGAGGAGAGAGTGTGTAAGTGAAGCTCAA 532
Db 467 CAGTTATTGGGGCGAAAAATGCGATCGATGCGGAGGAGAGAGTGTGTAAGTGAAGCTCAA 526
QY 533 CTCAACGCCCTTGGGGCTTCGAACCTCCGACTACACGAGATACATGTCCTTACAGATGT 592
Db 527 CTCAACGCGTTGGGGCTTCGAACCTCAACGACTACACGAGATACCGGTCCTTACAGATGT 586
QY 593 TTTGAACGTTTTTAAAGCAAAATGGGCAATTTTCTCCACTGCCAATATTCAAGATGA 652
Db 587 TTTCAAGCTTTCAAAAGGCCAAATGGGCAATTTCTGCTCTGAAATATTCAAGACAGA 646
QY 653 GGGAGATTTAGAGCGCTTCTCAATTTATTCAGGCGCTCCCTCGTGCCTTTCCCGGCGA 712
Db 647 TGAAGAGATCAGAGCGCTTGAATTTATTCGGGCGCTCCCTCATTTGCTTCCAGGGGA 706
QY 713 GAAAGTTATGATGAAGCTGAAACATTTCTACAAATATTTAAGAGAAAGCCCTGCMAAA 772
Db 707 GAAATTTATGATGAGGCTGAATCTTCTACCAATATTTAAGAAAGCCCTGCMAAA 766
QY 773 GATTCCGCGATCCAGTATACCTTTCACTAGAGATACGGGACGTTCTGGAATATGTTGCA 832
Db 767 GATTCGCGTCTCCAAGT--CTTTCGCGAGAGATCGGGACGTTTGGATATGTTGCA 823
QY 833 CACCAATTTGCCACGCTTGAAGCAAGAAATTAATGAGCGTCTTGGACAGACACTAA 892
Db 824 CACATATTTCGCGCGATTTGAAGCAAGAAATTAATGAGCGTCTTGGACAGACACTGA 883
QY 893 AAATAGAACGCG-----CGCCGAGAACTTTTGAAGCTTGCMAAATTGGAATTCAA 943
Db 884 GAACACGAAGTCATATGTGAAGAGCAAAAACTTTAGAACTCGCAAAATTGGAGTTCAA 943
QY 944 TATATTCACTCCTTACAAGAGAGAGATTAAACATGTTTCCGATGCTGAAAAAGACTC 1003
Db 944 CATCTTCAATCCTTACAAAAAGAGGAGTTAGAAAAGTCTGCTCAGATGCTGAAAAAGATC 1003
QY 1004 GGGTCTCTGAGATGACCTTCTGTGCAATGCTCACGTTGAATATAAGCTTTGGCTTC 1063
Db 1004 GGGTCTCTGAGATGACCTTCTGTGCAATGCTCACGTTGAATATAAGCTTTGGCTTC 1063
```

```
Db 1004 GGGTTTTCTGAGATGACCTTCTGCCGACATCGTCAACGTGGAATACTACACTTTGGCTTC 1063
QY 1064 CTGATTTGCGTTGAGCGCTCAACATTTCTGATTCAAGCTCGGCTTTTACCAAGATGTTCA 1123
Db 1064 CTGATTTGCGTTGAGCGCTCAACATTTCTGATTCAAGCTCGGCTTTTACCAAGATGTTCA 1123
QY 1124 TCTTATCAAGCTTCTTGAAGCAATGTAAGAGCTCTTCCGACAGTAGAGAGCTGGAAT 1183
Db 1124 TCTTATCAAGCTTCTTGAAGCAATGTAAGAGCTCTTCCGACAGTAGAGAGCTGGAAT 1183
QY 1184 CTTGACGCGACATTAAGAGATGGGATCCGTCGCGATGGAATGCTTCCAGAATATAT 1243
Db 1184 CTTGACGCGACATTAAGAGATGGGATCCGTCCTCGATGATAGATTGCTTCCAGAATATAT 1243
QY 1244 GAAAGAGTGTACATGATGTTTATCACACCGTAATGAAATGCTCGAGTGCGACAGAGA 1303
Db 1244 GAAAGAGTGTACATGATGTTTATCACACCGTAATGAAATGCTCGAGTGCGACAGAGA 1303
QY 1304 GGCTCAAGGCGGAGACACGCTCAACTATGCAAGACAGGCTTTGGAGGCGGTTTGAATTC 1363
Db 1304 GGCTCAAGGCGGAGATACGCTCATATATGCTCGGGAAGCTTTGGAGGCGGTTATATGATTC 1363
QY 1364 GTATATGCAAGGAAGCAAAAGTGATGCGCACTGCTTATCTGCCACGTTGAGAGTACTT 1423
Db 1364 GTATATGCAAGGAAGCAAAAGTGATGCGCACTGCTTATCTGCCCTCTTGTAGTACTTA 1423
QY 1424 GGAGAACGGGAAAGTTAGCTCTGCTCATCGCCCATGCGCACTGCAACCCATTCTGACGTT 1483
Db 1424 CGAGAAATGGGAAAGTTAGCTGCTGCTCATCGCATATCCGCAATGCAACCCATTCTGACAA 1483
QY 1484 GGAATCCCTTTCTGATCAACATCTCAAGGAAGTTGACTTCCATCGAAAGCTCAATGA 1543
Db 1484 GGAATCCCTTTCTGATCAACATCTCAAGGAAGTTGACTTCCATCGAAAGCTCAATGA 1543
QY 1544 CTTGATATGATCATCTCTGATTAAGAGTGATACACGGTGCTTACAAGGACAGAGGCG 1603
Db 1544 CTTGATATGATCATCTCTGATTAAGAGTGATACACGGTGCTTACAAGGACAGAGGCG 1603
QY 1604 CCGTGAGAGAAAGCTTCTGCTATATCATGTTATATGAAGAAATTCCTGATTAAACGA 1663
Db 1604 TCGTGAGAGAAAGCTTCTGCTATATCATGTTATATGAAGAAATTCCTGAGTATCAGA 1663
QY 1664 AGAAGATGCTGTAATCATATCAACTTCATGATCAGGAGCGCAATCAGAAATTAATTG 1723
Db 1664 GGAAGATGCTCTGATCATATCAACGCAATGATCAGTACGTAATCAAAAGATTAAATTG 1723
QY 1724 GGAGCTTTAAAGCCAGACCAAGTGTCCCATCACTTCCAAAGAAACAGCATTTGACAT 1783
Db 1724 GGAATCTTCAAAACAGACATCAATGTTCCCATCTCGCGAAGAAACATGCTTTGACAT 1783
QY 1784 AAGCAGTTTGGCATCACGCTTACAGATACCGAGATGCTACAGCTTTGCCAAGCTTGA 1843
Db 1784 CGCCAGGCTTTCATTAACGCTTCAATAACGAGACGCGTACAGCTTGGCCAAGCTTGA 1843
QY 1844 AACAAAGATTTGGTGATGAGAACCGTCATTTGAACCTGTGCTTTGTAACAACACTTCAA 1903
Db 1844 AACGAAGATTTGGTGATGAGAACCGTCATTTGAATCTGTGCTTTGTAACAACACTCAA 1903
QY 1904 ATCTATGCTTATTAATCTGAGGATGCCCTATGCGGTATATATAGGGCACCAAAAATTAATAT 1963
Db 1904 ATCTATGCTTATGCTATGCTGCGGTTAAATATATATGTGGAAGGTAGCCGTTGATGTAGA 1963
QY 1964 GGTGTTGTTAGTAAAGCTGTAAATTTATGAAAAAAATTTGTAAGGTTGTAAGGTTGTAAG 2013
Db 1964 GGATTAAGTTGTTATTAATTTAATAAGTTGTAATTTTAAAAAATTTGTAAGGTTGTAAG 2013
```

RESULT 5
AAF73421
ID AAF73421 standard, cDNA; 1890 BP.
XX
AC AAF73421;
XX

| | | |
|----|---|---|
| DT | 30-APR-2001 | (first entry) |
| XX | | |
| DE | Grand fir monoterpene synthase coding sequence SEQ ID NO: 77. | |
| XX | | |
| KW | Monoterpene synthase; grand fir; cancer; (-)-camphene synthase; | |
| KM | myrcene synthase; (-)-limonene synthase; (-)-pinene synthase; | |
| KW | terpinolene synthase; insect resistance; nutrition; ss. | |
| XX | | |
| OS | Abies grandis. | |
| PN | WO200107565-A2. | |
| XX | | |
| PD | 01-FEB-2001. | |
| XX | | |
| PF | 24-JUL-2000; 2000WO-US020264. | |
| XX | | |
| PR | 26-JUL-1999; 99US-00360545. | |
| XX | | |
| PA | (UNITV) UNIV WASHINGTON STATE RES FOUND. | |
| XX | | |
| PI | Steele Cl., Bohlmann J, Croteau RB, Phillips MA; | |
| DR | WPI; 2001-182782/18. | |
| XX | P-PADB; AAB69393. | |
| PT | New nucleic acid encoding monoterpene synthases, for increasing terpene synthesis in plants, e.g. for increasing resistance to pests or for treatment of cancer. | |
| PS | Claim 18; Page 163-165; 175pp; English. | |
| CC | The present invention provides the protein and coding sequences of monoterpene synthases from the grand fir. These include (-)-camphene synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase and pinene synthase. The sequences can be used to produce transgenic plants expressing high levels of the enzymes, resulting in levels which are useful in protecting against and treating cancers, and to confer insect resistance on plants | |
| CC | | |
| SQ | Sequence 1890 BP; 550 A; 381 C; 441 G; 518 T; 0 U; 0 Other; | |
| | Query Match | 54.3%; Score 1092.4; DB 4; Length 1890; |
| | Best Local Similarity | 76.8%; Pred. No. 3.6e-299; |
| | Matches 1439; Conservative | 0; Mismatches 396; Indels 39; Gaps 7; |
| OY | 46 TTCTATTACTCCGCTGGTTTCCAGTCGTGCCTCAGTCTCTCAATGAGATTAAAGGCTC | 105 |
| Dd | | |
| | 26 TGCTTCCAAATCGGTCCTGCACAAATCGTGATCGTTCTTAATGAGCATTAAGGCTA | 85 |
| OY | 106 TCCTAGAACAATGCCAACCTCTTGAATCTGCAGGCCGGGGAATCCGTCGGCATTCOA | 165 |
| Dd | | |
| | 86 TCAGTAGAACAAATCCCMAATCTTGATGTGCGTGGCGAGGGAATCTGTGACACATTCCC | 145 |
| OY | 166 TAAACATGTGTTGACAAGCGTCGCATCTACTG--ATTCTGACAGAGACGGGTGGGCA | 222 |
| Dd | | |
| | 146 TGAGAAATGAGTTGAGCACCGCAGTCTCTGATGATCATGTGTGTAACAAAGCATAGTCG | 205 |
| OY | 223 ACTATCATTCCAACCCTGTGGAGCATGATTTCATACAGTCTCTGATCTCCAAGCCTTAG | 282 |
| Dd | | |
| | 206 AGTTTCATTCCAATCTGTGGAGCAGATTTCATACAATCTC--TATCAAGCCTTAG | 262 |
| OY | 283 GAGCACCTGATTACCGGAACGTCGTGACAGACTTATTGGGGAAGTAAGATATAATGT | 342 |
| Dd | | |
| | 263 GGACACCTTCATACCGTGAACGTCGTGATAGACTTATTGTGAAGTAAGGATATA--T | 319 |
| OY | 343 TCAATTTCAAAGTCGCTGGAAGATGAG-----GCAATGATCTCCTTCAAC | 387 |
| Dd | | |
| | 320 TCACTTCAATTTCAAGCGGAAGATGAGAACTAATCACTCCCCCTCAATGATCTCATTCAC | 379 |
| OY | 388 GACTTTTGGCTGCTGATGACGTTGAACGTTTGGGAATGCACAGGATTTCAAAAAAGAGA | 447 |
| Dd | | |
| | 380 GCCTTTTAATGCTGATAACGTTGAACGTTTAGGATGTAGATGACATTTCAAAAATGAGA | 439 |

| | | | |
|----|------|--|------|
| QY | 448 | TAATAACGGCAGCTGGATTAATGTTAAACAGTATTGGAAACGAAAAAGGCATTGGATGTGGGA | 507 |
| Db | 440 | TAATAAGCAGCACTAGACTATATGTTTACAGTTATTGGAAACGAAAAAGGCATTGGCAGTGGAA | 499 |
| QY | 508 | GGGAGAGTGTGTGACTGACCTCAACTCAACCGCTTGGGGCTTCGAACTCTCCGACTAC | 567 |
| Db | 500 | GTGATAGTGTGTGCTGATCTCAACTCAACCTGCCCTGGGGTTTCGAATTCTTCGACTAC | 559 |
| QY | 568 | ACGATACACTGTGTCTTCAGATGTTTGAACGTTTAAAGACAAAAATGGCA--AT | 624 |
| Db | 560 | ACGATACAGTGTCTTCAGATGTGTTGAACACTTCAAGAAGAGAGAAGAGAGGGGC | 619 |
| QY | 625 | TTTCCTCCACTGCCAATATTCAGATAGAGGAGAGATTAGAGCGTTCTCAATTATTCA | 684 |
| Db | 620 | AGTTGTATGTTCGGCCATCCAAACAGAGAGAGATAAAAAGCGTTCTGAATTATTTC | 679 |
| QY | 685 | GGGCTCCCTCGTCGCTTTCCTCCGGCGAGAAAGTTATGATGAAGCTGAACATTCTCTA | 744 |
| Db | 680 | GGGCTCCCTCAATGCTTTCCTGGGAGAAAGTTATGGAAGAGCGCTGAATCTTCTCTA | 739 |
| QY | 745 | CAAAATATTTAAAGAGAAAGCCCTGCAAAAGATTCGGGCATCCAGTATACTTCACTAGAGA | 804 |
| Db | 740 | AAATATATTTAAAGAGACCTTACAAATATGTGCTGCTCCAGT--CTTCACGAGAGA | 796 |
| QY | 805 | TACGGAGCGTTTCGAATATGCTTGGCACACCAATTTGCCACGCTTGAAGCAAGGAATT | 864 |
| Db | 797 | TAGATACGTTCTGGAGCATGTTGGCAACAATATGCAAGATTGGAACAAGGAAT | 856 |
| QY | 865 | ACATGACGCTTTGGACAGCACACTAAAAATAAG-----AAGCCGCGAGAAAC | 915 |
| Db | 857 | ACATGATGTATGGGAGAGAACGATCGTATGAGACGTTATATGAACATGAGAAAC | 916 |
| QY | 916 | TTTGAACCTTGCAAAATTGGAATTCATATATTCTACTCTTACAAGAGAGAGATTAA | 975 |
| Db | 917 | TTTGAATTTGCAAAATTGAGATTCAATATTTTCACTCTTACAACAGAGAGAGCTAA | 976 |
| QY | 976 | AACATGTTTCCCGATGTTGGAAGAAAGACTCGGGTTCCTCTGAGATGACCTTCTGTCGACATC | 1035 |
| Db | 977 | AAGACCTCTCCAGATGTTGGAAGAAAGATTGGGTTTCCTCTCACTGACATTTCTCGGCATC | 1036 |
| QY | 1036 | GTCACGTGAATACACGCTTGGCTTCTCTGCAATTCGCTTGAAGCCTCAACATTTCTGGAT | 1095 |
| Db | 1037 | GTCATGTGAATCTACGCTCTGGCATCTTGCAATGAACGTATCGCAACATTTCCGAT | 1096 |
| QY | 1096 | TCAGACTCGGCTTTACCAAGATGTCATCTTATCACGCTTCTGACGACATGTACGACG | 1155 |
| Db | 1097 | TCAGACTCGGCTTTGCCAAATGTGTCATCTTATCACGGTTTGGACGATATATACACA | 1156 |
| QY | 1156 | TCTTCGGCACAGTAGACGAGCTGGAAGCTTTCACAGCGCAATTTAAGATGGATCCGT | 1215 |
| Db | 1157 | CCTTTGAACAATGAGAGAGCTGGAAGCTTTCACAGCATTTAAGAGATGGATCCGT | 1216 |
| QY | 1216 | CCGCGATGGAATGCTTCCAGATATATGAAAGAGTTCATGATGTTTATCACACCG | 1275 |
| Db | 1217 | CTGCCACAGATTTGCTTCCAGAGTATATGAAGGGTTGTACATGCTGTTTACGAAACCG | 1276 |
| QY | 1276 | TAAATGAATGGCTTCGAGTGGCAGAGAAAGGCTCAAGGCCGAGACACGCTCACTATGCA | 1335 |
| Db | 1277 | TAAATGAATGGCTTCGAGAGGCGACAGACAAGTCTCAAGGCCGAGAGACGCTCAACGATGCTC | 1336 |
| QY | 1336 | GACAGGCTTGGAGGCGGTGTTTGATTCGTATATGACGAAACGGAAGTTAGCTCTGCTCATCGCC | 1395 |
| Db | 1337 | GACGAGCTTGGAGGCGCTATCTTGATTCGTATATGAAAGAGCTGAGTGGATCTCCAGTG | 1396 |
| QY | 1396 | GTTATCTGCCCAACGTTTGAGAGTACTTGGAGAACGGGAAGTTAGCTCTGCTCATCGCC | 1455 |
| Db | 1397 | GTTATCTGCCCAACGTTTGAGAGTACATGAGACCGCAAGGAAGTTAGTTTGGTTATCGCA | 1456 |
| QY | 1456 | CATGCGCACTGAAACCAATCTTGACGTTGGAACATCCCTTTCCTGATCACATCTCAAGG | 1515 |
| Db | 1457 | TATTCGATTTGAAACCAATCTCACTATGATGTTCCCTTACTCACACATCTCGAGG | 1516 |


```
Db 1038 GGGTTGGCTGAACTGACCTTTGGTCGGCATCGTCACGTGAATACTACACCCCTGAGCTC 1097
Oy 1064 CTGCATTGCGTTGAGCCCTCAACATTTGAGATTCAAGACTCGGCTTTACCAAGATGTCTCA 1123
Db 1098 TTGCATTGCGACTGAGCCCAACATTCTGCATTAGATTGGCTTTGCCAAAACGTGTCA 1157
Oy 1124 TCTTATCACGGTTCTTGACGACATGTACGACGTCTTCGGACAGTAGACGAGCTGGAAT 1183
Db 1158 TCTTATCACGGTTCTTGACGATATCTACGACACTTTCGGAACGATGATGAATCGAACT 1217
Oy 1184 CTTCAACGCGACAATTAAGAGATGGGATCCGTCGGCATGGAATGCCCTTCCAGAATATAT 1243
Db 1218 CTTCAACGCGAGCAATTAGAGATGGAATCCGTCGGAGAAAGAACGCCCTCCCAGAATATAT 1277
Oy 1244 GAAAGAGTGTACATGATGTTTATACACCGTAATGAATGAGTGGCTGAGTGCGAGAGAA 1303
Db 1278 GAAAGAAATCTACATGGCACTCTACGAAGCCTTAACCTGACATGGCGGAGAGGAGAGAA 1337
Oy 1304 GGCCTAAGCCGAGACACGCTCAACTATGACAGACAGGCTTGAGGCGCTGTTGATTTC 1363
Db 1338 GACACAAAGCCGAGACACGCTCAATTATGTAGAAAGCCTTGGAAGTTTATCTTGATTTC 1397
Oy 1364 GTATATGCGAAGCAAAAGTGATCGGCACTGTTATCTGCCACGTTTGAGAGTACTT 1423
Db 1398 GTATACACAGAACAAAGTGATCGCGCAGGGTTATCTGCCAACTTTCAGAGAGTACTT 1457
Oy 1424 GGAGAACGGAAAGTTAGCTCTGCTCATCGCCCATGCGCACTGCAACCCATTCTGACGTT 1483
Db 1458 AGAGAACGGCAAGGTTAGCTCTGCTCATCGTGCAGCGGCAATGACACCCCTCTGACATT 1517
Oy 1484 GGACATCCCTTTCTCTGATCATCATCTCTCAAGAAAGTTGACTTCCCATCGAAGCTCAATGA 1543
Db 1518 GGACGTACCGCTTCTCTGATGACGTCCTTGAAGGGAATAGATTTCCATCGAAGATTATGA 1577
Oy 1544 CTTGATATGTATCATCTCTGATTAGAGGTGATACAGGCTTACAGGAGAGACAGAGGCG 1603
Db 1578 TTTGGCATCTTCTCTCTTAGACTAAGAGGTGACACAGATGTACAGGAGAGACAGAGGA 1637
Oy 1604 CCGTGAGAGAAAGCTTCGTCTATATCATGTATATGAAGAACAAATCTGGATTAAACGGA 1663
Db 1638 CCGAGAGAGAAAGCGTCAAGCATATCGTGTATCATGAAGAACAAATCCCGGATTAAACAGA 1697
Oy 1664 AGAAGATGCTCTGAATCATATATCAATCTCAATGATCAGGAGCGCAATCAGAAATTAATTG 1723
Db 1698 GGAAGATGCTCTCAATCATATATCAATGCCATGATCAACGACATATCAAGAAATTAATTG 1757
Oy 1724 GGAGCTTCTAAAGCCAGACACAGTGTCCCATCACTTCCAGAAACACGCAATTGACAT 1783
Db 1758 GGAATCTTCAAAACCCGATAGCAATATTCCAATGAAGTGCACGGAACATGCTTATGAGAT 1817
Oy 1784 AAGCAGATTTGGCATCAGCGTTACAGATACCGAGATGGCTACAGCTTTGCCAACGTTGA 1843
Db 1818 AACCAAGCTTTCCACCACTTACAAATATAGAGATGGCTTCAGCGTTGCCACTCAAGA 1877
Oy 1844 AACCAAGAGTTGGTGATGAGAACCGTCAATTGAACCTGTGCCCTTTGTAACAACACTTCAA 1903
Db 1878 AACGAAAGTTGGTGAGAGAGAACGCTCTTGAACCAAGTGCCTTTTAACAATTTAAACC 1937
Oy 1904 ATCTACAATA 1913
Db 1938 TTCTATAATA 1947
```

RESULT 7
AAx08643
ID AAX08643 standard; cDNA; 2196 BP.
XX AAX08643;

XX 27-SEP-1999 (first entry)
XX Myrcene synthase gene.
DE

```
XX Myrcene synthase; limonene synthase; pinene synthase; flavour; aroma;  
KW defense; plant seed; oil; meal; ss.  
XX Abies grandis.  
OS  
FH Key Location/Qualifiers  
FT CDS 69..1952  
FT /+tag= a  
FT /product= "Myrcene synthase"  
XX  
PN MO9902030-A1.  
PD 21-JAN-1999.  
XX  
PF 10-JUL-1998; 98MO-US014528.  
XX  
PR 11-JUL-1997; 97US-0052249P.  
XX  
PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.  
XX  
PI Bohlmann J, Steele Cl, Croteau RB;  
XX  
DR WPI; 1999-120396/10.  
DR P-PSDB; AAW85700.  
XX  
PT New isolated gymnosperm monoterpene synthase DNA - obtained from Grand  
PT fir (Abies grandis), used to provide plants with modified production of  
PT monoterpenes, e.g. myrcene, limonene or pinene.  
XX  
PS Claim 9; Page 69-72; 121pp; English.  
XX  
CC Nucleotide sequences encoding myrcene synthase, limonene synthase and  
CC pinene synthase from Grand fir may be incorporated into any organism  
CC (e.g. intact plant, animal, microbe), or derived cell culture that  
CC produces geranyl diphosphate for the production of the aforementioned  
CC enzymes or their products. The sequences when expressed in transfected  
CC cells may also be used for the production or modification of flavour and  
CC aroma properties, improvement of defense capability, and the alteration  
CC of other ecological interactions mediated by myrcene, limonene, pinene,  
CC or their derivatives. In particular they can be used for the production  
CC of plant seeds for the extraction of oil or meal  
XX  
SQ Sequence 2196 BP; 684 A; 416 C; 468 G; 628 T; 0 U; 0 Other;
```

Query Match 53.2%; Score 1071.6; DB 2; Length 2196;
Best Local Similarity 75.0%; Pred. No. 3.1e-293;
Matches 1430; Conservative 0; Mismatches 441; Indels 36; Gaps 6;

```
Oy 68 CAGTCGTGCTCAGTCTTCTCTCATGAGATTAAAGGCTCTCCGTAGAACATCCCACTCT 127  
Db 116 CAAGTCGTGATCAGTTCAATTCATGACATGAACATGAAGCTCCCTATAGAACATCCCAATCT 175  
Oy 128 TGAATCTGCAGGCGCGGAAATCCGTGCGCATTTCCATTAACATGTGTTGACAAAGCGT 187  
Db 176 TGAATGCGTAGCGGAGGAAATCTGTACAGCGCTTCCATGAGCATCAGTTGGCCACCGC 235  
Oy 188 CGCATCTACTGATTCTGTACAGAGACGCGTGGCAACTATCATTTCCAACTGTGGAGCGA 247  
Db 236 TGCACCTGATGATGTTGTACAAAGACGCAATGAGTACTACCATTCCAATATCTGGAGCGA 295  
Oy 248 TGATTTCAATCAGTCTCTGATCTCAACGCTTATGAGACACCTGATTAACGGGAACGTGC 307  
Db 296 TGATTTCAATCAGTCTC--TATCAACGCTTATGGGAAACCTCTTACCAAGAACGTGC 352  
Oy 308 TGACAGACTTAATGGGAGTAAGATATATATGTTCAATTTCAAGTGCCTGGAAGATGG 367  
Db 353 TGAGAGATTAATGTGAGAGTAAGAGATA--TTCAATTCATGTACCTGATGATGG 409  
Oy 368 AGG-----CAATGATCTCTTCAACGACTTTTGCTGTCGATGACGTTGA 412  
Db 410 AAGATTATGACTTCTCTTAATGATCTCATGCAACGCCCTTGATAGTCGATAGCGTTGA 469
```



```
QY 413 ACGTTTGGGAATCGACAGCATTTCAAAAAAGATMAAAACGGCACTCGATTATGTTAA 472
    |||||
Db 470 ACGTTTGGGAGTAGCTAGACATTTCAAGAACGAGATTAACATCAGCTCTGGATTATGTTT 529
QY 473 CAGTTATTTGGAACGAAAAAGCAATTGATGTGGAGGAGAGAGTGTGTAAGTCACTCA 532
    |||||
Db 530 CCGTTACTGGAGAGAAAAACGGCATTTGATGTGGAGAGACAGTAATTGTAAGTCA 589
QY 533 CTCAACCGCTTGGGGCTTGAAGTCTCCGACTACACGGATACAGTGTCTCAGATGT 592
    |||||
Db 590 CTCAACTGCGTTGGGGTTTCAAGTCTTCCGATTACACGGGTACACTGTATCTCCAGAGT 649
QY 593 TTTGAACGTTTAAAGACAAAATGGGCAATTTTCTCCACTGCCAATATTCAGATAGA 652
    |||||
Db 650 TTTAAAGCTTTTCAAGATCAAAATGAGACAGTTGTATGCTCCCC--GTCAGACAGA 706
QY 653 GGGAGAGATTAGAGCGGCTTCAATTTATTCAGGGCTCCCTGCTGCTTCCCGCGCA 712
    |||||
Db 707 GGGTGAATCAGAAAGCGTTCTTAATCTATATCGGGCTTCCCTCATTTGCTTCCCTGTGA 766
QY 713 GAAAGTTATGATGAAGCTGAACATTTCTCTACAATAATATTTAAGAAAGCCCTGCAAAA 772
    |||||
Db 767 GAAAGTTATGGAAGAGAGCTGAATCTTCCACAGATATTTGAAGAAGCTCTACAAAA 826
QY 773 GATTCGGCATCCAGTATATCTTCACTAGAGATACGGAGCTTCTGAATATGTGGCA 832
    |||||
Db 827 GATTCAGTCTCCGCT--CTTTCACAGAGATTAAGTTGTTATGGAATATGCTGGCA 883
QY 833 CACCAATTTGCCACGCTTGGAGACAGAAATTACATGACGCTTTGGACACACACTA- 891
    |||||
Db 884 CACAAATTTGCCAAGATTGGAGACAGAAATTACATAGACACACTTTGAAGAAAGACACAG 943
QY 892 -----AAATAGAACGCCCCGAGAAACTTTAGAACTTGCAAAATTGAATTCAA 943
    |||||
Db 944 TGCATGCTCAATAAAAATGCTGGAGAGAGCTTTAGAACTTGCAAAATTGAAGTTCAA 1003
QY 944 TATATTTCACTCCTTACAGAGAGAGATTAACAATGTTTCCGATGCTGGAAGACTC 1003
    |||||
Db 1004 TATATTTAACTCCTTACAAACAAAAGAAATTACAATATCTTTGAGATGCTGGAAGACTC 1063
QY 1004 GGGTCTCTCGATGAGTACCTTCTGACATCGTCAAGTGAATTAACGCTTTGCTTC 1063
    |||||
Db 1064 GGAATTTGCCTAAATTAACATTTGCTGGCATCGTCAATGGAATCTACACTTTGGCTTC 1123
QY 1064 CTGCATTCGCTTGCAGCTCAACATCTGGAATTCAGACTCGGCTTTACCAAGATGCTCA 1123
    |||||
Db 1124 TTGTATTTGCCATTTGACCCAAAACATTTCTGCATTCAGACTAGGCTTCGCCAAAATGTCTCA 1183
QY 1124 TCTTATCAAGGTTCTTGAAGACATGTAACGCTTTCGGCAAGTGAAGAGCTGGAAT 1183
    |||||
Db 1184 TCTTGTACAGATTTTGAAGCATATTAACGACACTTTTGAACGATTTGAAGCTTGAAT 1243
QY 1184 CTTCAAGCGACAAATTAAGAGATGGATCCGCTCCGATGGAATGCTTCCAGAAATATAT 1243
    |||||
Db 1244 CTTCAATCTGCAATTAAGAGATGAATTCATCAGAGATAGAACACTTCCAGAAATATAT 1303
QY 1244 GAAAGAGTGTATCATGATGTTTATCAACCGTAATGAATGGCTGAGTGGCAGAGAA 1303
    |||||
Db 1304 GAAATGTGTATCATGCTGTGTTGAACCTGTAATGAACGACAGAGCGGAGAA 1363
QY 1304 GGGTCAAGCGCGAGACACGCTCAACTATGTTGAAAGGCTTGGAGGCTTATTTGATTC 1363
    |||||
Db 1364 GACTCAAGGAGAAACACTCTCAACTATGTTGAAAGGCTTGGAGGCTTATTTGATTC 1423
QY 1364 GTATATGACGAGCAAGCAAGTGAATCGCACTGTTATCTGCCACGTTTGAAGTACTT 1423
    |||||
Db 1424 ATATATGAGAGAGCAAAATGATCTCTAATGTTATCTGCCAATGTTGAAGAGTACCA 1483
QY 1424 GGAGAACGGGAAAAGTTAGCTCTGCTATCGCCCATGCGCACTGCAACCCATTTGACGTT 1483
    |||||
Db 1484 TGAGAAATGGGAAAAGTGAGCTCTGCATATTCGCGTAGCAACATTTGCAACCCATCTCTCACTTT 1543
QY 1484 GGACATCCCTTTCTCTGATCAGATCTCTCAAGGAAGTTGACTTCCCATCGAAGCTCAATGA 1543
```

```
Db 1544 GAATGCATGGCTTCCCTGATTAATCTTGAAGGGAATGATTTTCCATCCAGTTCAATGA 1603
QY 1544 CTGATATGTATCATCTTTCGATTAAGAGTGATACACGGTCTACAAGCAGACAGAGGC 1603
    |||||
Db 1604 TTTGGCATCGTCTCTTCCCTTGGGCTACGAGGTGACACACGCTGTCTACAAGCCGATAGGA 1663
QY 1604 CCGTGAAGAGAAAGCTTCTGCTATATCATGTTATATGAAGACAAATCCTGATTAAACGA 1663
    |||||
Db 1664 TCGTGTGAAGAAAGCTTCTGCTATATCATGTTATATGAAGACAAATCCTGATCAACCGA 1723
QY 1664 AGAAGATGCTTGAATCATATCACTTCATGATCAGGACGCAATCAGAAATTAATTG 1723
    |||||
Db 1724 AGAAGATGCTTCAATCATATCAATGCCATGTCATGATCAAAAGAAATTAATTG 1783
QY 1724 GGAGCTTCTAAAGCCAGACAAAGTGTCCCATCATCTTCCAAGAAACACGATTTGACAT 1783
    |||||
Db 1784 GGAATCTTAAGATCCCAACGACATATTCATATGATGCTGGCCAGAAACATGCTTTGACAT 1843
QY 1784 AAGCAGTTTGGCATCACGGTTACAGATACCCGAGATGGCTACAGCTTTGCCAAGTTGA 1843
    |||||
Db 1844 AACAGAGCTCTCCACCATCTCTACATATATCGAGATGGCTTTAGTGTGCCAACAAGGA 1903
QY 1844 AACAAAGATTGTGTGATGAGAACCCGTCATTTGAACCTGTGCTTTGTAACAACACTTCA 1903
    |||||
Db 1904 AACAAAAAATTGTTATGGAACACTCTTGAATCTATGCTTTTAACTATAACCATATA 1963
QY 1904 ATCTACATATTTAAGTGAAGATGCCCTATGGGTATATAGGSCACA 1950
    |||||
Db 1964 TCCATATATTAATTAAGCTCATATATGCTTAAATTATTGGCTTATGACATA 2010

RESULT 8
AAA38927
ID AAA38927 standard; DNA; 2196 BP.
XX
AC AAA38927;
XX
DT 25-AUG-2000 (first entry)
XX
DE Grand fir myrcene synthase DNA sequence SEQ ID NO:29.
XX
KW Synthase; protein co-ordinate data; active site; modification; terpenoid;
KW 3-dimensional coordinate; alpha carbon atom; plant; terpene synthase;
KW isoprenoid; breeding programme; fragrance; flavour; pheromone;
KW defensive agent; pigment; antitumour; steroid hormone;
KW signal transduction pathway; bile acid; affinity purification;
KW photoreceptor; enzymatic synthesis; nutrient supplement;
KW immunological reagent; ds.
XX
OS Abies grandis.
XX
PN WO200017327-A2.
XX
PD 30-MAR-2000.
XX
PF 17-SEP-1999; 99WO-US021419.
XX
PR 18-SEP-1998; 98US-010093P.
PR 22-APR-1999; 99US-0130628P.
PR 23-AUG-1999; 99US-0150262P.
XX
PA (KENT ) UNIV KENTUCKY RES DEPT.
PA (SALK ) SALK INST BIOLOGICAL STUDIES.
XX
PI Chappell J, Manna KR, Noel JP, Starks CM;
XX
DR WPI; 2000-292839/25.
DR P-PSDB; AAY90842.
XX
PT Novel terpene synthase enzymes, useful for producing terpene
PT hydrocarbons, e.g. fragrances or antitumor agents, are derived from known
PT enzymes by specific amino acid alterations.
```

XX
PS Disclosure; Page 387-390; 450pp; English..

The present invention describes an isolated terpene synthase (I) comprising a region with at least 20% identity to region 265-535 of a 548 amino acid (aa) sequence (Ia), given in AAY90831. (I) contains nine alpha-carbon atoms (alphaC) that have interatomic distances, between each other, within tabulated ranges, have a centre point (within a sphere of radius 2.3 Angstrom) within tabulated ranges, and have an ordered arrangement of R groups (defining aa side chains), excluding specific tabulated arrangements (tables given in the specification). (I), and related enzymes, are used to produce a wide range of terpenoids (e.g. cyclic, acyclic, optionally hydroxylated), useful e.g. as fragrances, flavours, pheromones, defensive agents, pigments, anticancer agents, components of signal transduction pathways, precursors of steroid hormones and bile acids, as photoreceptors and as co-factor side chains. Some synthases with little or no catalytic activity (and nucleic acids encoding them) are used as controls in the analysis of products formed by enzymatic synthesis; as nutrient supplements; for affinity purification of isoprenoids; or to develop immunological reagents or nucleic acids for monitoring expression of terpene synthase or inheritance of the gene in plant breeding programs. The new synthases may produce novel terpene products. AAA38910 to AAA38938 and AAY90831 to AAY90859 represent sequences used in the exemplification of the present invention

SQ Sequence 2196 BP; 684 A; 416 C; 468 G; 628 T; 0 U; 0 Other;

| | | | | |
|----------------------------|-------|---------------------|------------|--------------|
| Query Match | 53.2% | Score 1071.6; | DB 3; | Length 2196; |
| Best Local Similarity | 75.0% | Pred. No. 3.1e-293; | | |
| Matches 1430; Conservative | 0; | Mismatches 441; | Indels 36; | Gaps 6; |

| | | | |
|----|-----|--|-----|
| Qy | 68 | CAGGTCGTGCCTCAGTTCTTCTCATGAGATTAAAGGCTCTCCGTAGAACAATCCCAACTCT | 127 |
| | | | |
| Db | 116 | CAAGTCGTGATCAGTTCAATTCATGACATAAAGCCTCCCTATAGAACAAATCCCAATCT | 175 |
| | | | |
| Qy | 128 | TGGAATCTGCAGCGCGGGAATCCGTCCGCATTCCATTAACATGTGTTGACAAAGCT | 187 |
| | | | |
| Db | 176 | TGGAATGCGTAGGCGAGGAATCTGTCAAGCCTTCCATGAGCATCAGTTGGCCACCGC | 235 |
| | | | |
| Qy | 188 | CGCATCTACTGATTCGTACAGACGCGTGGGCAACTATCATTTCCAACCTGTGGAGCA | 247 |
| | | | |
| Db | 236 | TGCACCTGATGATGTGTACAAAGACCCATAGGTGACTACCATTTCCAATATCTGGAGCA | 295 |
| | | | |
| Qy | 248 | TGATTTTCATACAGTCTCTGATCTCAAGCCTTATGAGACACCTGATTACGGGAAAGTGC | 307 |
| | | | |
| Db | 296 | TGATTTTCATACAGTCTC--TATCAAGCCTTATGGGGAACCTCTTACAGGAACGTGC | 352 |
| | | | |
| Qy | 308 | TGACAGACTTATTTGGGAGTAAGATATAATGTTCAATTTCAAGTCGCTGGAAGATGG | 367 |
| | | | |
| Db | 353 | TGAGAGATTAATTGTGAGAGTAAGAGATA--TTCAATTCATGTACTCGATGATGG | 409 |
| | | | |
| Qy | 368 | AGG-----CAATGATCTCCTTCAACGACTTTTGTGTCGTCATGACGTTGA | 412 |
| | | | |
| Db | 410 | AAGATTATAGAGTTCCTTAATGATCTCATGCAACGCTTTGATAGTCGATAGCGTTGA | 469 |
| | | | |
| Qy | 413 | ACGTTTGGGAATCGACAGGCATTTCAAAAAAGAGATTAATAACGGCACTCGAATTATGTTAA | 472 |
| | | | |
| Db | 470 | ACGTTTGGGATAGCTAGACATTTCAAGAACGAGATTAACATCAGCTCTGGAATTATGTTT | 529 |
| | | | |
| Qy | 473 | CAGTTATTGGAACGAAAAAGGCATTGSGATGTGGGAGGAGAGTGTGTGACTGCACTCAA | 532 |
| | | | |
| Db | 530 | CCGTTACTGGGAGGAAAAAGGCATTGSGATGTGGGAGAGACAGATATTGTTACTGATCTCAA | 589 |
| | | | |
| Qy | 533 | CTCAACCGCCTTGGGGCTTCCAACTCTCCGACTACACGGATACACTGTGTCTTCAGATGT | 592 |
| | | | |
| Db | 590 | CTCAACTGCGTTGGGTTTCGAACCTTTCGATTACACGGGTACACTGTATCTCCAGAGGT | 649 |
| | | | |
| Qy | 593 | TTTGAACGTTTTTAAGACAATAAGGCAATTTTCTCCACTGCGCAATTCAGATAGA | 652 |
| | | | |
| Db | 650 | TTTAAAGCTTTTCAAGATCAAAATGACAGTTGTATGCTCCCC--GTCAGACAGA | 706 |
| | | | |
| Qy | 653 | GGAGAGATTAGAGCGTTCCTCAATTATTCAGGGCCTCCCTGTCGCTTTCCCGGCGA | 712 |
| | | | |

| | | | |
|----|------|---|------|
| Db | 707 | GGGTGAGATCAGAAGCGTTCCTTAACCTATATATCGGGCTTCCTCATTTGCCCTTCCTGGTGA | 766 |
| QY | 713 | GAAAGTTATGATGAAGCTGAAACATTCTCTACAAAATTTAAGAGAAAGCCCTGCAAAA | 772 |
| Db | 767 | GAAAGTTATGAAAGAGCTGAAATCTTCTCACAGATATTTGAAAGAAAGCTCTACAAA | 826 |
| QY | 773 | GATTCCGGCATCCAGTATACCTTTCAGTATAGAGATACGGACGTTCTGGAATATGTTGGCA | 832 |
| Db | 827 | GATTCAGTCTCCGCT---CTTTCACAGAGATAAAGTTTGTATGGAATATGGCTGCA | 883 |
| QY | 833 | CACCAATTTGCCACGCTTGGAAGCAAGGAATTACATGACGCTTTGGACAGACACTA- | 891 |
| Db | 884 | CACAAATTTGCCAAGATTGGAAGCAAGAAATTACATAGACACACTTGAGAAAGACACGAG | 943 |
| QY | 892 | -----AAATTAAGAACGCCGCCGAGAAACCTTTAGAACTTGCAAAATTGAAATTC | 943 |
| Db | 944 | TGCATGGCTCAATTAATAATGCTGGGAAGAGCTTTAGAACTTGCAAAATTGAGTTC | 1003 |
| QY | 944 | TATATTTCACTCGTTTACAAGAGAGAGAGTTAAACAATGTTCCGATGTTGAAAGACTC | 1003 |
| Db | 1004 | TATATTTAACTCTTTACAACAAAAGGAATTACAATATCTTTGAGATGTTGAAAGAGTTC | 1063 |
| QY | 1004 | GGGTTCTCCTGAGATGACCTTCTGTGACATCGTCAAGTGAATACACGCTTGGCTTC | 1063 |
| Db | 1064 | GGATTTGCCCTAAATTGACATTTGCTCGGCATCGTCAATGGAATTTCTACACTTTGGCTTC | 1123 |
| QY | 1064 | CTGCATTGCGTTGAGCGCTCAACATTTCTGATTCAAGCTCGGCTTTACCAAGATGTCTCA | 1123 |
| Db | 1124 | TTGTATTTGCCATTGACCCAAAACATTTCTGATTCAAGCTAGGCTTCGCCAAATGTGTCA | 1183 |
| QY | 1124 | TCTTATCAGGTTCTTTGACGACATGTACGACGTTCTCGCACAGTAGACGAGCTGAACT | 1183 |
| Db | 1184 | TCTTGTACAGTTTGGACGATATTATTACGACACTTTTGGAAACGATTGACGAGCTTGA | 1243 |
| QY | 1184 | CTTCACAGCGCAATTAAGAGATGGGATCCGTCGCGCATGGAATGCCCTTCAGAAATATAT | 1243 |
| Db | 1244 | CTTCACATCTGCAATTAAGAGATGGAATTCATCAGAGATAGAACACCTTCAGAAATATAT | 1303 |
| QY | 1244 | GAAAGAGTGTACATGATGTTTATCACACCCGTAAATGAAATGGCTCGAGTGGCAGAGAA | 1303 |
| Db | 1304 | GAAATGTGTACATGTCGTGTTGAAACTGTAAATGAACCTGACACGAGAGCGGAGAA | 1363 |
| QY | 1304 | GGCTCAAGGCCGAGACACGCTCAACTATGCAAGACAGGCTTGGAGGCGTGTGTTGATTC | 1363 |
| Db | 1364 | GACTCAAGGAGAAACACTCTCAACTATGTTGAAAGGCTTGGAGGCTTATTTGATTC | 1423 |
| QY | 1364 | GTATATGACAGTACGAAAGTGGATCGCCACTGGTATCTGCCACGTTTGAGAGTACTT | 1423 |
| Db | 1424 | ATATATGGAAGTACGAAATGAGATCTTAATGGTTATCTGCCAATGTTTGAAGATACCA | 1483 |
| QY | 1424 | GGAGAACGGGAAGTTAGCTCTGCTCATCGCCCATGCGCACTGCACCCATTTCTGACGTT | 1483 |
| Db | 1484 | TGAGAAATGGAAAGTGAAGCTCTGCATATCGCGTAGCAACATTCACACCATCTCACTTT | 1543 |
| QY | 1484 | GGACATCCCCCTTTCCTGATCACATCTCAAGGAAGTTGACTTCCCATGGAAGCTCAATGA | 1543 |
| Db | 1544 | GAAATGATGCTTCTGATTAACATCTTGAAGGAATGATTTTCATCCAGGTTCAATGA | 1603 |
| QY | 1544 | CTTGATATGATCACTCTTGCATTAAGAGTGTACACGCTGCTACAGGACAGACAGGC | 1603 |
| Db | 1604 | TTTGGCATCGTCTTCTCGGCTACGAGGTGACACACGCTGCTACAGGCGGATGAGGA | 1663 |
| QY | 1604 | CCGTGAGAAAGCTTCGCTATATCATGTTATTAAGAAACAATCCTGATTAACGGA | 1663 |
| Db | 1664 | TCGTGTGAGAGAGCTTCGTATATCATGTTATTAAGAAACAATCCTGATCAACGGA | 1723 |
| QY | 1664 | AGAAGATGCTCTGAATCATATCAACTTCATGATCAAGGACGCAATCAGAGATTAATG | 1723 |
| Db | 1724 | AGAAGATGCCCTCAATCATATCAATGCCATGGTCAATGACATTAATCAAGAAATTAATG | 1783 |
| QY | 1724 | GGAGCTTTAAAGCCAGACAACAGTGTTCCTCATCTTCCAAGAAACGCAATTTGACAT | 1783 |
| Db | 1784 | GGAATCTTAAGATCAACGACAATATTTCCAATGCTGGCCCAAGAAACATGCTTTTGACAT | 1843 |

QY 1784 AAGCAGATTGGCATCAGGTTACAGATACGAGATGCTACAGCTTGGCAACGTTGA 1843
DB 1844 AACACAGCTCTCCACCATCTCTACATATATCGAGATGGCTTAGTGTGCCAACAGAGA 1903
QY 1844 AACAAAGAGTTGGTGTATGAGAACCGCTCATTTGAACCTGTGCCCTTTGTAACAACACTTCAA 1903
DB 1904 AACAAAAAAATTGGTATGAAACACTCTTGAATCTATGTCTTTTAACATAAACCATTA 1963
QY 1904 ATCTACATATTAAGTATGAGATGCCCTATGGGTATATAGGGCACA 1950
DB 1964 TCCATATATTAAGCTCATATATGCTAAATTATTGGCCTTATGACATA 2010

RESULT 9
AAF73371
ID AAF73371 standard; cDNA; 2196 BP.
XX
AC AAF73371;
XX
DT 30-APR-2001 (first entry)
XX
DE Grand fir myrcene synthase coding sequence SEQ ID NO: 1.
XX
KW Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;
KW myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;
KW terpinolene synthase; insect resistance; nutrition; ss.
XX
OS Abies grandis.
XX
PN WO200107565-A2.
XX
PD 01-FEB-2001.
XX
PF 24-JUL-2000; 2000MO-US020264.
XX
PR 26-JUL-1999; 99US-00360545.
XX
PA (UNIW) UNIV WASHINGTON STATE RES FOUND.
XX
PI Steele CL, Bohlmann J, Croteu RB, Phillips MA;
XX
DR WPI; 2001-182782/18.
DR P-PSDB; AAB69370.
XX
PT New nucleic acid encoding monoterpene synthases, for increasing terpene
PT synthesis in plants, e.g. for increasing resistance to pests or for
PT treatment of cancer.
XX
PS Claim 28; Page 103-106; 175bp; English.
XX
CC The present invention provides the protein and coding sequences of
CC monoterpene synthases from the grand fir. These include (-)-camphene
CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-
CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase
CC and pinene synthase. The sequences can be used to produce transgenic
CC plants expressing high levels of the enzymes, resulting in levels which
CC are useful in protecting against and treating cancers, and to confer
CC insect resistance on plants
XX
SQ Sequence 2196 BP; 684 A; 416 C; 468 G; 628 T; 0 U; 0 Other;

Query Match 53.2%; Score 1071.6; DB 4; Length 2196;
Best Local Similarity 75.0%; Pred. No. 3.1e-293;
Matches 1430; Conservative 0; Mismatches 441; Indels 36; Gaps 6;

QY 68 CAGTGTGCTCAGTCTTCTCATGAGATTAAAGCTCTCCGTAGAACATCCCACTCT 127
DB 116 CAAGTCGTGATCACTTCATATGACATTAAGCCTCCCTATAGAACATCCCAATCT 175
QY 128 TGAATCTGCAGCCCGGGAATCCGTGCGCATTCATTAACATGTGTTGACAAGCGT 187
DB 176 TGAATGCGTAGCGGAGGAATCTGTACGCTTCCATGAGCATCACTTTGGCCACCGC 235

QY 188 CGCATCTACTGATTCTGTACAGACGCGTGGCAACTATATCTCAACCTGTGGAGCA 247
DB 236 TGCACTGATGATGTGTACAAAGACGATAGTGACTACCATTCGAATATCTGGAGCA 295
QY 248 TGATTTCATACAGTCTCTGATCTCAACGCCCTTATGAGCACCCTGATTAACGGGAACGTGC 307
DB 296 TGATTTTACACAGTCTC--TATCAACGCCCTTATGGGGAACCCCTTACAGGAACGTGC 352
QY 308 TGACAGACTTATTTGGGAGATTAAGATATATATGTTCAATTTCAAGTCGCTGGAAGATGG 367
DB 353 TGAGAGATTAAATTGTGAGGTAAGAAGATA--TTCAATTCAATGTACCTGGATGATGG 409
QY 368 AGG-----CAATGATCTCCTTCAACGACTTTTGGCTGGTGCATGACGTTGA 412
DB 410 AAGATTAAAGATTCTCTTAATGATCTCATGCAACGCCCTTTGATAGTCGATAGCGTTGA 469
QY 413 ACGTTTGGGAATCGACAGGCACTTCAAAAAAGATTAATAAAGCGCACTCGATTATGTTAA 472
DB 470 ACGTTTGGGAGATAGCTAGACATTTCAAGAACGATTAACATCAGCTCTGATTATGTTT 529
QY 473 CAGTTATTCGAACGAAGAAAGCATTTGATGTGGAGGAGAGAGTGTGACTGACCTCAA 532
DB 530 CCGTTACTGGAGAGGAAACCGCATTTGATGTGGAGAGACAGTATTTACTGATCTCAA 589
QY 533 CTCAACCGCCTTGGGCTTGGACTCTCCGACTACACGAGATACGTGTCTTCAGATGT 592
DB 590 CTCAACTGCGTTGGGCTTCGAACCTTTCCATTACACGGGTACACTGTATCTCCAGAGGT 649
QY 593 TTTGAACGTTTAAAGACAAATAAGGCAATTTCTCCACTGCCAATATTAGATAGA 652
DB 650 TTTAAAGCTTTCAAGATCAAAATGACAGATTGTATGCTCCCC--GGTCAGACAGA 706
QY 653 GGGAGATTAGAGCGGCTTCTCAATTATTAGGGGCTCCCTGCTGCTTCCCGGCGA 712
DB 707 GGGTAGATCAGAAAGCGTCTTAATTAATATCGGGCTTCCCTGATGCTTCCCTGTGTA 766
QY 713 GAAAGTTATGATGAAGCTGAACATTTCTTCAAAAATATTTAAGAAAGCCCTGCAGAAA 772
DB 767 GAAAGTTATGAAAGAGCTGAATCTTCTCCACAGATATTTGAAGAAGAGCTTACAGAAA 826
QY 773 GATTCGGCATCCAGTATATCTTCACTAGAGATACGGAGCGTCTGGAATATGTTGCA 832
DB 827 GATTCCAGTCTCCGCT--CTTCAAGAGATTAAGTTGTATGGAATATGCTGCGCA 883
QY 833 CACCAATTTGCCACGCTTGGAGACAGCAATTTACATGAGCGTCTTTGGACAGCACACTA- 891
DB 884 CACAAATTTGCCAAGATTGGAGACAGCAAAATTTACATAGACACACTTGAAGAAAGACACAG 943
QY 892 -----AAATTAAGAACGCCCGCGAGAACTTTAGAACCTTGCAAAATTGGAATTCAA 943
DB 944 TGCAATGCTCAATTAATAATGCTGGAGAGAGCTTTAGAACCTTGCAAAATTGAGTTCAA 1003
QY 944 TATATTTCACTCCTTACAGAGAGAGATTAAACATGTTTCCGATGCTGGAAGAGACTC 1003
DB 1004 TATATTTCACTCCTTACAAACAAAGGAATTAATATATCTTTGAGATGCTGGAAGAGACTC 1063
QY 1004 GGGTTCCTGAGATGACCTTCTGTGACATCGTCAACGTGAATACTACGCTTTGGCTTC 1063
DB 1064 GGATTTGCTTAAATTGACATTTGCTGCGCATCGTATGTGAATTTCTACACTTTGGCCTC 1123
QY 1064 CTGCATTTGCTTGAAGCTTCAACATTTCTGATTTCAGACTCGGCTTACCAAGATGTCTCA 1123
DB 1124 TTTGATTTGCAATTTGACCCCAAAACATTTCTGCATTCAGACTAGGCTTCCGCAAAATGTCTCA 1183
QY 1124 TCTTATTCACGCTTCTTGAAGCATATTTACGACACTTTTGGAACGATTTGACGAGCTTGAAC 1183
DB 1184 TCTTGTACAGTTTGGACGATATTTACGACACTTTTGGAACGATTTGACGAGCTTGAAC 1243
QY 1184 CTTCACAGGACAAATTAAGAGATGGATCCGTCGCGATGGAATGCTTCCAGAAATATAT 1243
DB 1244 CTTCACATCTGCAATTAAGAGATGGAATTCATCAGAGATAGAACCTTCCAGAAATATAT 1303

| | | | |
|----|------|---|------|
| QY | 1244 | GAAAGAGGTGATCATGATGGTTTATCACACCCGTTAAATGAAATGGCTCGAGTGGCAGAGAA | 1303 |
| | 1304 | GAAATGTGTGTACATGGTCTGTGTTGAAACTGTAAATGAATGACACGAGAGGCGGAGAA | 1363 |
| QY | 1304 | GGCTCAAGGCCGAGACACGCTCAACTATGCAAGACAGCGTTGGAGCGGCTTTTGATTC | 1363 |
| Db | 1364 | GACTCAAGGAGAAACACTCTCAACTATGTTGAAAGCGTTGGAGGCTTATTTTGATTC | 1423 |
| QY | 1364 | GTATATGCAGAGCAAAAGTNGATCGCCACTGGTTATCTGCCCCAGTTTGAGAGTACTT | 1423 |
| Db | 1424 | ATATATGGAGAAGCAAAATGATCTCTAATGGTTATCTGCCAATGTTTGAAGAGTACCA | 1483 |
| QY | 1424 | GGAGAACGGGAAAGTTAGCTCTGCTCATCGCCCATGCGCACTGCAACCCATTCTGACGTT | 1483 |
| Db | 1484 | TGAGAAATGGGAAAGTGAGCTCTGCATATCGCGTAGCAACATTGCAACCCATCTCACATT | 1543 |
| QY | 1484 | GGACATCCCCCTTTCCTGATCAATCCTCAAGGAAAGTTGACTTCCATCGAAGCTCAATGA | 1543 |
| Db | 1544 | GAATGATGCTTCTCTGATTAATCATCTTGAAAGGAAATGATTTTCATCCAGGTTCAATGA | 1603 |
| QY | 1544 | CTTGATATGATCATCCTTCGATTAAAGAGTGATACACGCGTCTTCAAGGCAGACAGGC | 1603 |
| Db | 1604 | TTTGGCATCGTCTTCTCGGCTACGAGGTGACACACGCTGCTACAAGCCGATAGGGA | 1663 |
| QY | 1604 | CCGTGAGAGAAGAGCTTCGCTATATCATGTTATATGAAAGACAATCCTCGATTAAACGA | 1663 |
| Db | 1664 | TCGTGGTGAAGAAGCTTCGTGTATATCATGTTATATGAAAGACAATCCTCGATCAACGA | 1723 |
| QY | 1664 | AGAAATGCTCTGAATCATATCAACTTCATGATCAGGAGCGCAATCAGAGAAATTAATTG | 1723 |
| Db | 1724 | AGAAAGATGCCCTCAATCATATCAATGCCATGCTCAATGACATTAATCAAAAGAAATTAATTG | 1783 |
| QY | 1724 | GGAGCTTCTAAAGCCAGACAAGTGTTCCTCATCACTTCCAGAGAAACAGCATTTGACAT | 1783 |
| Db | 1784 | GGAACCTTCAAGATCCAAGCAACAATATTCCAATGCTGGCCAGAGAAACATGCTTTGACAT | 1843 |
| QY | 1784 | AAGCAGAGTTTGGCATGACGAGTTACAGATACCGAGATGGCTACAGCTTTGCCAAGCTTGA | 1843 |
| Db | 1844 | AACAAGAGCTCTCCACCACTCTCAATATATCGAGATGGCTTAAAGTTGCCAACAAGGA | 1903 |
| QY | 1844 | AACAAGAGTTTGGTGTATGAGAACCCGTCATTGAACTGTGCTTTGTAAACAACACTTCAA | 1903 |
| Db | 1904 | AACAAGAGTTTGGTGTATGAGAACCACTCCTTGAATCTATGCTTTTAACTATAACCATTA | 1963 |
| QY | 1904 | ATCTACAATATTAATCTGAGATGCCCTATGGGTGTATATAGGGCACA | 1950 |
| Db | 1964 | TCCATAATATAAGCTCATTAATGCTAAATTAATTATGGCCCTTAAGACATA | 2010 |

| RESULT 10 | ID | AAAX08663 | standard; cDNA; 2205 BP. |
|-----------|--------------|---|--------------------------|
| XX | AC | AAAX08663; | |
| XX | DT | 27-SEP-1999 | (first entry) |
| DE | XX | Grand Fir monoterpene synthase clone AG3.48. | |
| XX | KW | Myrcene synthase; limonene synthase; pinene synthase; flavour; | |
| KW | KW | monoterpene synthase; aroma; defense; plant seed; oil; meal; primer; PCR; | |
| KW | probe; ss. | | |
| OS | XX | Abies grandis. | |
| XX | XX | | |
| FH | Key | Location/Qualifiers | |
| FT | FT | 57..1940 | |
| FT | FT | /*tag= a | |
| XX | PN | /product= "Monoterpene synthase" | |
| XX | PN | WO9902030-A1. | |
| PD | 21-JAN-1999. | | |

| | | |
|----------|--|----------------|
| XX | 10-JUL-1998; | 98WO-US014528. |
| PF | | |
| XX | 11-JUL-1997; | 97US-0052249P. |
| PR | | |
| XX | (UNIV) UNIV WASHINGTON STATE RES FOUND. | |
| PA | | |
| XX | Bohlmann J, Steele CL, Croteau RB; | |
| PI | | |
| XX | WPI; 1999-120396/10. | |
| DR | P-PSDB; AAW85710. | |
| DR | | |
| XX | New isolated gymnosperm monoterpene synthase DNA - obtained from Grand | |
| PT | fir (<i>Abies grandis</i>), used to provide plants with modified production of | |
| PT | monoterpenes, e.g. mycrene, limonene or pinene. | |
| XX | | |
| PS | Example 3; Page 104-107; 121pp; English. | |
| XX | | |
| CC | Nucleotide sequences encoding mycrene synthase, limonene synthase and | |
| CC | pinene synthase from Grand fir may be incorporated into any organism | |
| CC | (e.g. intact plant, animal, microbe), or derived cell culture that | |
| CC | produces geranyl diphosphate for the production of the aforementioned | |
| CC | enzymes or their products. The sequences when expressed in transfected | |
| CC | cells may also be used for the production or modification of flavour and | |
| CC | axoma properties, improvement of defense capability, and the alteration | |
| CC | of other ecological interactions mediated by mycrene, limonene, pinene, | |
| CC | or their derivatives. In particular they can be used for the production | |
| CC | of plant seeds for the extraction of oil or meal | |
| XX | | |
| Sequence | 2205 BP; 703 A; 412 C; 463 G; 627 T; 0 U; 0 Other; | |

| | | | | |
|----------------------------|-------|---------------------|------------|--------------|
| Query Match | 53.2% | Score 1071.6; | DB 2; | Length 2205; |
| Best Local Similarity | 75.0% | Pred. No. 3.1e-293; | | |
| Matches 1430; Conservative | 0; | Mismatches 441; | Indels 36; | Gaps 6; |

| | | | |
|----|-----|--|-----|
| QY | 68 | CAGGTCGTGCTCAGTTCCTTCATGAGATTAAAGCTCTCCGTAGAACATCCCACTCT | 127 |
| | | | |
| Db | 104 | CAAGTCGTTGATCAGTTCAATTCATGAACATTAAGCCTCCCTATAGAACATCCCAATCT | 163 |
| | | | |
| QY | 128 | TGGAATCTGCAGGCCGGGAAATCCGTCGCCATTCATTAACATGTTGTGAACAAGCT | 187 |
| | | | |
| Db | 164 | TGGAATGCGTAGGCGAGGAAATCTGTCAAGCCTTCATGAGCATCAGTTTGGCCACCGC | 223 |
| | | | |
| QY | 188 | CGCATCTACTGATTCTGTACAGACGCCGTGGCACTATCATTTCAACCTGTGGACGA | 247 |
| | | | |
| Db | 224 | TGCACCTGATGATGGGTGTACAAAGCCATAGGTGACTACCATTTCCAATATCTGGACGA | 283 |
| | | | |
| QY | 248 | TGATTTCATACAGTCTCTGATCTCAACGCCCTTATGAGACACCTGATTAACGGGAACGTGC | 307 |
| | | | |
| Db | 284 | TGATTTCATACAGTCTC--TATCAACGCATTATGCGGAACCTCTTACCAAGAAAGTGC | 340 |
| | | | |
| QY | 308 | TGACAGACTTATTTGGGGAAGTAAAGATATTAATGTTCAATTTCAAGTCCTGGAAGATGG | 367 |
| | | | |
| Db | 341 | TGAGAGATTAATTTGTGAGAGTAAAGAAGATA--TTCATTTCAATGTACTCGATGATGG | 397 |
| | | | |
| QY | 368 | AGG-----CAATGATCTCCTTCAACGACTTTTGCTGGTCGATGACGTTGA | 412 |
| | | | |
| Db | 398 | AAGATTATGAGTTCCTTTATGATCTCATGCAACGCCCTTGATAGTCGATAGCGTTGA | 457 |
| | | | |
| QY | 413 | ACGTTTGGGAATCGACAGGCATTTCAAAAAAGAGATTAATAACGGCATTCGATTATGTTAA | 472 |
| | | | |
| Db | 458 | ACGTTTGGGATAGCTAGACATTTCAAGAACGAGATTAACATCAGCTCTCGATTATGTTTT | 517 |
| | | | |
| QY | 473 | CAGTTATTGGAAACGAAAAAGGCAATTGGATGTGGAGGAGAGAGTGTGTGACTGAACCTCAA | 532 |
| | | | |
| Db | 518 | CCGTTACTGGAGGAAACCGCATTTGGATGTGGAGAGACAGTATTTTAACTGATCTCAA | 577 |
| | | | |
| QY | 533 | CTCAACCGCCTTTGGGCTTCGAATCTCCGACTACACGGATACACTGTGCTTCAGATGT | 592 |
| | | | |
| Db | 578 | CTCAACTGCGTTGGGTTTCGAATCTTCGATTACACGGGTACACTGTATCTCCAGAGGT | 637 |
| | | | |
| QY | 593 | TTTGAACGTTTAAAGACAAAAATGGCAATTTTCTCCACTGCCAATATTCAGATAGA | 652 |
| | | | |

Db 638 TTTAAAGCTTTTCAAGATCAAAATGACAGTTGTATGCTCCCC--GGTCAGACAGA 694
QY 653 GGGAGATTAGAGGCGTTCTCAATTTATTCAGGCGCTCCCTCGTCCCTTTCCGCGCA 712
Db 695 GGGTGAGATCAGAAAGCGTTCTTAACCTTATATCGGGCTTCCCTCATTTGCCCTTCCGTGTA 754
QY 713 GAAAGTTATGATGAAGCTGAAACATTTCTCTACAAATATTTTAAGAAAGCCCTGCAAAA 772
Db 755 GAAAGTTATGGAAGAAGCTGAAATCTTCCACAAGATATTGAAGAAGCTCTACAAAA 814
QY 773 GATTCGGCATCCAGTATATCTTCACTAGAGATACGGAGCTTCTGGAATATGTTGGCA 832
Db 815 GATTCAGTCTCCGCT--CTTCAAGAGATAAAGTTGTATGGAATATGGCTGGCA 871
QY 833 CACCAATTTGCCACGCTTGGAGACAGAAATTACATGAGCGTCTTTGACACAGACACTA- 891
Db 872 CACAAATTTGCCAAGATTGGAAGCAAGAAATTACATAGACACACTTTGAGAAAGACACCAG 931
QY 892 -----AAATTAAGAACGCCCGCGAGAACTTTAGAACTTGCAAAATTGAATTCAA 943
Db 932 TGCATGGCTCAATAAAAATGCTGGAGAGAAGCTTTAGAACTTGCAAAATTGAGATTCAA 991
QY 944 TATATTTCACTCCTTACAGAGAGAGAGTTAAAAATGTTCCCGATGGTGAAAGACTC 1003
Db 992 TATATTTAACTCCTTACACAAAAGAAATTACAATATCTTTGAGATGGTGAAAGACTC 1051
QY 1004 GGGTCTCTGAGATGACCTTCTGTCATCGTCACGTGGAATACTAGCTTTGGCTTC 1063
Db 1052 GGATTTGCCCTAAATTGACATTTGCTCGGCATCGTCATGTGAATTTCACTTTGGCTC 1111
QY 1064 CTGCATTCGCTTCGAGCCTCAACATTTCTGATTTCAGACTCGGCTTTACCAAGATGTCTCA 1123
Db 1112 TTGTATTTGCCATTGACCCAAACATTTCTGATTTCAGACTAGGCTTCGCCAAATGTGTCA 1171
QY 1124 TCTTATCACGCTTCTTGACGACATGTACGACGCTCTTCGGCACAGTACAGAGCTGGAAT 1183
Db 1172 TCTTGTACAGTTTGTGACGATATTTAAGACACTTTTGGAAAGATTGACGAGCTTGAAT 1231
QY 1184 CTTTACAGCGCAATTAAAGAGATGGATCCGTCGCGATGGAATGCTTCCAGAAATATAT 1243
Db 1232 CTTTCACTCTGCAATTAAGAGATGAAATTCATCAGAGATAGAACACTTCCAGAAATATAT 1291
QY 1244 GAAAGAGTGTACATGATGTTTATCACACCGTAAATGAAATGGCTGAGTGGCAGAGAA 1303
Db 1292 GAAATGTGTACATGCTGTGTTGAAACTGTAAATGAACTGACAGAGCGGAGAA 1351
QY 1304 GGCTCAAGGCCGAGACACGCTCAACTATGCAAGACAGGCTTGGAGGCGTGTATTGATTC 1363
Db 1352 GACTCAAGGGGAGAAACACTCTCAACTATGTTCCGAAAGGCTTGGAGGCTTATTGATTC 1411
QY 1364 GTATATGCAAGAACAAAGTGGATCGCCACTGGTTATCTGCCACGTTTGAGAGTACTT 1423
Db 1412 ATATATGGAAGAACAAATGATCTCTAATGTATCTGCCAACGTTTGAAGAGTACCA 1471
QY 1424 GGAGAACGGGAAAAGTTAGCTCTGCTCATCGCCCATGCGACTGCAACCCATTCTGACGTT 1483
Db 1472 TGAGAAATGGGAAAAGTGAGCTCTGCAATTCGCGTAGCAACATTGCAACCCATCTCACTTT 1531
QY 1484 GGACATCCCTTCTCTGATCACATCTCAAGGAAGTTGACTTCCCATCGAAGCTCAATGA 1543
Db 1532 GAATGCAATGCTTCTCTGATTACATTTGAAGGAATTGATTTCCATCCAGGTTCAATGA 1591
QY 1544 CTTGATATGTATCATCTTCTGATTAAGAGTGTATACAGGTTGCTACAGGCAGACAGGCG 1603
Db 1592 TTTGGCATCTCTCTCTCTCGCTACGAGGTGACACACGCTGCTACAGGCCGATAGGGA 1651
QY 1604 CCGTGAGAGAAGAGCTTCGTATATCATGTATATGAAGAACAATCCTGATTAAACGGA 1663
Db 1652 TCGTGTGAAGAAGCTTCGTATATCATGTATATGAAGAACAATCCTGATTCAACCGA 1711
QY 1664 AGAAGATGCTCTGAATCATATCACTTCATGATCAGGAGCGCAATCAGAAATTAATTG 1723
Db 1712 AGAAGATGCCCTCAATCATATCAATGCCATGGTCAATGACATAATCAAGAATTAATTG 1771

QY 1724 GGAGCTTTAAAGCCAGACAGAGTGTCCCATCACTTCCAGAAACACGCAATTTGACAT 1783
Db 1772 GGAATCTTAAGATCCACAGACATATTTCCAAATGCTGGCCAGAAACATGCTTTGACAT 1831
QY 1784 AAGCAGATTTGGCATCACGGTTACAGATACCGAGATGGCTACAGCTTTGCCAACGTTGA 1843
Db 1832 AACACAGACTCTCCACCATCTTCAATATATGAGATGGCTTTAGTGTGCCAACAGGA 1891
QY 1844 AACAAAGATTGCTGATGAGAACCGTCATTTGAACCTGTGCTTTGTAAACAACCTTCAA 1903
Db 1892 AACAAAAAATTGTTATGGAACACTCCTGAATCTATGCTTTTAACTATAACCATATA 1951
QY 1904 ATCTACATATTAACTGAGATGCCCTATGGGTATATATAGGCACA 1950
Db 1952 TCCATATAATAAGCTCATTAATGCTAAATTATTGGCCTTATGACATA 1998

RESULT 11
AAF73391
ID AAF73391 standard; cDNA; 2205 BP.
XX
AC AAF73391;
XX
DT 30-APR-2001 (first entry)
XX
DE Grand fir monoterpene synthase coding sequence fragment SEQ ID NO: 31.
XX
KW Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;
KW myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;
KW terpinolene synthase; insect resistance; nutrition; ss.
XX
OS Abies grandis.
XX
PN WO200107565-A2.
XX
PD 01-FEB-2001.
XX
PF 24-JUL-2000; 2000WO-US020264.
XX
PR 26-JUL-1999; 99US-00360545.
XX
PA (UNIW) UNIV WASHINGTON STATE RES FOUND.
XX
PI Steele CL, Bohlmann J, Croteau RB, Phillips MA;
XX
DR WPI: 2001-182782/18.
XX
DR P-PSDB; AAB69380.
XX
PT New nucleic acid encoding monoterpene synthases, for increasing terpene
PT synthesis in plants, e.g. for increasing resistance to pests or for
PT treatment of cancer.
XX
PS Example 3; Page 135-137; 175pp; English.
XX
CC The present invention provides the protein and coding sequences of
CC monoterpene synthases from the grand fir. These include (-)-camphene
CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-
CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase
CC and pinene synthase. The sequences can be used to produce transgenic
CC plants expressing high levels of the enzymes, resulting in levels which
CC are useful in protecting against and treating cancers, and to confer
CC insect resistance on plants
XX
SQ Sequence 2205 BP; 703 A; 412 C; 463 G; 627 T; 0 U; 0 Other;

Query Match 53.2%; Score 1071.6; DB 4; Length 2205;
Best Local Similarity 75.0%; Pred. No. 3.1e-293;
Matches 1430; Conservative 0; Mismatches 441; Indels 36; Gaps 6;

QY 68 CAGTGTGCTCAGTCTTCTCATGAGATTAAGGCTCTCCGTAGAACATCCCAACTCT 127
Db 104 CAACTGTTGATCAGTTCAATTCATGAAACATAAGCCTCCCTATAGAACAAATCCCAATCT 163

```
QY 128 TGAATCTGCAGCGCCGGGAATCCGTCGCCATTCATMAACATGTTTGACAAGCGT 187
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 164 TGAATGCGTAGCGGAGGMAATCTGTCAAGCCCTTCATGAGCATGATTGGCCACCGC 223
QY 188 CGCATCTACTGATTTCTGTACAGAGCGGTGGCAACTATCATTCACACTGTGGAGCA 247
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 224 TGCACCTGATGATGCTGTACAAAGACGATAGTACTACCATTCACATATCTGGAGCA 283
QY 248 TGATTTCAACAGTCTCTGATCTCAAGCCTTATGAGACCTGATTAACCGGAACGTGC 307
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 284 TGATTTCAACAGTCTC--TATCAACGCATTATGGGAACCTCTTACAGGAACGTGC 340
QY 308 TGACAGACTTATTTGGGGAAGTAAGATTAATGTTCAATTTCAAGTCGCTGGAAGATGG 367
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 341 TGAGAGATTAAATTGTGAGAGTAAGAAGATA--TTCAATTCAATGTAACTTGATGATGG 397
QY 368 AGG-----CAATGATCTCCTTCAACGACTTTTGTGCTGATGACGTTGA 412
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 398 AAGATTAAAGAGTTCCTTAATGATCTCAATGCAACGCCCTTGGATAGTCGATAGCGTTGA 457
QY 413 ACGTTTGGGAATCGACAGCATTTCAAAAAAGAGTAAAAACGCACTCGATTATGTTAA 472
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 458 ACGTTTGGGAGTAGCTAGACATTTCAAGAACAGATAACATCAGCTCGGATTATGTTT 517
QY 473 CAGTTATGGAACGAAAAAGCATGTGATGCGGAGGAGAGAGTGTGACTGACCTCAA 532
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 518 CCGTTACTGGAAGGAAAAACGCATTTGATGTGGGAGAGACAGTATTTACTGATCTCAA 577
QY 533 CTCAACCCGCTTGGGCTTCGAATCTCCGACTACACGATACACTGTCTTCAGATGT 592
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 578 CTCAACTGCGTTGGGGTTTCAACTCTTCAATTACACGGGTACACTGTATCTCCAGAGGT 637
QY 593 TTTGAACGTTTTTAAAGACAAAAATGGGCAATTTCTCCACTGCCAATATTCAGATAGA 652
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 638 TTTAAAGCTTTTCAAGATCAAAATGACAGATTTGTATGCTCCCC--GGTCAGACAGA 694
QY 653 GGGAGAGTTAGAGCGCTTCTCAATTAATTCAGGGCCTCCCTCGTCGCTTTCCCGGCGA 712
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 695 GGGTGAATCAGAAAGCGTTCTTAATTAATTCGGGCTCCCTCATGCTTCCCTGTGTA 754
QY 713 GAAAGTTATGATGAAGCTGAACATTTCTTACAAATATTTAAGAGAACCCCTGC AAA 772
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 755 GAAAGTTATGGAAGAAAGCTGAATCTTCCACAAGATATTTGAAGAAAGCTCTACAAA 814
QY 773 GATTCGGGATCCAGTATATCTTCACTAGAGATACGGGAGCTTCTGAATATGTTGCA 832
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 815 GATTCAGTCTCCGCT--CTTTCACAGAGATTAAGTTGTATGGAATATGCTGCA 871
QY 833 CACCAATTTGCCACGCTTGGAAAGCAAGAAATTAATGAGCGCTTTGACACACACTA- 891
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 872 CACAAATTTGCCAAGATTGGAAGCAAGAAATTAATAGACACACTTGAGAAAAGACACAG 931
QY 892 -----AAATTAAGAACGCCCGGAGAACTTTAGAACTTGCAAAATTGGAATTCAA 943
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 932 TGATGCTCAATPAAAAATGCTGGAAAGCTTTAGAACTTGCAAAATTGGAATTCAA 991
QY 944 TATATTTCACTCTTACAGAGAGAGAGTAAAAATGTTCCCGATGCTGAAAAGACTC 1003
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 992 TATATTTAACTCTTACAAACAAAAGAAATTAACAATATCTTTGAGATGCTGAAAAGACTC 1051
QY 1004 GGGTTCCTGAGATGACCTTCTGCAATGCTCAGCTGGAATATAAGCTTTGCTTC 1063
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1052 GGATTTGCCATAAATTGACATTTGCTCGGCAATGCTCATGTGAATTTACACTTTGGCTC 1111
QY 1064 CTGCAATGGGTTGAGCGCTCAACATTTGGAATTCAGACTCGGCTTTACCAAGATGCTCA 1123
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1112 TTGTATGCAATGACCAAAACATTTGCAATTCAGACTAGGCTTCGCAAAATGTGTCA 1171
QY 1124 TCTTATCACGCTTCTTGACGACATGTACGAGCTTCCGCAACAGTACAGAGCTGGAAT 1183
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1172 TCTTGTACAGTTTGGACGATATTTACGACACTTTTGGAAAGATGACGAGCTTGAAT 1231
```

```
QY 1184 CTTACAGGCAATTAAGATGGGATCCGTCGCCGATGGAATGCCCTCCAGATATAT 1243
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1232 CTTCACTCTGCAATTAAGATGGAATTCATCAGAGATAGAACACCTTCCAGATATAT 1291
QY 1244 GAAAGAGTGTACATGATGTTTATCACACCGTAATGAATGGCTCGAGTGGCAGAGAA 1303
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1292 GAAATGTGTATCATGCTGCTGTTTGAACCTGTAATGAACTGACACGAGGCGGAGAA 1351
QY 1304 GGCTCAAGCGGAGACACAGCTCAACTATGCAAGACAGGCTTGGAGGGCTGTTGATTC 1363
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1352 GACTCAAGGAGAAACACTCTCAACTATGTTCGAAAGGCTTGGAGGCTTATTTGATTC 1411
QY 1364 GTATATGACGAAAGCAAAAGTGATGCGCACTGTTATCTGCCAGTTTGAGAGTACTT 1423
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1412 ATATATGGAAGAAACAAATGATCTTAATGTTATCTGCCAAGCTTGAAGATACCA 1471
QY 1424 GGAGAACGGGAAAGTTAGCTCTGCTCATCGCCCATGCGCACTGCAACCCATCTGACGTT 1483
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1472 TGAGAAATGGGAAAGTAGCTCTGCATATCGCGTAGCAACATTTGCAACCCATCTCACTT 1531
QY 1484 GGACATCCCTTCTCTGATCAATCTCAAGGAAGTGAAGTCTCCATTCGAAGCTCAATGA 1543
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1532 GAATGCAAGCTTCTGATTAATCTTGAAGGAATGATTTTCCATCCAGCTCAATGA 1591
QY 1544 CTTGATATGATGATCTCTGATTAAGAGTGATACACGGTGCTTCAAGGACAGACAGGC 1603
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1592 TTGGCATGCTGCTCTTCCGCTACGAGGTGACACACGCTGCTTCAAGGCCGATAGGGA 1651
QY 1604 CCGTGAGAGAAAGCTTCTGCTATATCATGTTATATGAAGAAATCCTGATTAACGGA 1663
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1652 TCGTGGAAGAAAGCTTCTGCTATATCATGTTATATGAAGAAATCCTGATCAACCGA 1711
QY 1664 AGAAGATGCTCTGAATCATATCAACTTCATGATCAGGAGCGCAATCAGAAATTAATTG 1723
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1712 AGAAGATGCGCTGAATCATATCAATGCCATGTCAATGACATMAATCAAAAGATTAATTG 1771
QY 1724 GAGCTTCTAAAGCCAGACACAGTGTCCCATCACTTCCAAAGAACGCAATTTGACAT 1783
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1772 GGAATCTTAAGATTCACAGCACAATATTCGAATGCTGGCCAAAGAAATGCTTTGACAT 1831
QY 1784 AAGCAGATTGTCATCACGTTTACAGATACCGAGATGGCTACAGCTTGGCCAAGCTGA 1843
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1832 AACAAAGCTCTCCACCATCTCTACATATATCGAGATGGCTTGTGTTGCCAACAAGGA 1891
QY 1844 AACAAAGATTGTTGTGATGAGAACCGTCAATGAACTGTGCTTTGTTAAACAACACTTCAA 1903
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1892 AACAAAAATTTGTTATGGAACACTCTTGAATCTATGCTTTTAACTATAACCATATA 1951
QY 1904 ATCTACAATTAATCTGAGGATGCCCTATGGGTATATAGGCGACA 1950
Db 1952 TCCATAATAATAAGCTCATATGCTTAATTAATTGGCCTTATGACATA 1998
RESULT 12
AAF73413
ID AAF73413 standard; cdna; 2429 BP.
XX
XX AAF73413;
AC
XX
XX 30-APR-2001 (first entry)
DE Grand fir monoterpene synthase coding sequence fragment SEQ ID NO: 68.
XX
XX Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;
KW myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;
KW terpinolene synthase; insect resistance; nutrition; ss.
XX
XX Abies grandis.
OS
XX
XX MO200107565-A2.
PN
XX
XX 01-FEB-2001.
PD
XX
```


Db 1763 ATCAGAGATTAAATTGGAGCTTCTCAGACGAGATAGCAAAAGTCCCATCTCTTCCAAG 1822
QY 1767 AACACAGCATTTGACATAGCAGAGTTTGGCATCACGGTTACAGATACCGAGATGGCTAC 1826
Db 1823 AACATGCTTTTGACATCACCAGAGCTTCCATCACCCTACAGATACCGAGATGGTTAC 1882
QY 1827 AGCTTGGCCACGTTGAAACAAGAGTTTGGTATGAGAACCCTCATTTGAACCTGTGCCT 1886
Db 1883 ACTGTGCGAGTAGTGAAACAAGATTGGTATGAAAAACAGTTCTTGAACCTGTGGCA 1942
QY 1887 TTGTAACACACTTCAA 1903
Db 1943 TTGTAAAAAATATCAA 1959

RESULT 13

AAK08645
ID AAK08645 standard; cDNA; 2089 BP.

XX AAK08645;

DT 27-SEP-1999 (first entry)

DE Limonene synthase gene.

XX Myrcene synthase; limonene synthase; pinene synthase; flavour; aroma;
KW defense; plant seed; oil; meal; ss.

XX Abies grandis.

FT Key Location/Qualifiers
CDS 73..1986
FT /*tag= a
FT /product= "Limonene synthase"

XX WO9902030-A1.

XX 21-JAN-1999.

XX 10-JUL-1998; 98WO-US014528.

XX 11-JUL-1997; 97US-0052249P.

PA (UNIW) UNIV WASHINGTON STATE RES FOUND.

PI Bohlmann J, Steele CL, Croteau RB;

DR WPI; 1999-120396/10.

DR P-PSDB; AAW85702.

PT New isolated gymnosperm monoterpene synthase DNA - obtained from Grand
fir (Abies grandis), used to provide plants with modified production of
monoterpenes, e.g. myrcene, limonene or pinene.

PS Claim 11; Page 79-82; 121pp; English.

XX Nucleotide sequences encoding myrcene synthase, limonene synthase and
pinene synthase from Grand fir may be incorporated into any organism
CC (e.g. intact plant, animal, microbe), or derived cell culture that
CC produces geranyl diphosphate for the production of the aforementioned
CC enzymes or their products. The sequences when expressed in transfected
CC cells may also be used for the production or modification of flavour and
CC aroma properties, improvement of defense capability, and the alteration
CC of other ecological interactions mediated by myrcene, limonene, pinene,
CC or their derivatives. In particular they can be used for the production
CC of plant seeds for the extraction of oil or meal

SO Sequence 2089 BP; 638 A; 415 C; 450 G; 586 T; 0 U; 0 Other;

Query Match 46.0%; Score 925.4; DB 2; Length 2089;

Best Local Similarity 70.6%; Pred. No. 9.8e-252;
Matches 1340; Conservative 0; Mismatches 506; Indels 51; Gaps 6;

QY 72 TCGTGCCTCAGTTCTTCTCATGAGATTAAAGCTCTCCGTAGAACAAATCCCACTCTTGA 131
Db 127 TCGTGATCAGTTCCAGCAATGTGCAGAAAGCTCTGTATCTCTACAGCAGTCCCAACA 186
QY 132 ATCTGACGCGCGGAAATCCGTCGCGCATTTCCATAAATATGTGTTGACAAGCTCGCA 191
Db 187 CTCAGAATGCGTAGGCGCACAGAAAGCTCTGGTCAATCAACATGAATTTGACCACTGTATCC 246
QY 192 TCTACTGATTCT-----GTACAGAGACGCGTGCGCACTTATTCATTTCCAAC 236
Db 247 CATCGTATGATTAATGCTGTGTGTACTGCAAAAGCATAGCCGATCATCATCCCAAC 306
QY 237 CTGTGGACGATGATTTTCATACAGTCTGTATCTCAACGCTTATGAGACCTGATTTAC 296
Db 307 CTGTGGAGATGATTTTCATACATCATCTGTCTCA---CCTTATGGGGATCTTCGTAC 363
QY 297 CGGAACGTGCTGACAGACTTATTGGGGAAGTAAAGATAT-----AATGTTCAAT 347
Db 364 AGTGAACGTGCTGAGACAGTCTGTGAGAAAGTAAAGAGATGTTCAATTCATACCAAT 423
QY 348 TTCAAGTCGCTGGAAGATGAGAGCAATGATCTCCTTCAACGACTTTGCTGTGATGAC 407
Db 424 AATAGAGATTATTTGTTTCCCAAATGATCTCTTACACGCTTTGATGATGATAGC 483
QY 408 GTGAACGTTTGGGAATCGACAGGCAATTTCAAAAAAGAGATAAAACGCACTCGATTAT 467
Db 484 ATTGAACGTCTGCGGATAGATAGACATTTCCAAAATGAGATTAAGATAGCCCTGATTAT 543
QY 468 GTTAACAGTTATTGGAACGAAA--AAGCATTTGATGTGGAGGAGAGTGTGTACT 524
Db 544 GTTACAGTTATTGGAAGAAAAGAAAGCAATGGGTGTGGCAGAGATTCTACTTTTCT 603
QY 525 GACCTCAACTCAACCGCCTTGGGCTTGAACCTCTCCACTACACGATACACTGTGTCT 584
Db 604 GATCTCAACTGACTGCTTGGCGCTTGAACCTCTGACTGACGAGTACAATGTGTCT 663
QY 585 TCAGATGTTTGAACGTTTAAAGCAAAAATGGCAATTTCTCCACTGCAATATAT 644
Db 664 TCAGATGTGCTGAATACTTCAAGATGAAGAGGGCATTTTGCCTGCAATCTTA 723
QY 645 CAGATAGAGGAGAGATTAGAGGCGTCTCAATTTATTCAGGGCTCCTGCTGCTTT 704
Db 724 ACCGAGGACAGATCACTAGAGGTCTTAATTTATATCGGGCTTCCCTGCTGCTTT 783
QY 705 CCGGCGGAGAAAGTTATGATGAAGCTGAACATTTCTCAAAATATTTAAGAGAAAGCC 764
Db 784 CCGGCGGAGAAAGTTATGAGAGAGGCTGAATCTTCTCGGCATCTTAATTGAAAAAAGTC 843
QY 765 CTGCAAAAGATTCCGGCATCCAGTATCTTCACTAGAGATACGGGCGTCTGGAATAT 824
Db 844 TTACAAAAGATTCCGGTCTCCAAT---CTTACAGAGAGATAGATATGTTTGAATAT 900
QY 825 GGTGGCACCAATTTGCCACGCTTGAAGCAAGAAATTACATGACGTCTTTGACACAG 884
Db 901 GGTGGCACCAATTTGCCGAGATTGGAAGCAAGAAATTATATGAGGTCTACGAGCAG 960
QY 885 CACACTAAAATA-----AGAACGCGCGGAGAAACTTTTGAACCTT 926
Db 961 AGCGGCTATGAAGCTTAACGAGATGCCATATATGAACATGAAGAACTTTTACAACCTT 1020
QY 927 GCAAAATTTGAATTCATATATTTCACTCTTACAGAGAGAGAGTTAAACATGTTTCC 986
Db 1021 GCAAAATTTGAATTCATATATTTCACTCTTTCACACTAAGAGAGTTACAATCTATCTCC 1080
QY 987 CGATGTGGAAGAGACTCGGGTCTCTCGAGATGACCTTCTGTGACATGCTCAGCTGGA 1046
Db 1081 AGATGTGGAAGAGATCAGGTCTCTCAACTGACTTTTACACGGGATGTCACGTGGAA 1140
QY 1047 TACTACGCTTTGCTTCTGCAATGCGTTGAGCCTCAACATCTGGAATTCAGACTCGGC 1106
Db 1141 TACTACACTATGCACTTGTCAATTTATGTTGCCAAAACATTCAGCTTTCAGAAATGAG 1200
QY 1107 TTACCAAGATCTCTCATCTTATCAAGGTTCTTGACGACATGTAAGACGTCTTGGCACA 1166

```
Db      1201 TTTGTCAAAGTGTGTCATCTTGTACAGTCTTCGATGATATATATGACACTTTGGACA 1260
Qy      1167 GTAGACGAGCTGGAAGCTTTCACAGCCAAATTAAGAGATGGATCCGCGATGGAA 1226
Db      1261 ATGAACGAACTCCAACTTTTACCGATGCAATTAAGAGATGGATTTGTCAACGACAAG 1320
Qy      1227 TGCCTTCCAGAAATATATGAAGAGAGTGTACATGATGTTTATCACACCGTAATGAATG 1286
Db      1321 TGGCTTCCAGAAATATATGAAGAGAGTGTACATGAGCTTGTATCAATGCAATTAATGAATG 1380
Qy      1287 GCTCGAGTGCAGAGAGGCTCAAGGCCGAGACACGCTCAACTATGCAAGAAGAGCTTGG 1346
Db      1381 GTGAAGAGGCTGAGAAGACTCAAGGCCGAGATATGCTCAACTATATTCAAAATGCTTGG 1440
Qy      1347 GAGGCGTGTTTGATTCGTATATGCAAGAACAAAGTGATCCCACTGTTATCTGCC 1406
Db      1441 GAAGCCCTATTGTATACCTTTATGCAAGAACAAAGTGATCTCCAGCACTTATCTCCA 1500
Qy      1407 ACGTTGAGAGAGTACTTGGAGAACGGGAAAGTTAGCTCTGCTCATCGCCCATGCGCACTG 1466
Db      1501 ACGTTGAGAGAGTACTTGAAGAAATGCAAAAAGTTAGTTCTGTTCTTCGCAATAGCCACATTA 1560
Qy      1467 CAACCCATTTGACGCTTGACATCCCTTCTCTGATCACATCCTCAAGGAAGTGAAGTTTC 1526
Db      1561 CAACCCATTTCACTTTGATGATGACCACTTCTGATTACATACAGCAAGAAATGATTAT 1620
Qy      1527 CCATCGAGCTCAATGACTTGATATGTAATCATCTTCGATTAAAGGTGATACACGGTGC 1586
Db      1621 CCATCCGATTCATAGAGTAGTTCCTTCCTTCATCTTCGACTACGAGTGACACGCGTGC 1680
Qy      1587 TACAAGGAGACAGGGCCGCTGAGAGAGAGCTTCGTCTATATCATGTTATATGAAGAAG 1646
Db      1681 TACAAGGCGGATAGGGCCCGTGAGAGAGAGCTTCAGCTATATCGTGTATATGAAGAAG 1740
Qy      1647 AATCCTGATTTAACGGAAGAGATGCTCTGAATCATATCAACTTCATGATCAGGAGCA 1706
Db      1741 CATCCTGATTCATAGAGAGATGCTCTCAATCATATCAACGCCCATGATCAGTATGCA 1800
Qy      1707 ATCAGAGAAATTAATTTGGAGCTTCTTAAAGCCAGACACAGTGTTCCTCATCTTCCAAG 1766
Db      1801 ATCAGAGAAATTAATTTGGAGCTTCTTCAAGCCGATAGCAAAAAGTTCCTCATCTTCCAAG 1860
Qy      1767 AAACACGATTTGACATTAAGCAGAGTTGGCATCACGGTTACAGATACCGAGATGGCTAC 1826
Db      1861 AAACATGCTTTTGCATCACCAGAGCTTTCATCATGTCTACAAATATTCAGATGGTTAC 1920
Qy      1827 AGCTTTGCCAACGTTGAACAAAGAGTTGGTATGAGAACCGTCAATGAACCTGTGCT 1886
Db      1921 ACTGTTTCCAACAACGAAACAAAGAAATTTGGTATGAAAAACCGTCTTGAACCTCTCGCT 1980
Qy      1887 TTGTAACACACTTCAATCTACAATATTAAGTGAAG 1923
Db      1981 TTGTAACACATATAGATGCAATTAATGTGGGAAG 2017

RESULT 14
AAA38938 standard; DNA; 2089 BP.
AC      AAA38938;
XX      25-AUG-2000 (first entry)
DE      Grand fir limonene synthase DNA sequence SEQ ID NO:57.
XX      Synthase; protein co-ordinate data; active site; modification; terpenoid;
KW      3-dimensional coordinate; alpha carbon atom; plant; terpene synthase;
KW      isoprenoid; breeding programme; fragrance; flavour; pheromone;
KW      defensive agent; pigment; antitumor; steroid hormone;
KW      signal transduction pathway; bile acid; affinity purification;
KW      photoreceptor; enzymatic synthesis; nutrient supplement;
KW      immunological reagent; ds.
```

```
XX      Abies grandis.
OS      WO200017327-A2.
XX      30-MAR-2000.
XX      17-SEP-1999; 99WO-US021419.
XX      18-SEP-1998; 98US-0100993P.
PR      22-APR-1999; 99US-0130628P.
PR      23-AUG-1999; 99US-0150262P.
XX      (KENT ) UNIV KENTUCKY RES DEPT.
PA      (SALK ) SALK INST BIOLOGICAL STUDIES.
PI      Chappell J, Manna KR, Noel JP, Starks CM;
XX      WPI; 2000-292839/25.
DR      P-PSDB; AAY90859.
XX      Novel terpene synthase enzymes, useful for producing terpene
PT      hydrocarbons, e.g. fragrances or antitumor agents, are derived from known
PT      enzymes by specific amino acid alterations.
XX      Disclosure; Page 445-448; 450pp; English.
XX      The present invention describes an isolated terpene synthase (I)
CC      comprising a region with at least 20% identity to region 265-535 of a 548
CC      amino acid (aa) sequence (Ia), given in AAY90831. (I) contains nine alpha
CC      -carbon atoms (alphac) that have interatomic distances, between each
CC      other, within tabulated ranges, have a centre point (within a sphere of
CC      radius 2.3 Angstrom ) within tabulated ranges, and have an ordered
CC      arrangement of R groups (defining aa side chains), excluding specific
CC      tabulated arrangements (tables given in the specification). (I), and
CC      related enzymes, are used to produce a wide range of terpenoids (e.g.
CC      cyclic, acyclic, optionally hydroxylated), useful e.g. as fragrances,
CC      flavours, pheromones, defensive agents, pigments, antitumor agents,
CC      components of signal transduction pathways, precursors of steroid
CC      hormones and bile acids, as photoreceptors and as co-factor side chains.
CC      Some synthases with little or no catalytic activity (and nucleic acids
CC      encoding them) are used as controls in the analysis of products formed by
CC      enzymatic synthesis; as nutrient supplements; for affinity purification
CC      of isoprenoids; or to develop immunological reagents or nucleic acids for
CC      monitoring expression of terpene synthase or inheritance of the gene in
CC      plant breeding programs. The new synthases may produce novel terpene
CC      products. AAA38910 to AAA38938 and AAY90831 to AAY90859 represent
CC      sequences used in the exemplification of the present invention
XX      SQ      Sequence 2089 BP; 638 A; 415 C; 450 G; 586 T; 0 U; 0 Other;

Query Match      46.0%; Score 925.4; DB 3; Length 2089;
Best Local Similarity 70.6%; Pred. No. 9.8e-252;
Matches 1340; Conservative 0; Mismatches 506; Indels 51; Gaps 6;

Qy      72 TCGTGCCCTCAGTTCTTCTCATGAGATTAAGGCTCTCCGTAGAACAAATCCCAACTCTTGA 131
Db      127 TCCTGATCAGTTCACGCAATGTGAGAGAGCTCTGTATCTCTACAGCAGTCCCAACA 186
Qy      132 ATCTGACGCGCGGGAATCCGCGCATTCATTAACATGCTTTGACACAAGCGTCGA 191
Db      187 CTCAGATGCGTAGGCGACAGAAAGCTCTGTCATCAACATGAATGACCACTGTATCC 246
Qy      192 TCTACTGATTTCT-----GTACAGAGACCGCGTGGCAACTATCATTTCCAAC 236
Db      247 CATCGTATGATTAATGTGTGTGTGTACTGCAAAAGACGCATAGCCGATCATCTCCAAC 306
Qy      237 CTGTGGAGCATGATTTTCATACAGTCTCTGATCTCAACGCCCTTATGAGACACCTGATTAC 296
Db      307 CTGTGGAGATGATTTTCATACATATGTTCTCA---CCTTATGGGGGATCTTCGTAC 363
Qy      297 CGGAACGTGCTGACAGACTTATTTGGGAAGTAAGGATAT-----AATGTTCAAT 347
```


Db 364 AGTGAACGCTGAGACAGCTGTTGAGGAAGTAAAGAGATGTTCAATTCATACCAAT 423
QY 348 TTCAAGTCGCTGGAAGATGAGGCAATGATCTCTTCAACGACTTTGCTGTCGATGAC 407
Db 424 AATAGAGAAATTTTGGTTCCCAAAATGATCTCTTACACGCCCTTTGGATGATGAC 483
QY 408 GTTGAACGTTGGGAATCGACAGGCAATTTCAAAAAAGAGATAAAAACGGCACTCGATTAT 467
Db 484 ATTGAACGCTGGGGATAGATAGACATTTCCAAAATAGATTAAGATAGAGTACCTCGATTAT 543
QY 468 GTTAACAGTTAATGGAACGAAA--AAGCAATGATGTGGAGGAGAGATGTTGACT 524
Db 544 GTTACAGTTAATGGAAGGAAAAGGAAGGCAATGGGTGTGGCAGAGATTTCTATTTCCT 603
QY 525 GACCTCAACTCAACCGCTTGGGCTTGAACCTCTCCGACTACACGATACACTGTGCT 584
Db 604 GATCTCAACTGACCTGCTTGGCGCTTGAACCTTCCGACTGACGGAATACATGTGCT 663
QY 585 TCAGATGTTTGAACGTTTAAAGACAAAATGGCAATTTCTCCACTGCCAATATT 644
Db 664 TCAGATGTGCTGGAATACTTCAAGAATGAAGGGCAATTTGCCCTGCCCTCAATCCTA 723
QY 645 CAGATAGAGGAGAGATTAAGAGCGCTTCTCAATTTATTCAGGCGCTCCCTGCTGCTT 704
Db 724 ACCGAGGAGACATCACTAGAAAGTGTCTTAAATTTATATCGGGCTTCCCTGCTGCTT 783
QY 705 CCGGCGGAGAAAGTTATGATGAGAGCTGAACATTTCTTACAAAATATTTAAGAGAGCC 764
Db 784 CCGGGGAGAAAAGTTATGGAAGAGCGTGAATCTTCTGGCATCTTATTTGAAAAAGTC 843
QY 765 CTGCAAAAGATCCGGCATCCAGTATACCTTCACTAGAGATACGGGCGTCTGGAATAT 824
Db 844 TTACAAAAGATCCGGTCTCCAAT--CTTTCAGGAGAGATAGAAATATGTTTGAATAT 900
QY 825 GGTGGCAGACCAATTTGGCCAGCGTTGGAAGCAAGGAATTACATGAGCGTCTTGGACAG 884
Db 901 GGTGGCAGACGAATTTGCCGAGATTTGAAGCAAGAAATATATCGAGTCTACGAGCAG 960
QY 885 CACACTAAAAATA-----AGAACGCCCGGAGAACTTTTGAACCTT 926
Db 961 AGCGGCTATGAAAGCTTAAACGAGATGCCATATATGAACATGAAGAGCTTTTACAACCT 1020
QY 927 GCAAAATTTGGAATTCATATATTTCACTCTCTTCAAGAGAGAGATTAAACATGTTCC 986
Db 1021 GCAAAATTTGAGTTCAATATCTTCACTCTTTGCAACTAAGAGAGTTCAATCTATCTCC 1080
QY 987 CGATGTGGAAGACTCGGGTCTCTGAGATGACCTTCTGTCGACATGTCACGTGAA 1046
Db 1081 AGATGTGGAAGAAATCAGGTTCTCTCACTCACTTTTACACGCGCATGTCACGTGAA 1140
QY 1047 TACTAGCGTTTGGCTTCTGTCATGCGTTGAGCGCTCAACATTTCTGATTCAGACTGCGC 1106
Db 1141 TACTACACTATGGCATCTTGCAATTTCTATGTTGCCAAAACATTCAGCTTTCAGAAATGAG 1200
QY 1107 TTTACCAAGATGCTCATCTTATCAACGCTTCTGAAGACATGTAAGCGTCTTGGCACA 1166
Db 1201 TTTGTCAAAGTGTGTCATCTTGAACAGTTCTCGATGATATATATGACACTTTTGAACA 1260
QY 1167 GTAGACGAGTGAACCTTTCACAGCGCAATTAAGAGATGGATCCGTCGCGATGAA 1226
Db 1261 ATGAACGAACTCCAACCTTTTACCGGATGCAATTAAGAGATGGATTTGTCAACGACAAGG 1320
QY 1227 TGCCTTCCAGATATATGAAGGAGTGTACATGATGCTTATACACCGTAAATGAATG 1286
Db 1321 TGGCTTCCAGATATATGAAGGAGTGTACATGACTTGTATCAATGCAATTAATGAATG 1380
QY 1287 GCTGAGTGCAGAGAGGCTCAAGGCCGAGACACGCTCAACTATGCAAGAGGCTTGG 1346
Db 1381 GTGGAAGAGCTGAGAAAGACTCAAGGCCGAGATATGCTCAACTATATTCAAAATGCTTGG 1440
QY 1347 GAGCGGTGTTTGAATTCGTATATGACAGAAAGAAAGTGAATGCGCACTGTTATCTGCC 1406
Db 1441 GAAGCCCTATTGATACCTTATGCAAGAGCAAAAGTGATCTCCAGAGTTATCTCCA 1500

QY 1407 ACGTTGAGAGTACTTGGAACCGGAAAGTTAGCTCTGCTCATCGCCCATGCGCACTG 1466
Db 1501 ACGTTGAGAGTACTTGGAAGAAATGCAAAAGTTAGTTCTGTTCTGCAATGACCACATTA 1560
QY 1467 CAACCATTTCTGACGTTGACATCCCTTCTCTGATCACATCTCAAGAAAGTTGACTTC 1526
Db 1561 CAACCATTTCTCACTTTGATGTACCACTTCTGATTAACATCTCAAGAAATGATTAT 1620
QY 1527 CCATGGAAGCTCAATGACTTGATATGATCATCTTCTGATTAAGAGTGATACACGCTG 1586
Db 1621 CCATCCAGATTCATGAGTAGTTCCTGATCCTTCTGACTACGAGTGACACGCGCTGC 1680
QY 1587 TACAAGGCGAGACAGGGCCCGTGAGAGAGAGCTTCTGCTATATCATGTTATGAAGAC 1646
Db 1681 TACAAGGCGAGTAGGGCCCGTGAGAGAGAGCTTCACTATATCGTGTATATGAAGAC 1740
QY 1647 AATCTGATTAACGGAAGAGATGCTGTAATCATATCACTTCATGATCAGGAGCGCA 1706
Db 1741 CATCTGATCATTAAGAGAGATGCTCTCAATCATATCAACGCCATGATCAGTATGCA 1800
QY 1707 ATCAGAGAAATTAATTTGGAGCTTCTTAAAGCCAGACAAAGTGTCCATCACTTCCAAG 1766
Db 1801 ATCAGAGAAATTAATTTGGAGCTTCTCAGACCGGATGACAAAAGTCCATCTCTTCCAAG 1860
QY 1767 AAACAGCAATTTGACATTAAGCAGAGTTTGCATCAGGTTACAGATACGAGATGCTTAC 1826
Db 1861 AAACATGCTTTGACATCACCAGAGCTTCCATCATGTCTACAAATATGAGATGTTAC 1920
QY 1827 AGCTTGGCAAGCTTGAACCAAGAGTTTGGTATGAGAAACCGTCAATGAACCTGTGCT 1886
Db 1921 ACTGTTTCCAAACAGAAAGAAATTTGGTATGAACCCGTTCTTGAACCTCTCGCT 1980
QY 1887 TTGTAAACAACATCTCAATCTTCAATATTAATGAGG 1923
Db 1981 TTGTAAAAACATATAGAAATGATTAATGTTGGGAG 2017

RESULT 15
AAF73373
ID AAF73373 standard; cDNA; 2089 BP.
XX
AC AAF73373;
XX
DT 30-APR-2001 (first entry)
XX
DE Grand fir (-)-limonene synthase coding sequence SEQ ID NO: 5.
XX
KW Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;
KW myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;
KW terpinolene synthase; insect resistance; nutrition; ss.
XX
OS Abies grandis.
XX
PN W0200107565-A2.
XX
PD 01-FEB-2001.
XX
PF 24-JUL-2000; 2000MO-US020264.
XX
PR 26-JUL-1999; 99US-00360545.
XX
PA (UNIW) UNIV WASHINGTON STATE RES FOUND.
XX
PI Steele CL, Bohlmann J, Croten RB, Phillips MA;
XX
DR MPI; 2001-182782/18.
XX
DR P-PSDB; AAB69372.
XX
PT New nucleic acid encoding monoterpene synthases, for increasing terpene
PT synthesis in plants, e.g. for increasing resistance to pests or for
PT treatment of cancer.
XX

PS Claim 33; Page 112-115; 175pp; English.

CC The present invention provides the protein and coding sequences of
CC monoterpene synthases from the grand fir. These include (-)-camphene
CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-
CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase
CC and pinene synthase. The sequences can be used to produce transgenic
CC plants expressing high levels of the enzymes, resulting in levels which
CC are useful in protecting against and treating cancers, and to confer
CC insect resistance on plants

SQ Sequence 2089 BP; 638 A; 415 C; 450 G; 586 T; 0 U; 0 Other;

Query Match 46.0%; Score 925.4; DB 4; Length 2089;

Best Local Similarity 70.6%; Pred. No. 9.8e-252;

Matches 1340; Conservative 0; Mismatches 506; Indels 51; Gaps 6;

| | | | |
|----|-----|---|-----|
| QY | 72 | TCGTGCTCAGTTCCTCTCATGAGATTAAAGGCTCTCCGTAGAACAAATCCCACTCTTGA | 131 |
| Db | 127 | TCGTGATCAGTTCACGAATGTGCAGAAAGGCTCTCTGTATCTTACAGCAGTCCCAACA | 186 |
| QY | 132 | ATCTGCAGCCGGGAAATCCGTCCGCATTCATTAACATGTGTTGCAAGCGTCGCA | 191 |
| Db | 187 | CTCAGAATGCGTAGGCGACAGAAAGCTCTGGTCATCAACATGAATGACCACCTGTATCC | 246 |
| QY | 192 | TCTACTGATTTCT-----GTACAGAGACGCGTGGGCACTATCATTTCCAAC | 236 |
| Db | 247 | CATCGTGAATGATTAATGTGGTGGTGTACTGCAAAAGACGATAGCCGATCATCCCAAC | 306 |
| QY | 237 | CTGTGGGACGATGATTTTCATATACAGTCTCTGATCTCAACGCTTATGAGACCTGATTAC | 296 |
| Db | 307 | CTGTGGGAAGATGATTTCAATACATCATTTGTCTCA--CCTTATGGGGATCTTCGTAC | 363 |
| QY | 297 | CGGGAACGTGCTGACAGACTTATGGGGAAGTAAAGATAT-----ATGTTCAAT | 347 |
| Db | 364 | AGTGAACGTGCTGAGACAGTCGTTGAGGAAGTAAAAAGAGATGTTCAATTCATACCAAT | 423 |
| QY | 348 | TTCAAGTCGCTGGAAGATGAGGCAATGATCTCCTTCAACGACTTTTGCTGTCGATGAC | 407 |
| Db | 424 | AATAGAGAATTATTGTGTTCCCAAAATGATCTCCTTACACGCTTTGGATGTGATAGC | 483 |
| QY | 408 | GTTGAACGTTTGGGAATGCACAGGCAATTTCAAAAAAGATAAAAACGGCACTCGATTAT | 467 |
| Db | 484 | ATTGAACGTCTGGGATAGATAGACATTTCCAAATGAGATTAAGAGTAGCCCTCGATTAT | 543 |
| QY | 468 | GTTAACAGTTATTGGAACGAAA--AAGCATTTGGATGTGGAGGAGAGAGTGTGTGACT | 524 |
| Db | 544 | GTTTACAGTTATTGGAAGGAAAAGGAGGCATTTGGGTGTGGCAGAGATTCTACTTTTCT | 603 |
| QY | 525 | GACCTCAACTCAACCGCCTTGGGGCTTGGAACTCTCCGACTACACGGATACACTGTGTCT | 584 |
| Db | 604 | GATCTCAACTGCACTGCCCTTGGCGCTTCGAACTCTTCGACTGCACGGATCAATGTGTCT | 663 |
| QY | 585 | TCAGATGTTTGAACGTTTAAAGCAAAAAATGGCAATTTTCTCCACTGCAATATTT | 644 |
| Db | 664 | TCAGATGTGCTGAATACTTCAAAAGTGAAGGAGGCGCATTTTGCTGCCCTGCAATCCTA | 723 |
| QY | 645 | CAGATAGAAGGAGAGATTAGAGCGTCTCAATTTATTCAAGGCGCTCCCTCGTGCCTTT | 704 |
| Db | 724 | ACCGAGGACAGATCACTAGAAGTGTTCTAAATTTATATCGGGCTTCCCTGCTGCCCTTT | 783 |
| QY | 705 | CCCCGCGAAGAAATTATGATGAAGCTGAACATTTCTTACAAATATTTAAGAGAAGCC | 764 |
| Db | 784 | CCCCGGGAGAAAATTATGGAAGAGGCTGAATCTTCTCGGCATCTTATTTGAAAAAAGTC | 843 |
| QY | 765 | CTGCAAAAAGATTCGGGCATCCAGTATACTTTCACTAGAGATACGGGACGTTCTGGAATAT | 824 |
| Db | 844 | TTACAAAAGATTCGGTCTCCAAT--CTTTCAGAGAGATAGAAATATGTTTGGAAATAT | 900 |
| QY | 825 | GCTTGGCACACCAATTTGCCACGCTTGAAGCAAGGAATTACATGACGCTTTTGGACAG | 884 |
| Db | 901 | GCTTGGCACACGAATTTGCCGAGATTGGAGCAAGAAATTATATCGAGGTTACGAGCAG | 960 |

| | | | |
|----|------|---|------|
| QY | 885 | CACACTAAAAATA-----AGAACGCCGCCGAGAAACTTTAGAACTT | 926 |
| Db | 961 | AGCGGCTATGAAGCTTAAACGAGATGCCATATATGAACATGAAGAACTTTTACAACCTT | 1020 |
| QY | 927 | GCAAAATTTGGAATTCATATATTTCTACTCCCTTACAAGAGAGAGAGTTAAAAACATGTTTCC | 986 |
| Db | 1021 | GCAAAATTTGAGTTCAATATCTTTCACTCTTTGCAACTAAGAGAGTTACAATCTATCTCC | 1080 |
| QY | 987 | CGATGTGGAAAGACTCGGGTCTCCTGAGATGACCTTCTGTGCACATCGTCAGGTGAA | 1046 |
| Db | 1081 | AGATGTGGAAAGAAATCAGGTTGCTCTCAACTGACTTTTACACGGCATCGTCAGGTGAA | 1140 |
| QY | 1047 | TACTACGCTTTGGCTTCTGCAATTTGCGTTGAGCCTCAACATTTCTGATTCAGACTCGGC | 1106 |
| Db | 1141 | TACTACACTATGGCACTCTTGCAATTTCTATGTGTCAAAACATTCAGCTTTCAAGATGGAG | 1200 |
| QY | 1107 | TTTACCAAGATGTCTCATCTTATCACCGGTTCTTGACGACATGTACGACGCTTCGGCACA | 1166 |
| Db | 1201 | TTTGTCAAAAGTGTCTCATCTTGTAAACAGTTCCTGATGATATATATGACACTTTTGAACA | 1260 |
| QY | 1167 | GTAGACGAGCTGGAATCTTTCACAGCGACAATTAAGAGATGGATCCGTCGCCGATGGAA | 1226 |
| Db | 1261 | ATGAACGAACCTCCAACTTTTACGGATGCAATTAAGAGATGGGATTGTCAACGACAAAG | 1320 |
| QY | 1227 | TGCCCTTCAGAAATATATGAAAGAGTGTACATGATGGTTTATCACACCCGTAAATGAAATG | 1286 |
| Db | 1321 | TGGCTTCAGAAATATATGAAAGAGTGTACATGACTTGTATCAATGCAATTAATGAATG | 1380 |
| QY | 1287 | GCTCGAGTGCAGAGAAAGGCTCAAGGCCGAGACACGCTCAACTATATGCAAGACAGGCTTG | 1346 |
| Db | 1381 | GTGAAAGAGGCTGAGAGACTCAAGGCCGAGATATGCTCAACTATATTCAAAATGCTTGG | 1440 |
| QY | 1347 | GAGGCGTGTTTGATTCGTATATGCAGAGCAAAAGTGATCGCCACTGGTTATCTGCC | 1406 |
| Db | 1441 | GAAGCCCTATTTGATACCTTATGCAAGAGCAAAAGTGATCTCCAGCAGTTATCTCCA | 1500 |
| QY | 1407 | ACGTTTGAGAGTACTTGGAGAACGGAAAGTTAGCTGTGCTCATCGCCATGGCACACTG | 1466 |
| Db | 1501 | ACGTTTGAGAGTACTTGAAGAATGCAAAAGTTAGTTCTGGTTCTCGCATAGCCACATTA | 1560 |
| QY | 1467 | CAACCCATTTGACGTTGGACATCCCCCTTCTGATCACATCCTCAAGGAAGTTGACTTC | 1526 |
| Db | 1561 | CAACCCATTTCTACTTTGGATGTACCACCTTCTGATTAACATACTGCAAGAAATTTGATTAT | 1620 |
| QY | 1527 | CCATCGAAGCTCAATGACTTGATATGTATCATCTTCCGATTAAGAGGTGATACACGGTGC | 1586 |
| Db | 1621 | CCATCCAGATTCATGAGTTAGCTTCGTCCATCTTCCGACTACGAGGTGACACGGCTGC | 1680 |
| QY | 1587 | TACAAGGCAGACAGGGCCGTGGAGAAAGACTTCGTATATCATGTTATATGAAGAAC | 1646 |
| Db | 1681 | TACAAGGCGATAGGGCCGTGGAGAAAGACTTCAGCTATATCGTGTATATGAAGAAC | 1740 |
| QY | 1647 | AATCCTGATTAAACGAGAAAGATGCTCTGAATCATATCAACTTCATGATCAGGACGCA | 1706 |
| Db | 1741 | CATCCTGATCAATGAGAGAAAGATGCTCTCAATCATATCAACGCCATGATCAGTATGCA | 1800 |
| QY | 1707 | ATCAGAGAATTAATTTGGAGCTTCTTAAAGCCAGCAACAGTGTTCCTCATCACTTCCAAG | 1766 |
| Db | 1801 | ATCAGAGAATTAATTTGGAGCTTCTCAGACCGGATAGCAAAAAGTCCCATCTCTTCCAAG | 1860 |
| QY | 1767 | AAACACGCAATTTGACATAAGCAGAGTTTGGCATCAACGGTTACAGATACCGAGATGGCTAC | 1826 |
| Db | 1861 | AAACATGCTTTTGACATCACACAGAGCTTTCATCATGTCTACAATATCGAGATGGTTAC | 1920 |
| QY | 1827 | AGCTTTGCCAACGTTGAAACAAAGAGTTTGGTATGAGAACCGTCATTTGAACCTGTGCCT | 1886 |
| Db | 1921 | ACTGTTTCCAAACACGAAACAAAGAAATTTGGTATGAAAAACCGTCTTGAACTCTCGCT | 1980 |
| QY | 1887 | TTGTAAACAACATTTCAATCTACAATATTTAACTGAGG | 1923 |
| Db | 1981 | TTGTAAAAACATATAGAAATGCAATTAATGTGGGAG | 2017 |

Tue Jul 27 08:32:44 2004

us-10-025-145a-64.rng

Page 21

Search completed: July 26, 2004, 10:16:48
Job time : 773 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 26, 2004, 09:57:57 ; Search time 4682 Seconds
(without alignments)
12839.079 Million cell updates/sec

Title: US-10-025-145A-64

Perfect score: 2013

Sequence: 1 tcttgacgtgcctctctatc.....aaaaaaaaaaaaaaaa 2013

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST: *
1: em_estba: *
2: em_esthum: *
3: em_estin: *
4: em_estmu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_htc: *
9: gb_est1: *
10: gb_est2: *
11: gb_htc: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estom: *
17: em_gss_hum: *
18: em_gss_inv: *
19: em_gss_pln: *
20: em_gss_vrt: *
21: em_gss_fun: *
22: em_gss_mam: *
23: em_gss_mus: *
24: em_gss_pro: *
25: em_gss_rod: *
26: em_gss_phg: *
27: em_gss_vrl: *
28: gb_gss1: *
29: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|----------------------------|
| 1 | 564.2 | 28.0 | 745 | 14 | CF477103 RTW3_5_A |
| 2 | 475.2 | 23.6 | 697 | 13 | BQ196773 NXLV105_B |
| 3 | 447.2 | 22.2 | 599 | 13 | BX680641 BX680641 |
| 4 | 428.2 | 21.3 | 599 | 12 | BG526917 BG526917 NXPV_057 |

| | | | | | | |
|----|-------|------|-----|----|----------|--------------------|
| 5 | 427 | 21.2 | 700 | 14 | CF474786 | CF474786 RTW2_7_B |
| 6 | 425.8 | 21.2 | 637 | 14 | CF476978 | CF476978 RTW3_5_A |
| 7 | 419.2 | 20.8 | 696 | 14 | CF401916 | CF401916 RTW1_15 |
| 8 | 413 | 20.5 | 669 | 14 | CF479802 | CF479802 RTW3_12 |
| 9 | 399.6 | 19.9 | 616 | 14 | CF663845 | CF663845 RTW3_12 |
| 10 | 388.6 | 19.3 | 516 | 13 | BQ698077 | BQ698077 NXPV_064 |
| 11 | 384.4 | 19.1 | 517 | 13 | BX677624 | BX677624 BX677624 |
| 12 | 384.2 | 19.1 | 804 | 14 | CF666338 | CF666338 RTW3_12 |
| 13 | 376 | 18.7 | 481 | 9 | AL750951 | AL750951 AL750951 |
| 14 | 375 | 18.6 | 740 | 14 | CF477562 | CF477562 RTW3_8_G |
| 15 | 352.4 | 17.5 | 539 | 10 | AM287756 | AM287756 EST0004_S |
| 16 | 343.8 | 17.1 | 557 | 14 | CF666483 | CF666483 RTW3_12 |
| 17 | 339.8 | 16.9 | 651 | 14 | CF479884 | CF479884 RTW3_12 |
| 18 | 327.4 | 16.3 | 682 | 14 | CF663768 | CF663768 RTW3_12 |
| 19 | 324.8 | 16.1 | 534 | 10 | AM287755 | AM287755 EST0003_S |
| 20 | 315.4 | 15.7 | 569 | 10 | AM287754 | AM287754 EST0002_S |
| 21 | 312.2 | 15.5 | 430 | 13 | BQ702557 | BQ702557 NXSI_129 |
| 22 | 302.4 | 15.0 | 591 | 14 | CA305371 | CA305371 haap004xk |
| 23 | 300.4 | 14.9 | 541 | 14 | CF672979 | CF672979 RTW3_12 |
| 24 | 284.2 | 14.1 | 618 | 9 | AL750955 | AL750955 AL750955 |
| 25 | 283.6 | 14.1 | 542 | 10 | BG039521 | BG039521 NXSI_099 |
| 26 | 264 | 13.1 | 574 | 14 | CF474640 | CF474640 RTW2_7_B |
| 27 | 264 | 13.1 | 733 | 14 | CF666270 | CF666270 RTW3_12 |
| 28 | 245.4 | 12.2 | 574 | 9 | AM065088 | AM065088 ST39E04_P |
| 29 | 239 | 11.9 | 597 | 14 | CF666416 | CF666416 RTW3_12 |
| 30 | 215.4 | 10.7 | 385 | 10 | AM697531 | AM697531 ST64A12_P |
| 31 | 211.6 | 10.5 | 725 | 14 | CF470471 | CF470471 RTDS1_17 |
| 32 | 197.4 | 9.8 | 634 | 14 | CF397946 | CF397946 RTDS3_23 |
| 33 | 197.2 | 9.8 | 725 | 14 | CF397293 | CF397293 RTDS3_23 |
| 34 | 193.2 | 9.6 | 353 | 14 | CA305444 | CA305444 haap015xd |
| 35 | 188.6 | 9.4 | 552 | 13 | BQ696735 | BQ696735 NXPV_044 |
| 36 | 187.8 | 9.3 | 529 | 13 | BQ698322 | BQ698322 NXPV_068 |
| 37 | 185 | 9.2 | 400 | 14 | CF672970 | CF672970 RTW3_12 |
| 38 | 181.8 | 9.0 | 601 | 9 | AM043070 | AM043070 ST28H10_P |
| 39 | 181.2 | 9.0 | 530 | 9 | AU298829 | AU298829 AU298829 |
| 40 | 180.6 | 9.0 | 537 | 9 | AM011129 | AM011129 ST17A09_P |
| 41 | 176.6 | 8.8 | 629 | 9 | AU299287 | AU299287 AU299287 |
| 42 | 176.2 | 8.8 | 487 | 14 | Z92688 | Z92688 SC1571/1_NO |
| 43 | 164 | 8.1 | 306 | 10 | AM226490 | AM226490 ST82H11_P |
| 44 | 162.4 | 8.1 | 730 | 13 | BX682869 | BX682869 BX682869 |
| 45 | 156.6 | 7.8 | 530 | 9 | AU298828 | AU298828 AU298828 |

ALIGNMENTS

RESULT 1
LOCUS CF477103 745 bp mRNA linear EST 08-SEP-2003
DEFINITION RTW3_5_A06.g1_A022 well-watered loblolly pine roots W3 Pinus taeda cDNA clone RTW3_5_A06_A022 5', mRNA sequence.
ACCESSION CF477103
VERSION CF477103.1 GI:34505972
KEYWORDS EST.
SOURCE Pinus taeda (loblolly pine)
ORGANISM Pinus taeda

REFERENCE
AUTHORS Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W., Dean, J., Gebremedhin, M., Dervinis, C., Martin, T., White, T., Davis, J. and Neale, D.
TITLE An EST database from well-watered loblolly pine (Pinus taeda) roots
JOURNAL Unpublished (2003)
COMMENT Other ESTs: RTW3_5_A06.b1_A022
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
RNA prepared and library constructed by W. Walter Lorenz, School of

Forestry, University of Georgia; plant material prepared at the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.
Seq primer: JENREV (CAGGAACGCTATGACC).

FEATURES
source
Location/Qualifiers

1..745
/organism="Pinus taeda"
/mol_type="mRNA"
/strain="CCLONES"
/db_xref="taxon:3352"
/clone="RTMW3 5 A06 A022"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="Well-watered loblolly pine roots MW3"
/note="Vector: pSL1180; Site_1: EcoRI; Site_2: XhoI; The library was prepared from polyA+ RNA from loblolly pine (Pinus taeda) roots watered to pot capacity every other day. Pre-dawn water potential remained -0.3 MPa +/-0.1. Roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL1180. Inserts excised with EcoRI (5' end) and XhoI (3' end)."

ORIGIN

Query Match 28.0%; Score 564.2; DB 14; Length 745;
Best Local Similarity 84.8%; Pred. No. 6e-90;
Matches 632; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

QY 1100 ACTCGGCTTTACCAAGATGTCATCTTATACGCGTTCTTGACGACATGACGCTCTT 1159
Db 1 ACTCGGCTTTGCCAAATCCTGTCAATCATCACCGTCTTGATGATATGTACGACACCTT 60
QY 1160 CGGCACAGTAGACGAGCTGGAACCTCTTCAACGACGCAATTAAGATGGATCCGTCGC 1219
Db 61 CGGAACACTCGACGAGCTCGAACTCTTCAACGCTGAATTAAGATGGATCCGTCGC 120
QY 1220 GATGGAATGCCTTCCAGAATATATGAAGAGTGTACATGATGTTTATCACACCGTAAA 1279
Db 121 GACAGAGTGCCCTTCCAGAATATATGAAGAGTTTACATGATAGTTTACAACACTGTAAA 180
QY 1280 TGAATGCTCGAGTGGCAGAGAGGCTCAAGCCGAGACACCGTCAACTATGCAAGACA 1339
Db 181 TGAATGCTCTCAGGAGGACAGACAGGCTCAAGCCGAGACACCGTCAACTATTGTCGACA 240
QY 1340 GCGTTGGAGGCGGTGTTGATTCGTATATGCAAGAGCAAAAGTGCCTGCTGCTTA 1399
Db 241 GCGTTGGAGGAATATATTGATTCGTATATGCAAGAGCAAAAGTGCCTGCTGCTGA 300
QY 1400 TCTGCCACGTTTGAGGAGTACTTGAGAAACGGAAAGTTAGCTGCTCATGCCCATG 1459
Db 301 GGTGCCAATTTGAGGAGTACTGAGAAACGGAAATTAAGCTGCTGCTCATGCCCATG 360
QY 1460 CGCACTGCAACCCATTCTGACGTTGACATCCCTTCTGATCAGATCCTCAAGAAAGT 1519
Db 361 GGCATGCAACCCATTCTGACGACCGACATCCCTTCTGAGCAGCGTCCCAAGAAAGC 420
QY 1520 TGACTTCCCATCGAAGCTCAATGATCTGATATGTATCATCCTTCATTAAGAGGTATAC 1579
Db 421 TGACATTCATCGAAGCTCAATGATCTGAGCATCTGCCATTCTTCATTAAGAGGATAC 480
QY 1580 ACGGTGCTACAAAGCAGACAGGCGCCGTGAGAGAAAGCTTCGTATATCATGTTATAT 1639
Db 481 GCGGTGCTACAAAGCAGACAGGCGCCGTGAGAGAAAGCTTCGTATATCTGTTATAT 540
QY 1640 GAAAGACAATCTTGATTAAACGGAAGATGCTCTGAATCATATCAACTTCATGATCAG 1699
Db 541 GAAAGACAATCTTGAGCAACGGAAGATGCTCTCAATCATATCAACGCCATGATCAG 600
QY 1700 GGACGCAATCAGAAATTAATTGGAGCTTCTAAAGCCAGACAAAGTGTCCCATCAC 1759
Db 601 TGATGTATTAATAAGATTAAATTGGAGCTTCTCAAAACCAACAGCGTTCCTCATATC 660

QY 1760 TTCGAAGAAACACGATTTGACATTAAGCAGAGTTTGGCATCACCGTTACAGATACCGACA 1819
Db 661 TGCCAAAACAATGCTTTTGACATTAAGCAGAGCTTCCATTATGGCTACAATAATCGACA 720
QY 1820 TGGCTACAGCTTTGCCAACGTTGAA 1844
Db 721 TGGCTACAGCGTTGCCAGCATTGAA 745

RESULT 2
B0196773
LOCUS
DEFINITION
B0196773 697 bp mRNA linear EST 07-MAY-2003
NXLV105 B02 F NXLV (Nsf Xylem Late wood Vertical) Pinus taeda cDNA
clone NXLV105 B02 5' similar to Arabidopsis thaliana sequence
At4g16730 limonene cyclase like protein see
http://mips.gsf.de/proj/thal/db/index.html, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
B0196773 GI:20379276
EST.
pinus taeda (loblolly pine)
pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
1 (bases 1 to 697)
Sederoff, R.
Molecular Basis of Wood Formation in the Pine Megagenome
Unpublished (2000)
Contact: Sederoff, Ron
Forest Biotechnology
North Carolina State University
840 Main Campus Drive, Centennial Campus, Campus Box 7247, Raleigh,
NC 27695, USA
Tel: 919 515 7800
Fax: 919 515 7801
Email: ron.sederoff@ncsu.edu, jerri.johnson@ncsu.edu
Please see http://web.ahc.umn.edu/biodata/nsfpine/ for further
information.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Seq primer: T3.

FEATURES
source
Location/Qualifiers

1..697
/organism="Pinus taeda"
/mol_type="mRNA"
/strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
/clone="NXLV105 B02"
/tissue_type="primary xylem"
/dev_stage="late wood"
/lab_host="X1-Blue"
/clone_lib="NXLV (Nsf Xylem Late wood Vertical)"
/note="Vector: pTribLx; Site_1: EcoRI; The library is from late (summer-August) wood, taken from below the crown of a 20 year old tree. The harvested xylem tissue was on the the cusp between transitional and mature wood. NOTE: The sequences contain a 'cDNA adapter' between the EcoRI site and the start of the EST. The adapter sequence is 'AATTCGCCCATTTATGCC'."

ORIGIN
Query Match 23.6%; Score 475.2; DB 13; Length 697;
Best Local Similarity 83.0%; Pred. No. 3.3e-74;
Matches 534; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

QY 1250 AGTTACATGATGTTATACACCGTAATGAATGGCTCGAGTGCAGAGAGGCTCA 1309
Db 22 AGTTACATGATGATTACAACTGTAAATGAATGTCTCAGAGGACAGACAAAGGCTCA 81
QY 1310 AGGCCGAGACAGCTCAACTATGCAAGACAGGCTTGGAGCGCTGTTGATTCGTATAT 1369
Db 82 AGGCCGAGACAGCTCAACTATGTGCAACAGGCTTGGAGGAATATATTGATGCGTATAT 141
QY 1370 GCAGAAACCAAGTGATCGCACTGTTATCTGCCCACTTTGAGAGTACTTGAGAA 1429
Db 142 GCAAGAACCAAGTGATCGCCCGTGTGAGGTGCCAACATTGAGAGTACTATGAGAA 201

| | | | |
|----|------|---|------|
| OY | 1430 | CGGGAAGTTAGCTCTGCTCATTCGCCCATGCGCACTGCAAACCCATTCTGACGTTGGACAT | 1489 |
| Db | 202 | CGGGAAGTTAGCTCTGCTCATTCGCCGTATCGGCATTGCACCATTCTGACGACCGACAT | 261 |
| OY | 1490 | CCCCCTTCCGTATCACATCCTCAAGGAAGTTGACTTCCCATCGAAGCTCAATGACTTGAT | 1549 |
| Db | 262 | CCCCCTTCCGTAGCACGCTCTCAAGGAAGTTGACATTCATCGAAGCTCAATGACTTGGC | 321 |
| OY | 1550 | ATGTATCATCCTTCGATTAAGAAGTGATACACGGTGCTACAAGCAGACAGAGGCCCGTG | 1609 |
| Db | 322 | ATCTGCATCTCTCGATTAAGAGGGGATACGCGCTGCTAACAGCGAGAGGCCCGTG | 381 |
| OY | 1610 | AGAAGAAGCTTCGTATAATCATGTTATATGAAGACAATCCTGGATTAAAGGAAGA | 1669 |
| Db | 382 | AGAAGAAGCTTCGTATAATCTGTTATATGAAGACAATCCTGGAACAACAGAGAAGA | 441 |
| OY | 1670 | TGCTCTGAATCATATCAACTTCATGATCAGGACGCAATCAGAGAATTAATTGGGAGCT | 1729 |
| Db | 442 | TGCTCTCATCATCTCAACGCCATGATCAGTAGTAATTAAGATTAAATTGGGAGCT | 501 |
| OY | 1730 | TCTAAAGCCAGACAACAGTGTCCCATCACTTCCAAGAAACAAGCATTTGACATTAAGCAG | 1789 |
| Db | 502 | TCTCAAATCAACAAGCAGCGTTCCCATATCTGCCAAAACAATGCTTTTGACATTAGCAG | 561 |
| OY | 1790 | AGTTTGGCATCACGGTTACAGATACCGAGATGGCTACAGCTTTGCCCAACGTTGAACA | 1849 |
| Db | 562 | AGCTTTCATTTGGCTACAAATAATCGAGATGGCTACAGCGTTGCCCAACATTTGAACNNN | 621 |
| OY | 1850 | GAGTTTGGTATGAGAACCGTCAATTGAACCTGTGCTTTGTA | 1892 |
| Db | 622 | NNGTTTTGGTGANNNNNNAACCGTCAATTGATCCTGTCACTTATNA | 664 |

| | |
|------------|--|
| RESULT 3 | |
| BX680641 | |
| LOCUS | BX680641 599 bp mRNA linear EST 28-OCT-2003 |
| DEFINITION | BX680641 RS Pinus pinaster cDNA clone RS46D06, mRNA sequence. |
| ACCESSION | BX680641 |
| VERSION | BX680641.1 GI:38015099 |
| KEYWORDS | EST. |
| SOURCE | Pinus pinaster |
| ORGANISM | Pinus pinaster |
| REFERENCE | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 599) |
| AUTHORS | Frigerio,J. and Plomion,C. |
| TITLE | Identification of water-deficit responsive genes in Maritime pine (Pinus pinaster Ait.) using an EST approach |
| JOURNAL | Unpublished (2002) |
| COMMENT | Contact: Frigerio JM Genetique et Amelioration 69 |
| | INRA |
| | route d'Arcachon 33612 Cestas CEDEX France |
| | Email: Frigerio@pierroton.inra.fr |
| | Email: Frigerio@pierroton.inra.fr |
| | Seq primer: T3. |

| FEATURES | Location/Qualifiers |
|----------|---------------------|
| source | 1. .599 |

```

/organism="Pinus pinaster"
/mol_type="mRNA"
/db_xref="taxon:71647"
/clone="RS46D06"
/tissue_type="root"
/dev_stage="6 weeks old seedling"
/lab_host="SOLR"
/clone_lib="RS"
/note="Vector: Uni-ZAP XR; ecotype: landes; The library
was made from the roots of 6 weeks old seedlings grown in
hydroponic conditions. A three weeks drought stress
treatment was applied by lowering the osmotic potential of
the nutrient solution to -0.45 Mpa using 170 g/l of
polyethylene glycol as an osmoticum. A mixture of

```

genotypes were used. Oligo-dT primed cDNA was directionally cloned into the EcoRI-XhoI lambda-ZAP vector arms and mass-excised to form a pBluescript phagemid"

| | | | | |
|---------------------------|-------|--------------------|-----------|-------------|
| Query Match | 22.2% | Score 447.2; | DB 13; | Length 599; |
| Best Local Similarity | 85.2% | Pred. No. 3.1e-69; | | |
| Matches 511; Conservative | 0; | Mismatches 88; | Indels 1; | Gaps 1; |

| | | | |
|----|------|---|------|
| QY | 1228 | GCCTTCCAGATATATGAAAGGAGTGATCATGATGGTTTATACACACCGTAATGAAATGG | 1287 |
| Db | 1 | GCCTTCCACAATATATGAAAGGAAT-TACATGATGGTTTACAACACCGTAAATGAAATGT | 59 |
| QY | 1288 | CTCGAGTGGCAGAGAAAGGCTCAAGGCCGAGACACGCTCAACTATGCAAGACAGGCTTGGG | 1347 |
| Db | 60 | CTGCGAGGCACAGAAAGGCTCAAGCCGAGACACTCTCAACTATGCTCGACAGGCTTGGG | 119 |
| QY | 1348 | AGGCGTGTTTGATTCGTATATATGCAAGAACAAAGTGATCGCCACTGTTATCTGCCA | 1407 |
| Db | 120 | AGGATTATCTTGATTCGTATATATGCAAGAACAAAGTGATAGCCACGGGTTATCTGCCA | 179 |
| QY | 1408 | CGTTGAGGAGTACTTTGGAGAACGGGAAAGTTAGCTCTGCTCATCGCCCATGCGCACTGC | 1467 |
| Db | 180 | CGTTGAGGAATACTTTGGAGAACGGGAAAGTTAGCTCTGCGCATCGCGCTTGC | 239 |
| QY | 1468 | AACCCATTTGACGTTGGACATCCCCCTTCTGTATCAATCCTCAAGGAAGTTGACTTCC | 1527 |
| Db | 240 | AACCCATGCTGACGATGGACATCCCCCTTCTCTTCAATCCTCAAGGAAGTTGACTTCC | 299 |
| QY | 1528 | CATGAAGCTCAATGACTTGATATGATATCATCCTTCGATTAAAGAGTGATACAGGTGCT | 1587 |
| Db | 300 | CATCCACCTCAATGACTTGGCATGTGCCATATCTCGATTACGAGTGATACCGAATGTT | 359 |
| QY | 1588 | ACAAGGCAGACAGGGCCCGCTGGAGAGAAGAGCTTCGTATATCATGTATATGAAAGACA | 1647 |
| Db | 360 | ATCAGGAGGACAGGGCTCGTGAGAGAAGAACTTCGTATATCTTGTATATGAAAGACA | 419 |
| QY | 1648 | ATCTGTGATTAAAGGAAGAGATGCTCTGATCATATCAACTTCATGATCAGGAGCGAA | 1707 |
| Db | 420 | ACCCTGAGCAAGAGAGAAAGATGCTCTTAATCATCTCAATGTCATGATCAGTGGCTTAA | 479 |
| QY | 1708 | TCAGAGATTAAATTGGGAGCTTCTAAAGCCAGACAACAGTGTTCCTACACTTCCAGA | 1767 |
| Db | 480 | TTAAGAATTAAATTGGGAGCTTCTCAAAACCGACACAAGTGTGCCATTCTTCCAAGA | 539 |
| QY | 1768 | AACACGCATTTGACATAAGCAGAGTTTGGCATCACGGTTACAGATACCGAGATGGCTACA | 1827 |
| Db | 540 | AAATTACTTTTGACATTACCGAGAGCTTTCATTACGGTTACAAATACCGAGATGGCTACA | 599 |

| | | | | |
|------------|---------------------|------------------------------------|-------------|-----------------|
| RESULT 4 | | | | |
| BG526917 | | | | |
| LOCUS | BG526917 | 599 bp | mRNA | linear |
| DEFINITION | NXPV_057_D04_F_NXPV | (Nsf Xylem Planings wood Vertical) | Pinus taeda | EST 07-MAY-2003 |

cdna clone NXPY_057_D04_5' similar to Arabidopsis thaliana sequence At4g16730 limonene cyclase like protein see <http://mips.gsf.de/proj/thal/db/index.html>, mRNA sequence.

| | |
|-----------|--|
| ACCESSION | BG526917 |
| VERSION | BG526917.1 |
| KEYWORDS | GI.13536796 |
| SOURCE | EST. |
| ORGANISM | Pinus taeda (loblolly pine) Pinus taeda |

| REFERENCE AUTHORS TITLE JOURNAL COMMENT |
|--|
| Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 599) Sederoff, R. Molecular Basis of Wood Formation in the Pine Megagenome Unpublished (2000) Contact: Sederoff, Ron |

Forest Biotechnology
North Carolina State University
840 Main Campus Drive, Centennial Campus, Campus Box 7247, Raleigh,
NC 27695, USA

Tel: 919 515 7800
Fax: 919 515 7801
Email: ron_sedero@ncsu.edu, jerri_johnson@ncsu.edu
Please see <http://web.ahc.umn.edu/biodata/nsfpine/> for further information.

Seq primer: T3.

FEATURES
Location/Qualifiers

source

```
1..599
/organism="Pinus taeda"
/mol_type="mRNA"
/strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
/clone="NXPV 057 D04"
/tissue_type="Xylem"
/cell_type="Planings (secondary)"
/dev_stage="Transitional"
/lab_host="XLI-Blue"
/clone_lib="NXPV (Nsf Xylem Planings wood Vertical)"
/note="Vector: Bluescript SK; Site_1: Eco RI; Site_2: XhoI; The library is from early (spring) secondary wood, taken from a ten year old tree in the transitional phase. The tree is a kind gift of the Westvaco Corporation. Secondary xylem was harvested from the tree by peeling back the bark and primary xylem and then removing the underlying tissue with a block plane. NOTE: The sequences contain a 'cDNA adapter' between the EcoRI site and the start of the EST. The adapter sequence is 'AATTCGGCACGAG'."
```

ORIGIN

Query Match 21.3%; Score 428.2; DB 12; Length 599;

Best Local Similarity 80.9%; Pred. No. 7e-66;

Matches 484; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

Oy 1216 CCGCGATGGAATGCCTTCCAGAATATATGAAAGGAGTGATCATGATGTTTATCACACCG 1275

Db 1 CCGCGACAGAGTGCCTTCCAGAATATATGAAAGGAGTTACATGATGTTTACAACACTG 60

Oy 1276 TAAATGAAATGGCTCGAGTGGCAGAGAAAGCTCAAGGCCGAGACGCTCAACTATGCAA 1335

Db 61 TAAATGAAATGCTCTCAGAGGACAGACAGGCTCAAGGCCGAGACGCTCAACTATTGTC 120

Oy 1336 GACAGGCTTGGAGGCGTGTGTTGATTGCTATATGCAAGAAAGAGATGATCGCCACTG 1395

Db 121 GACAGGCTTGGAGGAGATATATGATGCGTATATGCAAGAAAGAGATGATCGCCACTG 180

Oy 1396 GTTATCTGCCACGTTTGAGAGTACTTGAGAAAGGAAAGTTAGCTCTGCTCATCGCC 1455

Db 181 GTGAGGTGCCAATTTGAGAGTACTATGAGAACGGAAAGTTAGCTCTGCTCATCGCG 240

Oy 1456 CATGCGCACTGCAACCCATTTGACGTTGACATCCCTTCTCTGATCACATCCTCAAGG 1515

Db 241 TATCGGCAATTGCAACCCATTTGACGACCGACATCCCTTCTCTGAGCAGCTCCTCAAGG 300

Oy 1516 AAGTTGACTTCCCATCGAAGCTCAATGACTTGATATGATCATCCTTCGATTAAAGGTCG 1575

Db 301 AAGTTGACTTCCCATCGAAGCTCAATGACTTGCGATCTGCCATTCTTCGATTACGAGGGG 360

Oy 1576 ATACACGGTGCTACAAGGACAGACAGGCGCTGGAGAAAGCTTCGTTATATCATGTT 1635

Db 361 ATACGCGCTGCTACCNNGCGACAGGCGCTGGAGAAAGCTTCGTTATATCTTGT 420

Oy 1636 ATATGAAAGCAATCTGATTAAAGGAGAAAGATGCTCTGAATCATATCAACTTCATGA 1695

Db 421 ATATGAAAGCAATCTTNNAACAACAGAGAAAGATGCTCTCAATCATCTCAACGCCATGA 480

Oy 1696 TCAGGAGCGCAATCAGAGATTAATTGGAGCTTCTAAAGCCAGACAACAGTGTCCCA 1755

Db 481 TCAGTGATGTATTANANNNTAAATTGGAGCTTCTCAAAACCAACAGACAGCGTTCCCA 540

Oy 1756 TCACCTTCCAAGAAACAGCATTTGACATTAACGAGAGTTGGCATCAGCGTTACAGATA 1813

Db 541 TATCTGCCAANNNCATGCTTTGACATTANCNNNNNNTCCNNNTGTGGCTACAAATA 598

RESULT 5
CF474786
LOCUS
DEFINITION
RTMW2_7 B11.g1_A021 well-watered loblolly pine roots WW2 Pinus taeda cDNA clone RTMW2_7_B11_A021 5', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Pinus taeda (loblolly pine)

REFERENCE
AUTHORS
Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W., Dean, J., Gebremedhin, M., Dervinis, C., Martin, T., White, T., Davis, J. and Neale, D.

TITLE
JOURNAL
COMMENT
An EST database from well-watered loblolly pine (Pinus taeda) roots unpublished (2003)
Other ESTs: RTMW2_7_B11.b1_A021

Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu

RNA prepared and library constructed by W. Walter Lorenz, School of Forestry, University of Georgia; plant material prepared at the University of Florida; sequencing done in the laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.
Seq primer: JENREV (CAGGAACAGCTATGACC).

FEATURES

source

```
1..700
/organism="Pinus taeda"
/mol_type="mRNA"
/strain="CLONES"
/db_xref="taxon:3352"
/clone="RTMW2_7 B11_A021"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="well-watered loblolly pine roots WW2"
/note="Vector: pSL1180; Site 1: EcoRI; Site 2: XhoI; The library was prepared from polyA+ RNA from loblolly pine (Pinus taeda) roots watered to pot capacity every other day. Pre-dawn water potential remained -0.3 MPa +/- 0.1. Roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL1180. Inserts excised with EcoRI (5' end) and XhoI (3' end)."
```

ORIGIN

Query Match 21.2%; Score 427; DB 14; Length 700;

Best Local Similarity 75.7%; Pred. No. 1.1e-65;

Matches 529; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

Oy 1034 TCGTCACTGGAATACACGCTTTGGCTTCCTGCATTTGCCGTTGACGCTCAACATTTGCG 1093

Db 1 TCGTCACTGGAATACACCTTTAGCAGCTTGCAATGCAATGATCTTAACATTTCTGC 60

Oy 1094 ATTCAAGCTCGGCTTTACCAAGATGCTCATCTTATACGGTTCTTGACGACATGTACGA 1153

Db 61 GTTTCAGTAGAATTGGTAAATAAGTCATATGATGATCAGATTCTCGACGATATCTACGA 120

Oy 1154 CGTCTTGGCAGACGTAGACGAGCTGGAACCTTTCACAGCGCAATTAAGATGGGATCC 1213

Db 121 CACCTTCGGAACAATGAGAGAGCTCGAACTCTTAACCGCAGCGTTTAAGATGGGATCC 180

Oy 1214 GTCCGATGGAATGCTTCAGAAATATGAAGAGAGTGTACATGATGTTATCACAC 1273

Db 181 GTCTTCATAGAGTGTCTTCAGATTATATGAAGAGAGTGTACATGCGGTTACGACAA 240

[illegible]

| | |
|------------|--|
| RESULT | 6 |
| CF476978 | |
| LOCUS | CF476978 637 bp mRNA linear EST-08-SEP-2003 |
| DEFINITION | RTWw3_5_A06.b1_A022 well-watered loblolly pine roots wv3 Pinus taeda cDNA clone RTWw3_5_A06_A022 3', mRNA sequence. |
| ACCESSION | CF476978 |
| VERSION | CF476978.1 GI:34505847 |
| KEYWORDS | EST. |
| SOURCE | Pinus taeda (loblolly pine) |
| ORGANISM | Pinus taeda |
| REFERENCE | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 637) |
| AUTHORS | Pratt,P., Cordonnier-Pratt,M.-M., Lorenz,W.W., Dean,J., Gebremedhin,M., Derwinis,C., Martin,T., White,T., Davis,J. and Neale,D. |
| TITLE | An EST database from well-watered loblolly pine (Pinus taeda) roots unpublished (2003) |
| JOURNAL | |
| COMMENT | Other_ESTS: RTWw3_5_A06.g1_A022 |

Email: mmprat@uga.edu
RNA prepared and library constructed by W. Walter Lorenz, School of Forestry, University of Georgia; plant material prepared at the University of Florida; sequencing done in the laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.
Seq primer: M13-21 (TGTAACGACGCGCCAGT)
POLYA=Yes.

| FEATURES | Location/Qualifiers |
|----------|-------------------------|
| source | 1..637 |
| | /organism="Pinus taeda" |
| | /mol_type="mRNA" |

```

/strain="CCLONES"
/db_xref="taxon:3352"
/clone="RTW3_5_A06_A022"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="Well-watered loblolly pine roots W3"
/notes="Vector: pSL180; Site 1: EcoRI; Site 2: XhoI; The library was prepared from polyA+ RNA from loblolly pine (Pinus taeda) roots watered to pot capacity every other day. Pre-dawn water potential remained -0.3 MPa +/-0.1. Roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL180. Inserts excised with EcoRI (5' end) and XhoI (3' end)."
```

| | |
|---------------------------|-------------------------------------|
| ORIGIN | |
| Query Match | 21.2%; |
| Best Local Similarity | 85.3%; |
| Matches 475; Conservative | 0; Mismatches 82; Indels 0; Gaps 0; |

| | | | | | | |
|----|------|------------------------|---------------------|-----------------------|---------------|------|
| QY | 1336 | GACAGGCTTGGAGCGCGTGT | TTTGATTGCTGATATGCA | GGAAGCAAGTGATCGCCACTG | 1395 | |
| | | | | | | |
| | | | | | | |
| Db | 1 | GACAGGCTTGGAGGATATATTG | ATTCGTATATGCAAGCAAA | GTGATCGCCAGTG | 60 | |
| QY | 1396 | GTTATCTGCCACCTTTGAGG | AGTACTTGAGAAAGGAAAG | TAGCTCTGCTCATCGCC | 1455 | |
| | | | | | | |
| | | | | | | |
| Db | 61 | GTGAGTGCCAACTTTGAGG | AGTACTACGAAAGGAAAT | TAGCTCTGCTCATCGCG | 120 | |
| QY | 1456 | CATGCGCACTGCAACCCAT | TCTGACGTTGGACATCC | CTTCTGATCACA | TCTCAAGG | 1515 |
| | | | | | | |
| | | | | | | |
| Db | 121 | TATCGGCATTGCAACCCAT | TCTGACGACCGACATCC | CTTCTGAGCACG | TCTCAAGG | 180 |
| QY | 1516 | AAGTTGACTTCCCATTCGA | AGCTCAATGACTTGATAT | GTATCATCTTGATTA | GAGGTG | 1575 |
| | | | | | | |
| | | | | | | |
| Db | 181 | AAGCTGACATTCATCGAA | GCTCAATGACTTGCA | TCTGCCATCTTGATTA | GAGGAG | 240 |
| QY | 1576 | ATACACGGTGCTACGAAG | GCAGACAGGCGCTGGA | AGAAAGCTTCGTATAT | CATGTT | 1635 |
| | | | | | | |
| | | | | | | |
| Db | 241 | ATACGCGCTGTACGAGC | GCAGCGCCGTGGAGA | AGAACTTCGTATAT | CTTGTT | 300 |
| QY | 1636 | ATATGAAGAACAATCCTG | GATTTAACGGAAGAAGT | CTGATCATATCA | ACTTCATGA | 1695 |
| | | | | | | |
| | | | | | | |
| Db | 301 | ATATGAAGAACAATCCTG | AGCAACGGAAGAAGT | CTCTCAATCATAT | CAACGCCATGA | 360 |
| QY | 1696 | TCAGGAGCGCAATCAGA | GAATTTAATTGGAGCTT | CTAAAGCCAGACA | CAGTGTCCCA | 1755 |
| | | | | | | |
| | | | | | | |
| Db | 361 | TCAGTGATGTAATTAA | AGATTAAATTGGAGCTT | CTCAAAACCAAC | AGCAGCGTTCCA | 420 |
| QY | 1756 | TCACCTTCCAAGAAACA | CGCATTTGACATTAAG | CAGAGTTGGCATC | ACGGTTACAGATA | 1815 |
| | | | | | | |
| | | | | | | |
| Db | 421 | TATCTGCCAAAAACATG | CTTTTGACATTAGCAG | AGCTTCCATTATG | GTCTACAAATATC | 480 |
| QY | 1816 | GAGATGGCTACAGCTTTG | CCACGTTGAACAAGA | AGTTGGTGATGAG | AAACGTCATTG | 1875 |
| | | | | | | |
| | | | | | | |
| Db | 481 | GAGATGGCTACAGCGTTG | CCACGATTTGAACA | AGAAGTTGGTGAG | ACGGAACCGTCA | 540 |
| QY | 1876 | AACCTGTGCTTTGTAA | 1892 | | | |
| | | | | | | |
| | | | | | | |
| Db | 541 | ATGCTGTGACTTTATTA | 557 | | | |

| | |
|------------|---|
| RESULT | 7 |
| LOCUS | CF401916 |
| DEFINITION | CF401916 696 bp mRNA linear EST 29-AUG-2003 RTW1_15_B05_g1_A015 Well-watered loblolly pine roots Ww1 Pinus taeda cDNA clone RTW1_15_B05_A015 5' , mRNA sequence. |
| ACCESSION | CF401916 |
| VERSION | CF401916.1 GI:34360333 |
| KEYWORDS | BST. |
| SOURCE | Pinus taeda (loblolly pine) |
| ORGANISM | pinus taeda |
| REFERENCE | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; pinus. 1 (bases 1 to 696) Pratt,L., Cordonnier-Pratt,M.-M., Lorenz,W.W., Dean,J., |
| AUTHORS | |

TITLE
JOURNAL
COMMENT

Gebremedhin,M., Derwinis,C., Martin,T., White,T., Davis,J. and Neale,D.
An EST database from well-watered loblolly pine (Pinus taeda) roots
Unpublished (2003)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu

RNA prepared and library constructed by W. Walter Lorenz, School of Forestry, University of Georgia; plant material prepared at the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.
Seq primer: JENREV (CAGGAACAGCTATGACC).

FEATURES
source

1. .696
location/Qualifiers
/organism="Pinus taeda"
/mol_type="mRNA"
/strain="CCIONES"
/db_xref="taxon:3352"
/clone="RTMW1_15_B05_A015"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="Well-watered loblolly pine roots wW1"
/note="Vector: pSL180; Site 1: EcoRI; Site 2: XhoI; The library was prepared from polyA+ RNA from loblolly pine (Pinus taeda) roots watered to pot capacity every other day. Pre-dawn water potential remained -0.3 MPa +/-0.1. Roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL180. Inserts excised with EcoRI (5' end) and XhoI (3' end)."

ORIGIN

Query Match 20.8%; Score 419.2; DB 14; Length 696;
Best Local Similarity 75.1%; Pred. No. 2.6e-64;
Matches 523; Conservative 0; Mismatches 173; Indels 0; Gaps 0;

QY 1065 TGCATTGCGTTGAGCCTCAACATCTGGATTACAGACTCGGCTTTACCAAGATGTCTCAT 1124
|||||
Db 1 TGCATTGCAAAATGATCCTAAACATTTTGGCTTCGACTAGATTGGTAAATAAGTCAT 60
QY 1125 CTTATTCACGGTCTTGACGACATGTACGACGCTTCGCGACAGTAGACGAGCTGGAATC 1184
|||||
Db 61 ATGATCAGGATTCTCGACGATATCTACGACACCTTCGGAACATGAGGAGCTCGAATC 120
QY 1185 TTTCAGCGACAATTAAAGATGGATCCGTCGCGATGGAATGCTTCAGAAATATATG 1244
|||||
Db 121 TTAAACGACGCTTTAAAGATGGATCCGCTTCGATAGAGTGTCTCCAGATTATATG 180
QY 1245 AAAGAGTGTACATGATGTTTATCACACCGTAAATGAATGGCTCGAGTGCGAGAGAAG 1304
|||||
Db 181 AAAGAGTGTACATGCGGCTTACGACAACATCAACGAATGGCAGAGGCGCAGAAA 240
QY 1305 GCTCAAGCCGAGACACGCTCAACTATGCAAGACAGGCTTGGAGGCGTGTATTGATTG 1364
|||||
Db 241 ATTCAAGGCTGGGATACAGTCACTATGCTCGAAAATCTGGAGGCTTTTATTGTGCT 300
QY 1365 TATATGCAAGAAAGTGTATGCGCACTGTTATCTGCGCAAGCTTTGAGAGTACTTG 1424
|||||
Db 301 TATATACAAGAAAGCCCAAGTGGATTTCCAGTGTATCTCCACGTTCCAGAGTACCTC 360
QY 1425 GAGAAAGGGAAGTTAGTCTGCTCATGCCCCATGCGCACTGCAACCCATTCTGACGTTG 1484
|||||
Db 361 GAGAAAGGGAAGTTCAGCTTCGGCTCTCGCATTAACCAAGCTCGAACCCATGCTGACTTG 420
QY 1485 GACATCCCTTCTCTGATCACATCCTCAAGGAAGTTGACTTCCATCGAAGCTCAATGAC 1544
|||||
Db 421 GGGTTCTCTTCCGCTCGAATCCTGAGGAAGTGAATGACTTCCATCGAAAATTCAATGAT 480

QY 1545 TTGATATGTATCATCTTCGATTAAAGGTGATACACGGTGCTACAGGACAGAGGCC 1604
|||||
Db 481 TTGATATGTGCCATCTTCGACTGAAGGTGACACACTCAATGCTACAAAGCTGACAGGCG 540
QY 1605 CGTGAGAAAGAGCTTCGCTATATCATGTATATGAAACAATCCTGGATTACGGAA 1664
|||||
Db 541 CGTGAGAAAGAGCTTCGCGCTATCGTTATATGAAAGCAATCCTGGAATAACAGAG 600
QY 1665 GAAGATGCTCTGAATCATATCACTTCATGATCAGGAGCGCAATCAGAGATTAAATTGG 1724
|||||
Db 601 GAAGATGCTGTCAATCAAGTCAATGCTATGTCGATTAACCTTAACCAAGAACTGAATTGG 660
QY 1725 GAGCTTAAAGCCAGACACAGTGTCCCATCACT 1760
|||||
Db 661 GAGTTACTTAGACCCGACAGCGGTGTTCCCATCTCT 696

RESULT 8
CF479802/c 669 bp mRNA linear EST 08-SEP-2003
LOCUS
DEFINITION
RTMW3_12_D02_b1_A022 well-watered loblolly pine roots wW3 Pinus taeda cDNA clone RTMW3_12_D02_A022 3', mRNA sequence.
CF479802
CF479802.1 GI:34508671
VERSION
KEYWORDS
SOURCE
ORGANISM
Pinus taeda (loblolly pine)
Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.

REFERENCE
AUTHORS
Pratt,L., Cordonnier-Pratt,M.-M., Lorenz,W.W., Dean,J., Gebremedhin,M., Derwinis,C., Martin,T., White,T., Davis,J., Cannon,R., Owen,A. and Neale,D.
EST database from well-watered loblolly pine (Pinus taeda) roots Unpublished (2003)
Other ESTs: RTMW3_12_D02.g1_A022
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu

RNA prepared and library constructed by W. Walter Lorenz, School of Forestry, University of Georgia; plant material prepared at the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.
Seq primer: M13-21 (TGTAACAACGACGGCCAGT)
POLYA=NO.

FEATURES
source

1. .669
location/Qualifiers
/organism="Pinus taeda"
/mol_type="mRNA"
/strain="CCIONES"
/db_xref="taxon:3352"
/clone="RTMW3_12_D02_A022"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="Well-watered loblolly pine roots wW3"
/note="Vector: pSL180; Site 1: EcoRI; Site 2: XhoI; The library was prepared from polyA+ RNA from loblolly pine (Pinus taeda) roots watered to pot capacity every other day. Pre-dawn water potential remained -0.3 MPa +/-0.1. Roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL180. Inserts excised with EcoRI (5' end) and XhoI (3' end)."

ORIGIN

Query Match 20.5%; Score 413; DB 14; Length 669;
Best Local Similarity 76.1%; Pred. No. 3.3e-63;
Matches 509; Conservative 0; Mismatches 160; Indels 0; Gaps 0;

Db 491 GGAGAGCAAGTAGTGTCCAGCGTTATATACCCAGCTTGAGAGATTTGGAGAA 550
QY 1430 CGGAAAGTTAGCTCTGCTCATCGCCCATGCGCACTGCAACCCATTCTGACGTGACAT 1489
Db 551 CCGGAAGGTGAGTTTGGGTATCGACAGCCACTGCAACCCATTCTCAGTTGATAT 610
QY 1490 CCCCTT 1495
Db 611 TCCCTT 616

RESULT 10
BQ698077
LOCUS 516 bp mRNA linear EST 07-MAY-2003
DEFINITION NXPV_064_C05_F_NXPV (Nsf Xylem Planings wood Vertical) Pinus taeda
cDNA clone NXPV_064_C05_5' similar to Arabidopsis thaliana sequence
At1g61680 hypothetical protein see
http://mips.gsf.de/proj/thal/db/index.html, mRNA sequence.

ACCESSION BQ698077 GI:21823393
VERSION BQ698077.1
KEYWORDS EST.
SOURCE Pinus taeda (loblolly pine)
ORGANISM Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
1 (bases 1 to 516)
Sederoff, R.
REFERENCE Molecular Basis of Wood Formation in the Pine Megagenome
TITLE Unpublished (2000)
JOURNAL Contact: Sederoff, Ron
COMMENT Forest Biotechnology
North Carolina State University
840 Main Campus Drive, Centennial Campus, Campus Box 7247, Raleigh,
NC 27695, USA
Tel: 919 515 7800
Fax: 919 515 7801
Email: ron_sederoff@ncsu.edu, jerri_johnson@ncsu.edu
Please see http://web.ahc.umn.edu/biodata/nsfpine/ for further
information.
Seq primer: T3.

FEATURES
source location/Qualifiers
1..516

/organism="Pinus taeda"
/mol_type="mRNA"
/strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
/clone="NXPV_064_C05"
/tissue_type="Xylem"
/cell_type="Planings (secondary)"
/dev_stage="Transitional"
/lab_host="XLI-Blue"
/clone_lib="NXPV (Nsf Xylem Planings wood Vertical)"
/note="Vector: Bluescript SK; Site 1: Eco RI; Site 2:
XhoI; The library is from early (spring) secondary wood,
taken from a ten year old tree in the transitional phase.
The tree is a kind gift of the Westvaco Corporation.
Secondary xylem was harvested from the tree by peeling
back the bark and primary xylem and then removing the
underlying tissue with a block plane. NOTE: The sequences
contain a 'cDNA adapter' between the EcoRI site and the
start of the EST. The adapter sequence is
'AATTCGGCAGAG'."

ORIGIN

Query Match 19.3%; Score 388.6; DB 13; Length 516;
Best Local Similarity 84.7%; Pred. No. 7.3e-59;
Matches 436; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 1353 TGTTTGATTCGTATATGCAAGCAAGAGTGATGCGCACTGGTTATCTGCCACGTTT 1412
Db 2 TATATTGATGCGTATATGCAAGCAAGAGTGATGCGCACTGGTGAGTGCCCAACATTT 61

QY 1413 GAGAGTACTTGAGAACGGGAAAGTTAGCTCTGCTCATCCGCCATGCGCACTGCAACC 1472
Db 62 GAGAGTACTATGAGAACGGGAAAGTTAGCTCTGCTCATCCGTAATCGCAATTGCAACCC 121
QY 1473 ATTCTGACGTTGACATCCCTTTCTCTGATCACATCTTCAAGAAAGTTGACTTCCCATCG 1532
Db 122 ATTTGACGACCGACATCCCTTTCTCTGACACGTCCTCAAGAAAGTTGACATTCATCG 181
QY 1533 AAGCTCAATGACTTGATATGATCATCTTCTGATTAAAGGTGATACACGGTCTACAG 1592
Db 182 CAGCTCAATGACTTGACATCTGCCATCTTCTGATTACGAGGGGATACGCGTCTACAG 241
QY 1593 GCAGACAGGCGCGTGAGAGAAAGCTTCTATATCATGTTATGAAAGCAATCCT 1652
Db 242 GCGACAGGCGCGTGAGAGAAAGCTTCTGATATATCTGTTATGAAAGCAATCCT 301
QY 1653 GGATTAACGGAAGAGATGCTCTGAATCATATCAACTTCATGATCAGGACGCAATCAGA 1712
Db 302 GGAACAACAGAGAGAGATGCTCTCAATCATCTCAACGCCATGATCAGTGTATTA 361
QY 1713 GAATTAATTTGGAGCTTTAAAGCCAGACACAGATGTTCCATCACTTCCAGAAACAC 1772
Db 362 GGATTAATTTGGAGCTTTCAAAACCAACAGACAGCTTCCATATCTGCCAAAAACAT 421
QY 1773 GCATTTGACATTAAGCAGAGTTTGGCATCACGTTACAGATACCGAGATGGCTACAGCTT 1832
Db 422 GCTTTGACATTAAGCAGAGCTTTCATTTGTGCTACAAATATGAGATGGCTACAGCTT 481
QY 1833 GCCACGTTGAAACAAAGAGTTTGGTGATGAGAAC 1867
Db 482 GCCACATTTGAAACAAAGAGTTTGGTGAGAGAAC 516

RESULT 11
BX677624 517 bp mRNA linear EST 28-OCT-2003
LOCUS BX677624 RN Pinus pinaster cDNA clone RN42B08, mRNA sequence.
DEFINITION BX677624
ACCESSION BX677624
VERSION BX677624.1 GI:38011576
KEYWORDS EST.

SOURCE Pinus pinaster
ORGANISM Pinus pinaster
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
1 (bases 1 to 517)
REFERENCE Frigerio, J. and Plomion, C.
TITLE Identification of water-deficit responsive genes in Maritime pine
(Pinus pinaster Ait.) using an EST approach
JOURNAL Unpublished (2002)
COMMENT Contact: Frigerio JM
Genetique et Amelioration 69
INRA

route d'Arcachon 33612 Cestas CEDEX France
Email: Frigerio@pierroton.inra.fr
Email: Frigerio@pierroton.inra.fr
Seq primer: T3.

FEATURES
source location/Qualifiers
1..517

/organism="Pinus pinaster"
/mol_type="mRNA"
/db_xref="taxon:71647"
/clone="RN42B08"
/tissue_type="root"
/dev_stage="6 weeks old seedling"
/lab_host="SOLR"
/clone_lib="RN"
/note="Vector: Uni-ZAP XR; ecotype: Landes; The library
was made from the roots of 6 weeks old seedlings grown in
hydroponic conditions. A mixture of genotypes were used.
Oligo-dT primed cDNA was directionally cloned into the
EcoRI-XhoI lambda-ZAP vector arms and mass-excised to form
a pBluescript phagemid"

ORIGIN

| | | | |
|-----------------------|---|---|-----------------------------|
| Db | 658 | AGACGAGAGATAGAGATGTCCTCAATTATTTCGGGATCTCTCATGTGCTTCCTGG | 717 |
| Qy | 710 | CGAGAAAGTTATGATGAGCTGAACATTTCTACAAAAATATTTAAGAGAAGCCCTGCA | 769 |
| Db | 718 | CGAAAAAATTAATGAGGCGGCTGAATCTTCTACAATGTAATTAAGAATGCCCTACA | 777 |
| Qy | 770 | AAAGATTCCGGCATCCAGTAT | 790 |
| Db | 778 | AAAGATTCCGCCCTCCGGTCT | 798 |
| RESULT 13 | | | |
| LOCUS | AL750951 | 481 bp | mRNA linear EST 20-JUN-2002 |
| DEFINITION | AL750951 RS Pinus pinaster cDNA clone RS02D01 similar to PINENE | | |
| SYNTHASE | AL750951 | | Pinene sequence. |
| ACCESSION | AL750951 | | |
| VERSION | AL750951.1 | | GI:21492198 |
| KEYWORDS | EST. | | |
| SOURCE | Pinus pinaster | | |
| ORGANISM | Pinus pinaster | | |
| REFERENCE | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. | | |
| AUTHORS | Frigerio,J. and Plomion,C. | | |
| TITLE | Identification of water-deficit responsive genes in Maritime pine (Pinus pinaster Ait.) using an EST approach | | |
| JOURNAL | Unpublished (2002) | | |
| COMMENT | Contact: Frigerio JM | | |
| ORGANISM | Genetique et Amelioration 69 | | |
| REFERENCE | route d'Arcachon 33612 Cestas CEDEX France | | |
| AUTHORS | Email: Frigerio@pierroton.inra.fr | | |
| TITLE | Seq primer: T3. | | |
| JOURNAL | | | |
| COMMENT | | | |
| ORGANISM | | | |
| FEATURES | | | |
| source | 1. .481 | | |
| | location/Qualifiers | | |
| | /organism="Pinus pinaster" | | |
| | /mol_type="mRNA" | | |
| | /db_xref="taxon:71647" | | |
| | /clone="RS02D01" | | |
| | /tissue_type="root" | | |
| | /dev_stage="6 weeks old seedling" | | |
| | /lab_host="SOLR" | | |
| | /clone_lib="RS" | | |
| | /note="Vector: Uni-ZAP XR; ecotype: landes; The library was made from the roots of 6 weeks old seedlings grown in hydroponic conditions. A three weeks drought stress treatment was applied by lowering the osmotic potential of the nutrient solution to -0.45 MPa using 170 g/l of polyethylene glycol as an osmoticum. A mixture of genotypes were used. Oligo-dt primed cDNA was directionally cloned into the EcoRI-XhoI lambda-ZAP vector arms and mass-excised to form a pbluescript phagemid" | | |
| ORIGIN | | | |
| Query Match | 18.7%; | Score 376; | DB 9; Length 481; |
| Best Local Similarity | 86.5%; | Pred. No. 1.3e-56; | |
| Matches 415; | Conservative 0; | Mismatches 65; | Indels 0; Gaps 0; |
| Qy | 1038 | CACGTGAATACTACGCTTTGGCTTCTGCATTCGTTGAGCTCAACATTTCTGATTC | 1097 |
| Db | 2 | CAGTGTGAGTACTACACTTTGGCTTCCTGCATCGCGTTGAGCCCAACATTTCTGATTC | 61 |
| Qy | 1098 | AGACTGGCTTTACCAAGATGTCTCATCTTATCACGCGTTCTTGACAGACATGTAGCAGCTC | 1157 |
| Db | 62 | AGACTGGCTTTGCGAAGCGTGTCAATATTACTACTGTTCTCGACATATGTAGCAGCTC | 121 |
| Qy | 1158 | TTCCGACAGTAGACGAGCTGGAATCTTTCACAGCGACAATTAAGATGGATCCGCTCC | 1217 |
| Db | 122 | TTCCGACAGTAGATGAGCTCAAACTGTTTCACAGCCGCAATTAAGATGGATCCGCTCC | 181 |
| Qy | 1218 | GCGATGAATGCCTTCAGAAATATATGAAGAAGTGTACATGATGTTTATACACCCGTA | 1277 |

| | | | |
|-----------------------|--|---|-----------------------------|
| Db | 182 | GCCACAGATTGCCCTCCACATATATGAAGAATTTTACATGATGTTTACACACCCGTA | 241 |
| Qy | 1278 | AATGAATGGCTCGAGTGGCAGAGAAGGCTCAAGGCCGAGACACGCTCAACTATGCAAGA | 1337 |
| Db | 242 | AATGAATGTCTGCGGAGGCAAGAGGCTCAAGGCCGAGACACTCTCAACTATGCTGCA | 301 |
| Qy | 1338 | CAGGCTTGGGAGGCGGTGTTTGAATTCGTATATGACAGAACAAAGTGATCGCCACTGCT | 1397 |
| Db | 302 | CAGGCTTGGGAGGATTAATCTGATTCGTATATGACAGAACAAAGTGATAGCCACGGGT | 361 |
| Qy | 1398 | TATCTGCCACCGTTTGAGAGTAATTTGAGAACCGGAAAGTTAGCTTGCTCATCGCCCA | 1457 |
| Db | 362 | TATCTGCCAACGTTTGAGAGTAATTTGAGAACCGGAAAGTTAGCTTGCGCATCGCGTG | 421 |
| Qy | 1458 | TGCGCACTGCAACCCATTCGACGTTGGACATCCCTTCTGATCAGATCCTCAAGGA | 1517 |
| Db | 422 | TGCGCGTTGCAACCCATGCTGACATGACATCCCTTCTCTCCTCACATCCTCAAGGA | 481 |
| RESULT 14 | | | |
| LOCUS | CF477562/c | 740 bp | mRNA linear EST 08-SEP-2003 |
| DEFINITION | RTMW3_8 G10.g1_A022 well-watered loblolly pine roots WM3 Pinus taeda cDNA clone RTMW3_8_G10_A022 5', mRNA sequence. | | |
| ACCESSION | CF477562 | | |
| VERSION | CF477562.1 | | GI:34506431 |
| KEYWORDS | EST. | | |
| SOURCE | Pinus taeda (loblolly pine) | | |
| ORGANISM | Pinus taeda | | |
| REFERENCE | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. | | |
| AUTHORS | 1 (bases 1 to 740) | | |
| | Pratt,L., Cordonnier-Pratt,M.-M., Lorenz,W.W., Dean,J., Gebremedhin,M., Dervinis,C., Martin,T., White,T., Davis,J. and Neale,D. | | |
| | An EST database from well-watered loblolly pine (Pinus taeda) roots | | |
| | Unpublished (2003) | | |
| | Contact: Cordonnier-Pratt MM | | |
| | Laboratory for Genomics and Bioinformatics | | |
| | The University of Georgia, Department of Plant Biology | | |
| | Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA | | |
| | Tel: 706 542 1860 | | |
| | Fax: 706 583 0210 | | |
| | Email: mmp Pratt@uga.edu | | |
| | RNA prepared and library constructed by W. Walter Lorenz, School of Forestry, University of Georgia; plant material prepared at the University of Florida; sequencing done in the laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA. | | |
| | Seq primer: JENREV (CAGGAACAGCTATGACC). | | |
| FEATURES | | | |
| source | 1. .740 | | |
| | location/Qualifiers | | |
| | /organism="Pinus taeda" | | |
| | /mol_type="mRNA" | | |
| | /strain="CLONES" | | |
| | /db_xref="taxon:3352" | | |
| | /clone="RTMW3_8 G10_A022" | | |
| | /lab_host="DH10B-T1 phage-resistant E. coli" | | |
| | /clone_lib="Well-watered loblolly pine roots WM3" | | |
| | /note="Vector: pSL180; Site 1: EcoRI; Site 2: XhoI; The library was prepared from polyA+ RNA from loblolly pine (Pinus taeda) roots watered to pot capacity every other day. Pre-dawn water potential remained -0.3 MPa +/-0.1. Roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL180. Inserts excised with EcoRI (5' end) and XhoI (3' end)." | | |
| ORIGIN | | | |
| Query Match | 18.6%; | Score 375; | DB 14; Length 740; |
| Best Local Similarity | 76.1%; | Pred. No. 1.6e-56; | |

Matches 462; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

| | | | |
|----|------|---|------|
| QY | 1307 | TCAAGGCCGAGACACCGCTCAACTATGCAAGACAGAGCGCTTGGAGGCGCTGTTTGATTCGTA | 1366 |
| Db | 740 | TCAAGGCTGGGATACAGTCAAGCTATGCTCGAAAATCTTGGAGGCTTTTATTTGGTGCCTTA | 681 |
| QY | 1367 | TATGACGAGAAAGCAAGTGGATCGCCACTGGTTATCTGCCCCAGTTTGAGGAGTACTTGGGA | 1426 |
| Db | 680 | TATACAGAAGCCCAAGTGGATTTCCAGTGGTATCTTCCACGTTCCAGAGTACCTCGA | 621 |
| QY | 1427 | GAACGGGAAAGTTAGCTCTGCTCATCGCCCATGCGCACTGCAACCCATTCTGACGTTGGA | 1486 |
| Db | 620 | GAATGGGAAGGTCAAGCTTCGGCTCTCGCATTAACCAACGCTCGAAACCATGCTGACTTTGGG | 561 |
| QY | 1487 | CATCCCCCTTCCCTGATCACATCCTCAAGGAAGTTGACTTCCCATCGAAAGCTCAATGACTT | 1546 |
| Db | 560 | GTTTCCTCTCCGCTCGAATCCTGCAGGAATTGACTTTCATCGAAATTCATGATTT | 501 |
| QY | 1547 | GATATGTATCATCCTTCGATTAAGAGGTGATACACGGTGTCTACAAGGCAGACAGGGCCG | 1606 |
| Db | 500 | GATATGTGCCATCCTTCGACTGAAAGGTGACACTCAATGTCTACAAGGCTGACAGGGCGCG | 441 |
| QY | 1607 | TGGAGAAGAAGCTTCGCTATATCATGTTATATGAAGACAATCCTGGATTAACGGAGA | 1666 |
| Db | 440 | TGGAGAAGAAGCTTCGCGCGGTATCGTTATATGAAGACCATCCTGGAATTAACAGAGGA | 381 |
| QY | 1667 | AGATGCTCTGAATCATATCAACTTCATGATCAGGAGCGCAATCAGAGAATTAATTGGGA | 1726 |
| Db | 380 | AGATGCTGTCAATCAAGTCAATGCTATGTCGATTAACCTTAACCAAGGAACCTGAATTTGGGA | 321 |
| QY | 1727 | GCTTCTAAAGCCAGACACAAGTGTTCGCCATCATCTTCCAAGAAACACGCATTTGACATTAAG | 1786 |
| Db | 320 | GTTACTTAGACCCGACAGCGGTGTTCCCATCTCTTACAGAAGAGTTGCTTTTGACATTTTG | 261 |
| QY | 1787 | CAGAGTTTGGCATCACCGTTTACAGATACCGAGATGGCTTACAGCTTTGCCAACGTTGAAC | 1846 |
| Db | 260 | CAGAGTTTTCATTACGGTTACAAATACAGAGATGGCTTCAGTGTTCGCCAGTATTTGAAT | 201 |
| QY | 1847 | AAAGAGTTTGGTATGAGAAACCGTCATTGAACCTGTGCTTTGTAAACAACACTTCAATC | 1906 |
| Db | 200 | AAAGAAATTTGGTAAACAAGAACCGTGGTTGAAACTGTGCTTTGTAGCCACACATGAATG | 141 |
| QY | 1907 | TACAATA 1913 | |
| Db | 140 | TACAATA 134 | |

| | |
|------------|---|
| RESULT 15 | |
| LOCUS | AW287756 |
| DEFINITION | AW287756 539 bp mRNA linear EST 07-JAN-2000 |
| ACCESSION | EST0004 Sitka spruce drill-wounded bark Picea sitchensis cDNA clone |
| VERSION | 25-1-3 5' similar to mono-terpene synthase, mRNA sequence. |
| KEYWORDS | AW287756 |
| SOURCE | AW287756.1 GI:6681768 |
| ORGANISM | EST. |
| | Picea sitchensis (Sitka spruce) |
| | Picea sitchensis |
| | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; |
| | Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea. |
| REFERENCE | 1 (bases 1 to 539) |
| AUTHORS | Wang, S.X., Hunter, W. and Plant, A.L. |
| TITLE | Isolation of terpene synthase gene-specific probes from Sitka |

```

Bark tissue
PCR Primers
FORWARD: Mult-F10
BACKWARD: Mult-B18
Insert Length: 539      Std Error: 0.00
Seq primer: M13 Reverse and M13 Forward
High quality sequence stop: 539.

```

| FEATURES | Location/Qualifiers |
|----------|---------------------|
| Source | 1. .539 |

```

/organism="Picea sitchensis"
/mol_type="mRNA"
/db_xref="taxon:3332"
/clone="25-1-3"
/tissue_type="bark"
/clone Tib="Sitka spruce drill-wounded bark"
/notes="mRNA isolated from drill-wounded bark tissues;
RT-PCR product"

```

ORIGIN

| | | | | |
|---------------------------|-------|--------------------|-----------|-------------|
| Query Match | 17.5% | Score 352.4; | DB 10; | Length 539; |
| Best Local Similarity | 79.1% | Pred. No. 1.8e-52; | | |
| Matches 419; Conservative | 0; | Mismatches 111; | Indels 0; | Gaps 0; |

| | | | |
|----|------|---|------|
| QY | 1135 | TTCTTGACGACATGTACGACGCTTCGGCCACAGTAGACGAGCTTGAAGCTCTTACACGGCA | 1139 |
| DB | 1 | TGCTCGACGACCTGTACGACACATTCGGAACAATGACGAAATCGAACTCTTACACGAAG | 60 |
| QY | 1195 | CAATTAAGAGATGGGATCCGTCGCCGATGGAAATGCTTCCAGATATATGAAAGAGTGT | 1254 |
| DB | 61 | CAGTCAGAGATGGGATCCGTCGGAGACAGAGAGCTTCCAGACTATATGAAAGAGTGT | 120 |
| QY | 1255 | ACATGATGGTTTATCACACCGTAAATGAAATGGCTCGAGTGGCAGAGAGGCTCAAGGCC | 1314 |
| DB | 121 | ACATGTAATCTACGAAAGCCCTTAATGAAATGGCTCAAGAGGCGGAGAAAACACAAGGCC | 180 |
| QY | 1315 | GAGACACGCTCAACTATGCAAGACAGGCTTGGAGGCGTGTGATTCTGTATATGCAGG | 1374 |
| DB | 181 | GAGACACGCTCAACTATGCTCGAAAGGCTTGGAGATTATCTTGATTCGTATATTCAG | 240 |
| QY | 1375 | AAGCAAGTGAATCGCCACTGTTATCTGCCACGTTTGAGAGTACTTGGAAACGGGA | 1434 |
| DB | 241 | AAGCAAGTGAATCGCCAGTGTATCTGCCAACATTCAGAGTACTTGGAAACGGGA | 300 |
| QY | 1435 | AAGTTAGCTGCTCATCGCCCATGCGCACTGCAACCCATTTGACGTTGACATCCCT | 1494 |
| DB | 301 | AAATTAGCTGCTGCTTATCGCGCAGCGCATTGACACCCATCTCACATTGACGTAACGC | 360 |
| QY | 1495 | TTCCTGATCACATCCTCAAGGAAGTTGACTTCCCATCGAAGCTCAATGACTTGATATGTA | 1554 |
| DB | 361 | TTCCTGAATACATCTTGAAGGAATTGATTTCCATCGAGATTCAATGATTTGGCATCTT | 420 |
| QY | 1555 | TCATCCTTGCATTAAAGAGGTGATACACGGTGTCTACAAGGCAGACAGGGCCCGTGAGAA | 1614 |
| DB | 421 | CCTTCCTTGCATTAAGAGGTGACACACGCTGCTACAAGGCGGATAGGGCCCGTGAGAA | 480 |
| QY | 1615 | AAGCTTCGTTATATCATGTTATATGAAAGACAATCCTGGAATTAACGGA | 1664 |
| DB | 481 | AAGCTTCGTTATCTTGTCTACATGAAGGACCACTGCTACATGAA | 530 |

Search completed: July 26, 2004, 13:44:34
Job time : 4687 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2004, 09:01:22 ; Search time 19 Seconds
(without alignments)
1679.203 Million cell updates/sec

Title: US-10-025-145A-65

Perfect score: 3251

Sequence: 1 MALLSTPLVSRSCLSSEHE.....FANVETKSLVMRTVIEPVPL 618

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------------------------------|
| 1 | 3251 | 100.0 | 618 | 4 | US-09-360-545-65 Sequence 65, Appl |
| 2 | 2453 | 75.5 | 628 | 4 | US-09-360-545-4 Sequence 4, Appl |
| 3 | 2453 | 75.5 | 628 | 4 | US-09-398-395A-20 Sequence 20, Appl |
| 4 | 2453 | 75.5 | 628 | 4 | US-09-887-586A-20 Sequence 20, Appl |
| 5 | 2453 | 75.5 | 628 | 4 | US-09-895-752-20 Sequence 20, Appl |
| 6 | 2453 | 75.5 | 628 | 4 | US-09-903-012B-20 Sequence 20, Appl |
| 7 | 2453 | 75.5 | 628 | 4 | US-09-900-797-20 Sequence 20, Appl |
| 8 | 2264 | 69.6 | 630 | 4 | US-09-360-545-67 Sequence 67, Appl |
| 9 | 2200.5 | 67.7 | 627 | 4 | US-09-360-545-2 Sequence 2, Appl |
| 10 | 2200.5 | 67.7 | 627 | 4 | US-09-398-395A-30 Sequence 30, Appl |
| 11 | 2200.5 | 67.7 | 627 | 4 | US-09-887-586A-30 Sequence 30, Appl |
| 12 | 2200.5 | 67.7 | 627 | 4 | US-09-895-752-30 Sequence 30, Appl |
| 13 | 2200.5 | 67.7 | 627 | 4 | US-09-903-012B-30 Sequence 30, Appl |
| 14 | 2200.5 | 67.7 | 627 | 4 | US-09-900-797-30 Sequence 30, Appl |
| 15 | 2197.5 | 67.6 | 627 | 4 | US-09-360-545-32 Sequence 32, Appl |
| 16 | 2137 | 65.7 | 630 | 4 | US-09-360-545-78 Sequence 78, Appl |
| 17 | 2084.5 | 64.1 | 637 | 4 | US-09-360-545-69 Sequence 69, Appl |
| 18 | 2031.5 | 62.5 | 637 | 4 | US-09-360-545-6 Sequence 6, Appl |
| 19 | 2031.5 | 62.5 | 637 | 4 | US-09-398-395A-58 Sequence 58, Appl |
| 20 | 2031.5 | 62.5 | 637 | 4 | US-09-887-586A-58 Sequence 58, Appl |
| 21 | 2031.5 | 62.5 | 637 | 4 | US-09-895-752-58 Sequence 58, Appl |
| 22 | 2031.5 | 62.5 | 637 | 4 | US-09-903-012B-58 Sequence 58, Appl |
| 23 | 2031.5 | 62.5 | 637 | 4 | US-09-900-797-58 Sequence 58, Appl |
| 24 | 1295.5 | 39.8 | 580 | 3 | US-09-234-393-48 Sequence 48, Appl |
| 25 | 1295.5 | 39.8 | 580 | 4 | US-09-865-171-48 Sequence 48, Appl |
| 26 | 1295.5 | 39.8 | 581 | 3 | US-09-234-393-20 Sequence 20, Appl |
| 27 | 1295.5 | 39.8 | 581 | 3 | US-09-234-393-46 Sequence 46, Appl |

| | | | | | |
|----|--------|------|-----|---|-------------------------------------|
| 28 | 1295.5 | 39.8 | 581 | 4 | US-09-865-171-20 Sequence 20, Appl |
| 29 | 1295.5 | 39.8 | 581 | 4 | US-09-865-171-46 Sequence 46, Appl |
| 30 | 1295.5 | 39.8 | 581 | 4 | US-09-398-395A-48 Sequence 48, Appl |
| 31 | 1295.5 | 39.8 | 581 | 4 | US-09-887-586A-48 Sequence 48, Appl |
| 32 | 1295.5 | 39.8 | 581 | 4 | US-09-895-752-48 Sequence 48, Appl |
| 33 | 1295.5 | 39.8 | 581 | 4 | US-09-903-012B-48 Sequence 48, Appl |
| 34 | 1295.5 | 39.8 | 581 | 4 | US-09-900-797-48 Sequence 48, Appl |
| 35 | 1291.5 | 39.7 | 581 | 3 | US-09-234-393-44 Sequence 44, Appl |
| 36 | 1291.5 | 39.7 | 581 | 4 | US-09-865-171-44 Sequence 44, Appl |
| 37 | 1250.5 | 38.5 | 577 | 4 | US-09-360-545-18 Sequence 18, Appl |
| 38 | 1240.5 | 38.2 | 862 | 3 | US-09-315-861-2 Sequence 2, Appl |
| 39 | 1240.5 | 38.2 | 862 | 4 | US-09-398-395A-44 Sequence 44, Appl |
| 40 | 1240.5 | 38.2 | 862 | 4 | US-09-887-586A-44 Sequence 44, Appl |
| 41 | 1240.5 | 38.2 | 862 | 4 | US-09-895-752-44 Sequence 44, Appl |
| 42 | 1240.5 | 38.2 | 862 | 4 | US-09-903-012B-44 Sequence 44, Appl |
| 43 | 1240.5 | 38.2 | 862 | 4 | US-09-593-253-2 Sequence 2, Appl |
| 44 | 1240.5 | 38.2 | 862 | 4 | US-09-900-797-44 Sequence 44, Appl |
| 45 | 1231 | 37.9 | 593 | 3 | US-09-234-393-24 Sequence 24, Appl |

ALIGNMENTS

| | | | | | | | | | |
|--|-----|--|-----|--|--|--|--|--|--|
| RESULT 1 | | | | | | | | | |
| US-09-360-545-65 | | | | | | | | | |
| ; Sequence 65, Application US/09360545 | | | | | | | | | |
| ; Patent No. 6429014 | | | | | | | | | |
| ; GENERAL INFORMATION: | | | | | | | | | |
| ; APPLICANT: Croteau, Rodney B | | | | | | | | | |
| ; APPLICANT: Bohlmann, Joÿg | | | | | | | | | |
| ; APPLICANT: Steele, Christopher L | | | | | | | | | |
| ; APPLICANT: Phillips, Michael A | | | | | | | | | |
| ; TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS) | | | | | | | | | |
| ; FILE REFERENCE: wau13865 | | | | | | | | | |
| ; CURRENT APPLICATION NUMBER: US/09/360,545 | | | | | | | | | |
| ; CURRENT FILING DATE: 1999-07-26 | | | | | | | | | |
| ; EARLIER APPLICATION NUMBER: 60/052,249 | | | | | | | | | |
| ; EARLIER FILING DATE: 1997-11-07 | | | | | | | | | |
| ; EARLIER APPLICATION NUMBER: PCT/US98/14528 | | | | | | | | | |
| ; EARLIER FILING DATE: 1998-07-10 | | | | | | | | | |
| ; NUMBER OF SEQ ID NOS: 107 | | | | | | | | | |
| ; SOFTWARE: PatentIn Ver. 2.0 | | | | | | | | | |
| ; SEQ ID NO 65 | | | | | | | | | |
| ; LENGTH: 618 | | | | | | | | | |
| ; TYPE: PRT | | | | | | | | | |
| ; ORGANISM: Abies grandis | | | | | | | | | |
| ; US-09-360-545-65 | | | | | | | | | |
| Query Match | | | | | | | | | |
| Best local Similarity 100.0%; Score 3251; DB 4; Length 618; | | | | | | | | | |
| Matches 618; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | | | | | | | |
| QY | 1 | MALLSTPLVSRSCLSSEHEIKALRTIPTLGICRPGKSVASHINMCLTSVASTDSVQR | 60 | | | | | | |
| DB | 1 | MALLSTPLVSRSCLSSEHEIKALRTIPTLGICRPGKSVASHINMCLTSVASTDSVQR | 60 | | | | | | |
| QY | 61 | VGNYHSNMDDDFIOSLISTPYGADYRERADRLIGEVKDIMFNKSLDGGNDLQRL | 120 | | | | | | |
| DB | 61 | VGNYHSNMDDDFIOSLISTPYGADYRERADRLIGEVKDIMFNKSLDGGNDLQRL | 120 | | | | | | |
| QY | 121 | LVDDVERLGIDRHFKEIKTALDVVNSYWNKIGCGRESVTTDLNSTALGLRTLHGY | 180 | | | | | | |
| DB | 121 | LVDDVERLGIDRHFKEIKTALDVVNSYWNKIGCGRESVTTDLNSTALGLRTLHGY | 180 | | | | | | |
| QY | 181 | TVSSDVLVNFKDKNGQFSSTANIQIEGEIRGVNLFRASLVAFEGEKVMDAETFTSKYL | 240 | | | | | | |
| DB | 181 | TVSSDVLVNFKDKNGQFSSTANIQIEGEIRGVNLFRASLVAFEGEKVMDAETFTSKYL | 240 | | | | | | |
| QY | 241 | REALQKIPASSILSLERDVLEYGHTNLPRLARNYMDVFGHTKNKVAEKLLELAKL | 300 | | | | | | |
| DB | 241 | REALQKIPASSILSLERDVLEYGHTNLPRLARNYMDVFGHTKNKVAEKLLELAKL | 300 | | | | | | |
| QY | 301 | EFNIFSLQERELKHSRWKDGSGPEMTFCRRHRHVEYYALASCIAPFQHSGLGFTK | 360 | | | | | | |

|||||
Db 301 EFNIFSHLOERELKHVSRWVKDGSPEMTFCRHRHVEYYALASCLAFEPQHSGRIGFTK 360
Qy 361 MSHLITVLDMDYDFGTVDLELEFTATIKRWDPNAMECLPEYMKGYMMVYHTVENMARV 420
Db 361 MSHLITVLDMDYDFGTVDLELEFTATIKRWDPNAMECLPEYMKGYMMVYHTVENMARV 420
Qy 421 AEKQGRDTLNARQAWACFDSYQEAQWIATGYLPTFEETYLENGKVSSAHRPCALQPI 480
Db 421 AEKQGRDTLNARQAWACFDSYQEAQWIATGYLPTFEETYLENGKVSSAHRPCALQPI 480
Qy 481 LTLIDIPFPDHLKEVDFPSKLANDLICILRLRGDTRCYKADRARAGEEASSISCYMKDNP 540
Db 481 LTLIDIPFPDHLKEVDFPSKLANDLICILRLRGDTRCYKADRARAGEEASSISCYMKDNP 540
Qy 541 LTEEDALNHINFMIRDAIRELNWELLKPDNSVPITSKGAFDISRWHGYYRDRDYSFA 600
Db 541 LTEEDALNHINFMIRDAIRELNWELLKPDNSVPITSKGAFDISRWHGYYRDRDYSFA 600
Qy 601 NVEETKSLVMRTVIEBPVL 618
Db 601 NVEETKSLVMRTVIEBPVL 618

RESULT 2
US-09-360-545-4
; Sequence 4, Application US/09360545
; Patent No. 6429014
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B
; APPLICANT: Bohlmann, Jorg
; APPLICANT: Steele, Christopher L
; APPLICANT: Phillips, Michael A
; TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
; FILE REFERENCE: wsu13885
; CURRENT APPLICATION NUMBER: US/09/360,545
; CURRENT FILING DATE: 1999-07-26
; EARLIER APPLICATION NUMBER: 60/052,249
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: PCT/US98/14528
; EARLIER FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Abies grandis
US-09-360-545-4

Query Match 75.5%; Score 2453; DB 4; Length 628;
Best Local Similarity 75.3%; Pred. No. 9.9e-230;
Matches 475; Conservative 59; Mismatches 81; Indels 16; Gaps 6;
Qy 1 MALISITPLVSRSC-----SSSHEIKALRTIPTLGICRPGKSAHSINMCLTSVASTD 55
Db 1 MALVSTAPLASKSCLHKSLSSTHELKALSRITIPALGMSRRGKSITPSISMSSTTVTTDD 60
Qy 56 SVORRVGNVHSNLMWDDFIQSLISTPYGAPDYRERADRLIGEYKDIMFNFKSLLEDG--- 112
Db 61 GVRRRMGDFHSNLMWDDVIQSL-PLAYEEKSYLERAEKLIGEVKN-MFNSMSLEDGELMS 118
Qy 113 --NDLLQRLLLVDDVERLIGIDRHFKKEIKTALDYVNSYWNKEGIGCGRESVTTDLNSTAL 170
Db 119 PLNDLIQRLMIWDSLERLGIHRHFDEIKSALDYVYSYWGENGIGCGRESVTTDLNSTAL 178
Qy 171 GLRTLRHLGTYVSSDVLANVFKDKNGQFSSSTANIQIEGEIRGVNLFRASLVAFPEKXMD 230
Db 179 GLRTLRHLGYPVSSDVFKAFKQNGQFSCSENIQTDEEIRGVNLFRASLIAFPEKXMD 238
Qy 231 EAETFTSKYLREALQKIPASSISLSLEIRDVLEYGWHNTNLPRLAARNYMDVFGQHTKXNA 290
Db 239 EAETFTSKYLREALQKIPVSS-LSRREIGDVLEYGWHNTYLPRLAARNYITQVFGQDTEINTKS 297

Qy 291 ---AEKLLBELAKLEFNIFHSLQERELKHVSRWVKDGSPEMTFCRHRHVEYYALASCLAF 347
Db 298 YVSKSKLLELAKLEFNIFQSLQKRELESVLRWVKESGFPENTFCRHRHVEYYTLASCLAF 357
Qy 348 EPOHSGERLGFETKMSHLITVLDMDYDFGTVDLELEFTATIKRWDPNAMECLPEYMKGVY 407
Db 358 EPOHSGERLGFETKMSHLITVLDMDYDFGTVDLELEFTATMKRWDPSSIDCLPEYMKGVY 417
Qy 408 MMVYHTVENMARVAEKAQGRDTLNARQAWACFDSYQEAQWIATGYLPTFEETYLENGK 467
Db 418 IAVYDTVENMAREAEAAQGRDTLTYAREAWAYIDSYMQEARWIATGYLPSFDEYYENGK 477
Qy 468 VSSAHRPCALQPILTLDIPFPDHLKEVDFPSKLANDLICILRLRGDTRCYKADRARAGEE 527
Db 478 VSGCHRISALQPILTMDIPFPDHLKEVDFPSKLANDLACAILRLRGDTRCYKADRARAGEE 537
Qy 528 ASSISCYMKDNPGLTEEDALNHINFMIRDAIRELNWELLKPDNSVPITSKGAFDISRWH 587
Db 538 ASSISCYMKDNPVSEEDALDHINAMISDVIKGLNWELLKPDINVPISAKGAFDIARAF 597
Qy 588 HHGYRXYRDRGYSFANVETKSLVMTVIEBPVL 618
Db 598 HHGYRXYRDRGYSVANVETKSLVMTVIEBPVL 628

RESULT 3
US-09-398-395A-20
; Sequence 20, Application US/09398395A
; Patent No. 6468772
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64687721, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/398,395A
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Abies grandis
US-09-398-395A-20

Query Match 75.5%; Score 2453; DB 4; Length 628;
Best Local Similarity 75.3%; Pred. No. 9.9e-230;
Matches 475; Conservative 59; Mismatches 81; Indels 16; Gaps 6;
Qy 1 MALISITPLVSRSC-----SSSHEIKALRTIPTLGICRPGKSAHSINMCLTSVASTD 55
Db 1 MALVSTAPLASKSCLHKSLSSTHELKALSRITIPALGMSRRGKSITPSISMSSTTVTTDD 60
Qy 56 SVORRVGNVHSNLMWDDFIQSLISTPYGAPDYRERADRLIGEYKDIMFNFKSLLEDG--- 112
Db 61 GVRRRMGDFHSNLMWDDVIQSL-PLAYEEKSYLERAEKLIGEVKN-MFNSMSLEDGELMS 118
Qy 113 --NDLLQRLLLVDDVERLIGIDRHFKKEIKTALDYVNSYWNKEGIGCGRESVTTDLNSTAL 170
Db 119 PLNDLIQRLMIWDSLERLGIHRHFDEIKSALDYVYSYWGENGIGCGRESVTTDLNSTAL 178
Qy 171 GLRTLRHLGTYVSSDVLANVFKDKNGQFSSSTANIQIEGEIRGVNLFRASLVAFPEKXMD 230
Db 179 GLRTLRHLGYPVSSDVFKAFKQNGQFSCSENIQTDEEIRGVNLFRASLIAFPEKXMD 238
Qy 231 EAETFTSKYLREALQKIPASSISLSLEIRDVLEYGWHNTNLPRLAARNYMDVFGQHTKXNA 290


```
Db 239 EAEFSTKYLKEALOKIPVSS-LSREIGDVLEYGWHNTYLPRLRARNYIOVFQDTEINTKS 297
Qy 291 ---AEKLELAKLEFNI FHSLOERELKHVS RWMKDSGSPMTFCRHRHVEYYALASCI AF 347
Db 298 YVKS KULELAKLEFNI FOSLOKRELES LVRWKESGFPEMTFCRHRHVEYYTLASCI AF 357
Qy 348 EPOHSGFRLGFTKMSHLITVLDMDYDVGTVDELELFTATIKRWDPSAMECLPEYMKGVY 407
Db 358 EPOHSGFRLGFAKTCHLITVLDMDYDVGTVDELELFTATMKRWDPSIDCLPEYMKGVY 417
Qy 408 MMVYHTVNMARVAEKAQGRDTLVNARQAWACFDSYMOEAKWATGYLPTFEEYLENGK 467
Db 418 IAVYDTVNEMAREAEBAQGRDTLVAREAWAAYIDSYMOEARWATGYLPSFDEYENGK 477
Qy 468 VSSAHRPCALQPILTLDIPFPDHILKEVDFPSKNDLICIILRLRGDTRCYKADRARGE 527
Db 478 VSCGHRISALQPILTMDIPFPDHILKEVDFPSKNDLACAILRLRGDTRCYKADRARGE 537
Qy 528 ASSISCYMKDNPGLTEBDALNHINMIRDAIRELNWELKPDNSVPITSKGAFDISR W 587
Db 538 ASSISCYMKDNPGVSEEDALDHINAMISDVIKGLNWELKPDINVPISAKGAFDIARAF 597
Qy 588 HHGYRYRDGYSFANVETKSLVMRTVIEBPVL 618
Db 598 HHGYKRYRDGYSVANVETKSLVTRITLESVPL 628
```

RESULT 4
US-09-887-586A-20
; Sequence 20, Application us/09887586A
; Patent No. 6495354
; GENERAL INFORMATION:

; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64953541, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/887, 586A
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Abies grandis
US-09-887-586A-20

Query Match 75.5%; Score 2453; DB 4; Length 628;
Best Local Similarity 75.3%; Pred. No. 9.9e-230;
Matches 475; Conservative 59; Mismatches 81; Indels 16; Gaps 6;

```
Qy 1 MALSTPLVSRSC-----SSSHEIKALRRTIPTLGICRPGKSAHSINMCLTSVASTD 55
Db 1 MALVSTAPLASKSCLHKSLSISSTHEIKALSRTIPALGMSRGRKSTPSISMSSTTVTDD 60
Qy 56 SVQRRVGNVHNSLWDDDFIQSLISTPYGAPDYRERADRLIGEVDIMFNFKSLDEG--- 112
Db 61 GVRRRMGDFHNSLWDDDVIOQL-PTAYEEKSYLERAEKLI GEVKN-MENSM SLEDGELMS 118
Qy 113 --NDLLQRLLLVDVERLIGIDRHFKKEIKTALDYVNSYWNKEGIGCGRESVVTDLNSTAL 170
Db 119 PLNDLIQRLMIWDSLERLGIHRHFKDEIKSALDYVYSYWGENGIGCGRESVVTDLNSTAL 178
Qy 171 GLRTRLHGTVSSDVLVNFKDKNGQFSSTANIQIEGIRGVNLNFRASLVAFPGEKAMD 230
```

```
Db 179 GLRTRLHGYPVSSDVFKA FKQNGQFS CSENIQTDEIRGVNLNFRASLIAFPGEKIMD 238
Qy 231 EAEFSTKYLREALOKIPASSISLEIRDVLEYGWHNTLPRLRARNYMDVFGQHTKXNA 290
Db 239 EAEFSTKYLKEALOKIPVSS-LSREIGDVLEYGWHNTYLPRLRARNYIOVFQDTEINTKS 297
Qy 291 ---AEKLELAKLEFNI FHSLOERELKHVS RWMKDSGSPMTFCRHRHVEYYALASCI AF 347
Db 298 YVKS KULELAKLEFNI FOSLOKRELES LVRWKESGFPEMTFCRHRHVEYYTLASCI AF 357
Qy 348 EPOHSGFRLGFTKMSHLITVLDMDYDVGTVDELELFTATIKRWDPSAMECLPEYMKGVY 407
Db 358 EPOHSGFRLGFAKTCHLITVLDMDYDVGTVDELELFTATMKRWDPSIDCLPEYMKGVY 417
Qy 408 MMVYHTVNMARVAEKAQGRDTLVNARQAWACFDSYMOEAKWATGYLPTFEEYLENGK 467
Db 418 IAVYDTVNEMAREAEBAQGRDTLVAREAWAAYIDSYMOEARWATGYLPSFDEYENGK 477
Qy 468 VSSAHRPCALQPILTLDIPFPDHILKEVDFPSKNDLICIILRLRGDTRCYKADRARGE 527
Db 478 VSCGHRISALQPILTMDIPFPDHILKEVDFPSKNDLACAILRLRGDTRCYKADRARGE 537
Qy 528 ASSISCYMKDNPGLTEBDALNHINMIRDAIRELNWELKPDNSVPITSKGAFDISR W 587
Db 538 ASSISCYMKDNPGVSEEDALDHINAMISDVIKGLNWELKPDINVPISAKGAFDIARAF 597
Qy 588 HHGYRYRDGYSFANVETKSLVMRTVIEBPVL 618
Db 598 HHGYKRYRDGYSVANVETKSLVTRITLESVPL 628
```

RESULT 5
US-09-895-752-20
; Sequence 20, Application US/09895752
; Patent No. 6559297
; GENERAL INFORMATION:

; APPLICANT: Chappell, Joseph
; APPLICANT: No. 65592971, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/895,752
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Abies grandis
US-09-895-752-20

Query Match 75.5%; Score 2453; DB 4; Length 628;
Best Local Similarity 75.3%; Pred. No. 9.9e-230;
Matches 475; Conservative 59; Mismatches 81; Indels 16; Gaps 6;

```
Qy 1 MALSTPLVSRSC-----SSSHEIKALRRTIPTLGICRPGKSAHSINMCLTSVASTD 55
Db 1 MALVSTAPLASKSCLHKSLSISSTHEIKALSRTIPALGMSRGRKSTPSISMSSTTVTDD 60
Qy 56 SVQRRVGNVHNSLWDDDFIQSLISTPYGAPDYRERADRLIGEVDIMFNFKSLDEG--- 112
Db 61 GVRRRMGDFHNSLWDDDVIOQL-PTAYEEKSYLERAEKLI GEVKN-MENSM SLEDGELMS 118
Qy 113 --NDLLQRLLLVDVERLIGIDRHFKKEIKTALDYVNSYWNKEGIGCGRESVVTDLNSTAL 170
```


Db 1 MALVISISPLASKSCLRKSLISSIHEHKPPYRTIPNLGMRRGKSVTPSMSISLATAAPDD 60
Qy 56 SVORRVGNHNSNLMDDDFIQSLISTPYGAPDYRERADRLIGEVDIMFNKSLJEDG--- 112
Db 61 GVGRRIGDYHSNIWDDDFIQSL-STPYGEPSTYQERAERLIVEVKI-FNSMYLDDGRLMS 118
Qy 113 --NDLLQRLLLVDDVERLIGIDRHFKKEIKTALDYVNSYWNKEGIGCGRESVTDLNSTAL 170
Db 119 SFNDLMQRLMIWDSVERLGIARHFKEIETSDLDYFRYWEENGIGCGRDSIVTDLNSTAL 178
Qy 171 GLRTRLHGTYVSSDVLNVFKDKNGQFSSSTANIQIEGEIRGVNLFRASLVAFPGEKVM 230
Db 179 GFRTRLHGTYVSPVLKAFQDQNGQFVCSPG-QTEGEIRSVLNLFRASLIAFPGEKVM 237
Qy 231 EAETSTKYLRALQKIPASSILSLEIRDVLEYGWHNTNLPRLAARNYMDVFGQHTK---N 287
Db 238 EAEIFSTRYLKEALQKIPVSA-LSQEIKFVMEYGWHNTNLPRLAARNYIDTLEKDTSAWLN 296
Qy 288 KNAAEKLELAKLEFNIHSLQERELKHVSRWKDSGSPEMTFGRHVEYYALASCIAP 347
Db 297 KNAGKLELAKLEFNIHSLQERELKHVSRWKDSGSPEMTFGRHVEYYALASCIAP 356
Qy 348 EPOHSGFRIGFTKMSHLITVLDWMYDVGTVDELELFTATIKRWDPSAMECLPEYMKGVY 407
Db 357 DPKHSAFRLGFAKMHVTLVLDIYDTFTGIDELFTSAIKRWNSSEIEHLPEYMKGVY 416
Qy 408 MMVYHTVNEMARVAEKAQGRDTLNYARQAMEACFDSYMOEAKWIATGYLPTFEEYLENGK 467
Db 417 MNVFEYVNELTREAEKTQGRNTLNYVRKAMEAYFDSYMEAKWISNGYLPMEFEYHENGK 476
Qy 468 VSSAHRPCALQPIITLDIPFPDHIKEVDFPSKLNLDLCIILRLRGDTRCYKADRRGEE 527
Db 477 VSSAYRVATLQPIITLNAWLPDYILKIGIDFSPRFNDLASSFLRLRGDTRCYKADRRGEE 536
Qy 528 ASSISCYMKDNPGLTEEDALNHINFMIRDAIRELNMWELKPDNSVPITSKKHAFDISRW 587
Db 537 ASSISCYMKDNPGLTEEDALNHINAVNDI IKELNMWELLRSDNIPMLAKKHAFDITRAL 596
Qy 588 HHGYRYRDGYSPANVETKSLVMRTVIE 614
Db 597 HHLTYIRDFGSVANKETKCLVMETLLE 623

RESULT 10
US-09-398-395A-30
; Sequence 30, Application US/09398395A
; Patent No. 6468772
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64687721, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/398,395A
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Abies grandis
US-09-398-395A-30

Query Match 67.7%; Score 2200.5; DB 4; Length 627;
Best Local Similarity 68.1%; Pred. No. 3.8e-205;

Matches 427; Conservative 77; Mismatches 106; Indels 17; Gaps 7;
Qy 1 MALISITPLVSRCL-----SSSHEIKALRRTIPTLGICRPGKSVAHSIMCLTSVASTD 55
Db 1 MALVISISPLASKSCLRKSLISSIHEHKPPYRTIPNLGMRRGKSVTPSMSISLATAAPDD 60
Qy 56 SVORRVGNHNSNLMDDDFIQSLISTPYGAPDYRERADRLIGEVDIMFNKSLJEDG--- 112
Db 61 GVGRRIGDYHSNIWDDDFIQSL-STPYGEPSTYQERAERLIVEVKI-FNSMYLDDGRLMS 118
Qy 113 --NDLLQRLLLVDDVERLIGIDRHFKKEIKTALDYVNSYWNKEGIGCGRESVTDLNSTAL 170
Db 119 SFNDLMQRLMIWDSVERLGIARHFKEIETSDLDYFRYWEENGIGCGRDSIVTDLNSTAL 178
Qy 171 GLRTRLHGTYVSSDVLNVFKDKNGQFSSSTANIQIEGEIRGVNLFRASLVAFPGEKVM 230
Db 179 GFRTRLHGTYVSPVLKAFQDQNGQFVCSPG-QTEGEIRSVLNLFRASLIAFPGEKVM 237
Qy 231 EAETSTKYLRALQKIPASSILSLEIRDVLEYGWHNTNLPRLAARNYMDVFGQHTK---N 287
Db 238 EAEIFSTRYLKEALQKIPVSA-LSQEIKFVMEYGWHNTNLPRLAARNYIDTLEKDTSAWLN 296
Qy 288 KNAAEKLELAKLEFNIHSLQERELKHVSRWKDSGSPEMTFGRHVEYYALASCIAP 347
Db 297 KNAGKLELAKLEFNIHSLQERELKHVSRWKDSGSPEMTFGRHVEYYALASCIAP 356
Qy 348 EPOHSGFRIGFTKMSHLITVLDWMYDVGTVDELELFTATIKRWDPSAMECLPEYMKGVY 407
Db 357 DPKHSAFRLGFAKMHVTLVLDIYDTFTGIDELFTSAIKRWNSSEIEHLPEYMKGVY 416
Qy 408 MMVYHTVNEMARVAEKAQGRDTLNYARQAMEACFDSYMOEAKWIATGYLPTFEEYLENGK 467
Db 417 MNVFEYVNELTREAEKTQGRNTLNYVRKAMEAYFDSYMEAKWISNGYLPMEFEYHENGK 476
Qy 468 VSSAHRPCALQPIITLDIPFPDHIKEVDFPSKLNLDLCIILRLRGDTRCYKADRRGEE 527
Db 477 VSSAYRVATLQPIITLNAWLPDYILKIGIDFSPRFNDLASSFLRLRGDTRCYKADRRGEE 536
Qy 528 ASSISCYMKDNPGLTEEDALNHINFMIRDAIRELNMWELKPDNSVPITSKKHAFDISRW 587
Db 537 ASSISCYMKDNPGLTEEDALNHINAVNDI IKELNMWELLRSDNIPMLAKKHAFDITRAL 596
Qy 588 HHGYRYRDGYSPANVETKSLVMRTVIE 614
Db 597 HHLTYIRDFGSVANKETKCLVMETLLE 623

RESULT 11
US-09-887-586A-30
; Sequence 30, Application US/09887586A
; Patent No. 6495354
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64953541, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/887,586A
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Abies grandis
US-09-887-586A-30

; CURRENT FILING DATE: 1999-07-26
; EARLIER APPLICATION NUMBER: 60/052,249
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: PCT/US98/14528
; EARLIER FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Abies grandis
; US-09-360-545-32

Query Match 67.6%; Score 2197.5; DB 4; Length 627;
Best Local Similarity 68.1%; Pred. No. 7.5e-205;
Matches 427; Conservative 77; Mismatches 106; Indels 17; Gaps 7;

QY 1 MALSTITPLVSRCL-----SSSHEIKALRTIPTLGICRPGKSVASHINMCLTSVASTD 55
Db 1 MALVISISPLASKSCLRKSLISSIHEHKPPYRTIPNLGMRRGKSVTPSMSISLATAPDD 60
QY 56 SVQRRVGNVHNSLWDDDFIQSLISTPYGAPDYRERADRLIGEVDIMFNFKSLBDGG--- 112
Db 61 GVQRRIGDYHSNIWDDDFIQSL-STHYGEPSPYQERAERLIVEVKI-FNSMYLDDGRLMS 118
QY 113 --NDLLQRLLLVDYDVERLGIDRHFKKIKTALDYVNSYWNKGIQGGRESVTDLNSTAL 170
Db 119 SFNDLMQRLWIVDSVERLGIAHFKEITSLADYVFRYWEENGICGRDSIVTDLNSTAL 178
QY 171 GLRTLRHGYTVSSDVLNVFKDKNGQFSSSTANIQIEGEIRGYLNLFRASLVAFPGKXMD 230
Db 179 GFRTLRHGYTVSPVLKAFQDQNGQFVCSPG-QTEGEIRSVNLVYRASLIAFPGEKXME 237
QY 231 EAETPSTKYLRALQKIPASSISLSLRDYLEYGMHTNLPRLKARNYMDVFGQHTK--N 287
Db 238 EABISTRYLKEALQKIPVSA-LSQETIKFVMEYGMHTNLPRLKARNYIDTLEKDTSAMLN 296
QY 288 KNAEKLLELAKLEFNI FHSLOERELKHSRWKWDGSGPEMTFCRRHVEYYALASCI AF 347
Db 297 KNAGKLELAKLEFNI FNSLQCKELQYLLRWKESDLPKLTFAHRHVEFYTLASCI AI 356
QY 348 EPOHSGFRLGFTKMSHLITVLDDMYDVGTVDELELFTATIKRWDSAMECLPEYMKGVY 407
Db 357 DPKHSAFRLGFAKCHLVTLDDIYPTFGTIDELFTSAIKRWNSSEIHLPEYMKCVY 416
QY 408 MMVYHTVNEMARVAEKAQGRDTLNVQAWEACFDSYMOEAKWIAATGYLPTFEEYLENGK 467
Db 417 MVMFETVNELTREAEKTOGRNTLVYKAWAYFDSYMEBAKWISNGYLPTEEEYHENGK 476
QY 468 VSSAHRPCALQPILTLDIPFPDHLKEVDPPSKLNDLICIIILRGDTRCYKADRARGE 527
Db 477 VSSAYRYATLQPILTNLAMLPDYILKGIDPSPRFNDLASSFLRLRGDTRCYKADRGE 536
QY 528 ASSISCTYMKDNPGLTEDALNHINEMIRDAIRELNWELLKPDNSVPITSSKHAFDISRW 587
Db 537 ASCISCTYMKDNPGSTEEDALNHINAMNDI IKELNWELLRSNDNIPMLAKKHAFDITRAL 596
QY 588 HHGYRRYRGYSFANVETKSLVMRTVIE 614
Db 597 HHLXYIRDGFSVANKETKCLVMETLLE 623

Search completed: July 23, 2004, 09:04:45
Job time : 21 secs

This Page Blank (uspto)

| | | | | | | | | | | |
|----|-----|------------------------|--------------------|----------------|-----------|----------|-------------|--------|---------|-----|
| Qy | 121 | LVDDVERLGIDRHFKEIKTALD | VNSY | WNEKIGCG | RESV | VDL | N | TALGLR | TLRLHG | 180 |
| | | | | | | | | | | |
| Db | 121 | LVDDVERLGIDRHFKEIKTALD | VNSY | WNEKIGCG | RESV | VDL | N | TALGLR | TLRLHG | 180 |
| | | | | | | | | | | |
| Qy | 181 | TVSSDVLNVFKDKNGQFS | TANIQIEGEIR | GVNLFRASL | VAFPG | EKMDEA | ET | FT | ST | 240 |
| | | | | | | | | | | |
| Db | 181 | TVSSDVLNVFKDKNGQFS | TANIQIEGEIR | GVNLFRASL | VAFPG | EKMDEA | ET | FT | ST | 240 |
| | | | | | | | | | | |
| Qy | 241 | REALQKIPASSILSLEIR | DVLEYGWHTNLPRLEARN | MDVFQ | HTKNKNAE | KLLE | IAKL | | | 300 |
| | | | | | | | | | | |
| Db | 241 | REALQKIPASSILSLEIR | DVLEYGWHTNLPRLEARN | MDVFQ | HTKNKNAE | KLLE | IAKL | | | 300 |
| | | | | | | | | | | |
| Qy | 301 | EFNIFHSLQERELKHS | RWVKD | SGSP | EMTFCRHRH | VEYYALAS | CIAF | EQHSG | FRLG | 360 |
| | | | | | | | | | | |
| Db | 301 | EFNIFHSLQERELKHS | RWVKD | SGSP | EMTFCRHRH | VEYYALAS | CIAF | EQHSG | FRLG | 360 |
| | | | | | | | | | | |
| Qy | 361 | MSHLITVLDDMYDVF | GTVDELELTATIKR | WDPSAMECLPEY | MKGVMY | YHTV | NEMARV | | | 420 |
| | | | | | | | | | | |
| Db | 361 | MSHLITVLDDMYDVF | GTVDELELTATIKR | WDPSAMECLPEY | MKGVMY | YHTV | NEMARV | | | 420 |
| | | | | | | | | | | |
| Qy | 421 | AEKAQGRDTLNYARQ | WEACFDSY | MOEAKMIATGYLPT | FEY | LENGKVS | SAHRPCALQPI | | | 480 |
| | | | | | | | | | | |
| Db | 421 | AEKAQGRDTLNYARQ | WEACFDSY | MOEAKMIATGYLPT | FEY | LENGKVS | SAHRPCALQPI | | | 480 |
| | | | | | | | | | | |
| Qy | 481 | LTLDIPFPDHI | LKEVDFPSK | NDLICILRLRG | DTRCYKADR | ARGEASIS | ICYMKD | NP | | 540 |
| | | | | | | | | | | |
| Db | 481 | LTLDIPFPDHI | LKEVDFPSK | NDLICILRLRG | DTRCYKADR | ARGEASIS | ICYMKD | NP | | 540 |
| | | | | | | | | | | |
| Qy | 541 | LTEEDALNHINFMIR | DAIREL | NWELLKPDNS | VPIT | SKGAFDIS | RVWHG | GYR | RDGYSFA | 600 |
| | | | | | | | | | | |
| Db | 541 | LTEEDALNHINFMIR | DAIREL | NWELLKPDNS | VPIT | SKGAFDIS | RVWHG | GYR | RDGYSFA | 600 |
| | | | | | | | | | | |
| Qy | 601 | NVETKSLVMRTVIE | VPPL | | | | | | | 618 |
| | | | | | | | | | | |
| Db | 601 | NVETKSLVMRTVIE | VPPL | | | | | | | 618 |
| | | | | | | | | | | |

```

RESULT 2
US-09-887-586A-20
; Sequence 20, Application US/09887586A
; Patent No. US20020094556A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20020094556A1, Joseph P
; APPLICANT: Stark, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/887,586A
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Abies grandis
US-09-887-586A-20

```

| | | | | |
|---------------------------|-------|---------------------|------------|-------------|
| Query Match | 75.5% | Score 2453; | DB 9; | Length 628; |
| Best Local Similarity | 75.3% | Pred. No. 5.9e-226; | | |
| Matches 475; Conservative | 59; | Mismatches 81; | Indels 16; | Gaps 6; |

```
Qy      1 MALLSITPLVSRCL-----SSSHEIKALRRTIPTIGICRPGKSVAH SINCLTSVASTD 55
      |||:| || |:||| |||:|:||| ||| |||:| |||:| |||:|
Db      1 MALVSTAPLASKSCHLKSLSISTHEIKALSRITPALGMSRRGKSITPISMSITVTTDD 60
```

| | | | |
|----|-----|--|-----|
| OY | 56 | SVÖRRVGNTHSNLWDDDFIÖSLISTPYGAPDYRERADRLIGEYVDIMFNFKSLEDGG--- | 112 |
| Db | 61 | GVRRRMGDPFHSNLWDVVIOQL-PTAYEBSXYLERAEKLIGEVKN-MENSMILEDGELMS | 118 |
| OY | 113 | --NDLLÖRLLLVDVERLGIDHFEKKEIKTALDYNNSYWNEKGJCGGRESVTDLNSTAL | 170 |
| Db | 119 | PLNDLIÖRLMIWDSLERLGIRHFKEIKSALDVYSYWGENGJCGGRESVTDLNSTAL | 178 |
| OY | 171 | GLRTLRLHGTVSSDVLVNFEKDNGQFSSTANIÖIEGEIRGVTLNFRASLVAFPGEKMD | 230 |
| Db | 179 | GLRTLRLHGVPVSSDVFAKFGONGQFSCENIQTDEIRGVTLNFRASLIAFPGEKIMD | 238 |
| OY | 231 | EAFSTSTKYLRREALÖKIIPASSILSLEIRDVLEYGWHTNLPRLPEARNYMVFQÖHTKNKA | 290 |
| Db | 239 | EAEIFSTKYLKREALÖKIPVSS-ISREIGDVLEYGWHTYLPRLPEARNTYÖVFGÖDTENTKS | 297 |
| OY | 291 | ---AEKLLELAKEFNIFHSIQERELKHVSRWMKDGSPEMTFCRHRYEYYALASCIAF | 347 |
| Db | 298 | YVSKKLLELAKEFNIFÖSLÖKRELDSLVRWWKESGFPEMTFCRHRYEYYTLASCIAF | 357 |
| OY | 348 | EPÖHSGFRLGFTKMSHLITVLDMYDVFGTVDELFLFTATIKRWDBSAMECLEPEYMKGVY | 407 |
| Db | 358 | EPÖHSGFRLGFAKTCHLITVLDMYDTFGTVDELELFTATMKRWBPSSIDLPEYMKGVY | 417 |
| OY | 408 | MMVYHTVNEMARVAEKAQGDRTLNYARQAWBEACFDPSYMÖEAKWIATGYLPTFEELYENGX | 467 |
| Db | 418 | IAVYDTVNEMAREABEAQGDRTLTAREABEAYIDSYMÖEARWIATGYLPSFDEYYENGX | 477 |
| OY | 468 | VSSAHRPCALOPILTLDIPPEDHILKEVDFPSKLANDLICILRLRGPTRCYKADRARGEE | 527 |
| Db | 478 | VSCGRISALÖPILTMDIPEDHILKEVDFPSKLANDLACAILRLRGPTRCYKADRARGEE | 537 |
| OY | 528 | ASSISCYMKDNPGLTEEDLNNHINFMIRDAIRELNMWELLKPDNSVPLTSKGAFDISRVM | 587 |
| Db | 538 | ASSISCYMKDNPGVSEEDLADHINAMISDVIKGLNMWELLKPDINVPISAKKHAFDIARAF | 597 |
| OY | 588 | HHGYYRDGYSFANVETKSLVMRTVIEPVPL | 618 |
| Db | 598 | HYGYKYRDGYSVANVETKSLVTRTLLESVPL | 628 |

```

RESULT 3
US-09-903-012-20
; Sequence 20, Application US/09903012
; Patent No. US20020094557A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20020094557A1, Joseph F.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903,012
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for windows Version 3.0
; SEQ ID NO 20
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Abies grandis
US-09-903-012-20

```

| | | | | |
|-----------------------|------------------|---------------------|------------|-------------|
| Query Match | 75.5%; | Score 2453; | DB 9; | Length 628; |
| Best Local Similarity | 75.3%; | Pred. No. 5.9e-226; | | |
| Matches 475; | Conservative 59; | Mismatches 81; | Indels 16; | Gaps 6; |

```
Qy 1 MALSTITPLVSRCL-----SSSHEIKALRRTIPTLGICRPGKSVASHINMCLTSVASTD 55
Db 1 MALVSTAPLASKSCLHKSLSISSTHELKALSRITIPALGMSRGRKSTIPTSISMSSTTVTDD 60
Qy 56 SVQRRVGNVHNSLWDDDFIQSLISTPYGADYRERADRLIGEVDKIMFNFKSLEDGG--- 112
Db 61 GVRRRMGDFHNSLWDDDVIOQL-PTAYEKSXYLERAEKLIGEVDK-MENSMLEDGELMS 118
Qy 113 --NDLQRLLLVDVERLIGIDRHFKKEIKTALDVNSYWNKGIICGGRSVTDLNSTAL 170
Db 119 PLNDLIQRLMIVDSLERLGIHRHFKEIKSALDYVYSYWGENGICGGRSVTDLNSTAL 178
Qy 171 GLRTLRLHGYTVSSDVLNVFKDKNGQFSSSTANIQIEGEIRGVNLFRASLVAFPGEKVD 230
Db 179 GLRTLRLHGYTVSSDVFKAFAKQNGQFSSCENIQTDEIRGVNLFRASLIAFPGEKIMD 238
Qy 231 EAETFTKYLRREALQKIPASSILSLERDYLEYGMHTNLPRLAARNYMDVFGQHTKNKA 290
Db 239 EAETFTKYLRREALQKIPVSS-LSREIGDYLEYGMHTYLPRLAARNYIQVFGQDTEHTKS 297
Qy 291 --AEKLELAKLEFNIHSLQERELKHSRWKSDSGSPMTFCRHRHVEYYALASCIAP 347
Db 298 YVKSCKLLELAKLEFNIHSLQERELSLVWVKESGFPMTFCRHRHVEYYTLASCIAP 357
Qy 348 EPQHSGRFGFTKMSHLITVLDMDYDVGTVDELELFTATIKRWDPSAMECLPEYMKGVY 407
Db 358 EPQHSGRFGFAKTCHLTITVLDMDYDFTGTVDELELFTATMKRWDPSIDCLPEYMKGVY 417
Qy 408 MMVYHTVNEARVAEKAQGRDTLNYARQAWAECFDSYMOEAKWIATGYLPTFEYLENGK 467
Db 418 IAVYDTVNEARAEAEQAQGRDTLTAREAMEAYIDSYMOEARWIAATGYLPSFDEYENGK 477
Qy 468 VSSAHRPCALQPIILTDIPFPDHIKEVDPPSKLNDLICIILRLRGDTRCYKADRAGEE 527
Db 478 VSCGHRISALQPIILTMDIPFPDHIKEVDPPSKLNDLACAILRLRGDTRCYKADRAGEE 537
Qy 528 ASSISCYMKDNPGLTEEDALNHINFMIRDAIRELNWELLKPDNSVPITSKKHAFDISRVA 587
Db 538 ASSISCYMKDNPVSEEDALDHINAMISDVIKGLNWELLKPDINVPISAKKGAFDIARAF 597
Qy 588 HHGYYRDRGYSFANVETKSLVMRTVIEPVPL 618
Db 598 HYGKYYRDRGYSVANVETKSLVTRTLLESVPL 628
```

RESULT 4
US-09-900-797-20

```
; Sequence 20, Application US/09900797
; Publication No. US20030087406A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20030087406A1, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/900,797
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for windows Version 3.0
; SEQ ID NO 20
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Abies grandis
; US-09-900-797-20
```

Query Match 75.5%; Score 2453; DB 10; Length 628;
Best Local Similarity 75.3%; Pred. No. 5.9e-226;
Matches 475; Conservative 59; Mismatches 81; Indels 16; Gaps 6;

```
Qy 1 MALSTITPLVSRCL-----SSSHEIKALRRTIPTLGICRPGKSVASHINMCLTSVASTD 55
Db 1 MALVSTAPLASKSCLHKSLSISSTHELKALSRITIPALGMSRGRKSTIPTSISMSSTTVTDD 60
Qy 56 SVQRRVGNVHNSLWDDDFIQSLISTPYGADYRERADRLIGEVDKIMFNFKSLEDGG--- 112
Db 61 GVRRRMGDFHNSLWDDDVIOQL-PTAYEKSXYLERAEKLIGEVDK-MENSMLEDGELMS 118
Qy 113 --NDLQRLLLVDVERLIGIDRHFKKEIKTALDVNSYWNKGIICGGRSVTDLNSTAL 170
Db 119 PLNDLIQRLMIVDSLERLGIHRHFKEIKSALDYVYSYWGENGICGGRSVTDLNSTAL 178
Qy 171 GLRTLRLHGYTVSSDVLNVFKDKNGQFSSSTANIQIEGEIRGVNLFRASLVAFPGEKVD 230
Db 179 GLRTLRLHGYTVSSDVFKAFAKQNGQFSSCENIQTDEIRGVNLFRASLIAFPGEKIMD 238
Qy 231 EAETFTKYLRREALQKIPASSILSLERDYLEYGMHTNLPRLAARNYMDVFGQHTKNKA 290
Db 239 EAETFTKYLRREALQKIPVSS-LSREIGDYLEYGMHTYLPRLAARNYIQVFGQDTEHTKS 297
Qy 291 --AEKLELAKLEFNIHSLQERELKHSRWKSDSGSPMTFCRHRHVEYYALASCIAP 347
Db 298 YVKSCKLLELAKLEFNIHSLQERELSLVWVKESGFPMTFCRHRHVEYYTLASCIAP 357
Qy 348 EPQHSGRFGFTKMSHLITVLDMDYDVGTVDELELFTATIKRWDPSAMECLPEYMKGVY 407
Db 358 EPQHSGRFGFAKTCHLTITVLDMDYDFTGTVDELELFTATMKRWDPSIDCLPEYMKGVY 417
Qy 408 MMVYHTVNEARVAEKAQGRDTLNYARQAWAECFDSYMOEAKWIATGYLPTFEYLENGK 467
Db 418 IAVYDTVNEARAEAEQAQGRDTLTAREAMEAYIDSYMOEARWIAATGYLPSFDEYENGK 477
Qy 468 VSSAHRPCALQPIILTDIPFPDHIKEVDPPSKLNDLICIILRLRGDTRCYKADRAGEE 527
Db 478 VSCGHRISALQPIILTMDIPFPDHIKEVDPPSKLNDLACAILRLRGDTRCYKADRAGEE 537
Qy 528 ASSISCYMKDNPGLTEEDALNHINFMIRDAIRELNWELLKPDNSVPITSKKHAFDISRVA 587
Db 538 ASSISCYMKDNPVSEEDALDHINAMISDVIKGLNWELLKPDINVPISAKKGAFDIARAF 597
Qy 588 HHGYYRDRGYSFANVETKSLVMRTVIEPVPL 618
Db 598 HYGKYYRDRGYSVANVETKSLVTRTLLESVPL 628
```

RESULT 5

```
US-09-893-820-20
; Sequence 20, Application US/09893820
; Publication No. US20040053386A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20040053386A1, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/893,820
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US/09/398,395A
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for windows Version 3.0
; SEQ ID NO 20
```

```

; LENGTH: 628
; TYPE: PRT
; ORGANISM: Abies grandis
US-09-893-820-20

```

| | | | | |
|---------------------------|-------|---------------------|------------|-------------|
| Query Match | 75.5% | Score 2453; | DB 12; | length 628; |
| Best Local Similarity | 75.3% | Pred. No. 5.9e-226; | | |
| Matches 475; Conservative | 59; | Mismatches 81; | Indels 16; | Gaps 6; |

| | | | | | | | | | | |
|----|-----|---------------|------------------------------|--------------------|-----------------|-------------|------------|-------------|---------|-----|
| QY | 1 | MALLSTPLVSRSC | -----SSSHEIKALRRTIPTLGI | CRPGKSAVH | SINMCLTS | VASTD | 55 | | | |
| Db | 1 | MALVSTAPLASKS | CLHKSLSISSTHEIKALSRITIPALGMS | RRGKSITP | PSISMSST | TVVTD | 60 | | | |
| QY | 56 | SVQRRVGNH | SNLWDDDFIOQLISTPYGADY | RRERADRLIGE | VKOIMFNEK | SIEDG | 112 | | | |
| Db | 61 | GVRRRMGDF | HSNLWDDDVIOQL | -PTAYEEKSYLERAEKLI | GEVKN-MFNSMSLED | GELMS | 118 | | | |
| QY | 113 | --NDLLQRL | LLVDDVERLGIDRHFKKEIKTAL | DVNSYMN | KEGIGCGRES | VTDLNSTAL | 170 | | | |
| Db | 119 | PLNDLIQRL | WIVDSLERTGHRHFKEIKSAL | DVYSYNGEN | GICGRES | VTDLNSTAL | 178 | | | |
| QY | 171 | GLRTLRLHGY | TSSDVLNVEFKDKNGOFS | TANIQIEGEIR | GVNLFRASL | VAFGEKMD | 230 | | | |
| Db | 179 | GLRTLRLHGY | PVSSDVFKAFKGQNGOFS | CSENIQTDEIR | GVNLFRASL | VAFGEKIMD | 238 | | | |
| QY | 231 | EAETESTKY | LREALOKIPASSILSLEIR | DVEYGWHTNLPRLEARN | MYDVFQGH | TAKNA | 290 | | | |
| Db | 239 | EAEIFSTKY | LKEALOKIPVSS-LSREIG | DVEYGMHTYLPRL | EARNYIQVFGQ | TENTKS | 297 | | | |
| QY | 291 | ---AEKLL | ELAKLEFNIFHSLQERELKH | SRMWKDSGSP | EMTF | CRHRHVEY | ALLASCI | 347 | | |
| Db | 298 | YKSKKLL | ELAKLEFNIFQSLQKRE | LESVRMWKESG | FPEMTFCRHRH | VEY | YLLASCI | 357 | | |
| QY | 348 | EPQHS | GRLGFTKMSHLITVL | DMYDVEGT | VELELFTATI | KRWDPSAME | CLEPEYKGVY | 407 | | |
| Db | 358 | EPQHS | GRLGFAKTCHLITVL | DMYDFTG | YDELELFTATM | KRWDPSIDC | LEPEYKGVY | 417 | | |
| QY | 408 | MMVYHTV | NEMARVAEKAQGRDTL | NVARQAMEAC | FDSYMOEAK | MIATGYLPT | FEEYLENGK | 467 | | |
| Db | 418 | IAYVDTV | NEMAREAEAEQGRDTL | TYAREAMEAY | IDSYMOE | ARMIATGYLPS | FDEYENGK | 477 | | |
| QY | 468 | VSSAHR | PCALQPI | LTDIPFPDHILKE | YDFPSK | LNDLICII | LRLRGDT | RCYKADRARGE | 527 | |
| Db | 478 | VSCGHR | ISALQPI | LTM DIPFPDHILKE | YDFPSK | LNDLACAILRL | RGDT | RCYKADRARGE | 537 | |
| QY | 528 | ASSIS | CYMKDNPGLT | EBDALNHINFM | IRDAIRELN | WELLPK | PNDSVP | ITSKGA | FDISRWV | 587 |
| Db | 538 | ASSIS | CYMKDNPGV | SEEDALDHINAM | ISDVIKGLN | WELLPK | PDINVP | ISAKGA | FDIARAF | 597 |
| QY | 588 | HGGRY | RDGYSFAN | VE | TKSLVMRT | VE | PVPL | 618 | | |
| Db | 598 | HYGYK | RDGYSVAN | VE | TKSLVTR | IL | ESVPL | 628 | | |

RESULT 6
US-10-041-007-22

```

: Sequence 22, Application US/10041007
: Publication No. US20020164736A1
: GENERAL INFORMATION:
: APPLICANT: Matsuda, Seichi P.T.
: APPLICANT: Schepmann, Hala G
: TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase
: FILE REFERENCE: P02081US1
: CURRENT APPLICATION NUMBER: US/10/041,007
: CURRENT FILING DATE: 2002-01-07
: PRIOR APPLICATION NUMBER: US 60/259,881
: PRIOR FILING DATE: 2001-01-05
: NUMBER OF SEO ID NOS: 41
: SOFTWARE: PatentIn version 3.1
: SEO ID NO 22
: LENGTH: 628
: TYPE: PRT
: ORGANISM: Abies grandis
:

```

US-10-041-007-22

| | | | | |
|---------------------------|-------|---------------------|------------|-------------|
| Query Match | 75.5% | Score 2453; | DB 13; | Length 628; |
| Best Local Similarity | 75.3% | Pred. No. 5.9e-226; | | |
| Matches 475; Conservative | 59; | Mismatches 81; | Indels 16; | Gaps 6; |

```

QY 1 MALLSTPLVSRSC-----SSSHEIKALRRTIPTLGICRPGKSAVHSINMCLTSVASTD 55
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 1 MALVSTAPLASKSCLHKSLISSTHELKALSRITPALGMSRRGKSITPISIMSSITTVTDD 60
QY 56 SVQRVGNVHNSLWDDDFIQSLISTPYGAPDYRERADRLLIGEVDIMFNFKSLDGG--- 112
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 61 GYRRRMGDFHNSLWDDDDVIQSL-PTAYEEKSYLERAekliGEVKN-MFNSMSLEDGELMS 118
QY 113 --NDLLQRLLLVDDVERLIGIDRHEKKEIKTALDYVNSYWNKGI GCGRESVTDLNSTAL 170
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 119 PLNDLIQRLMIVDSLRLGIHRHFEDEIKSALDYVYSYWGNGICCGRESVTDLNSTAL 178
QY 171 GURLRLHGYTVSSDVLVNFKDKNGOFSSSTANIQIEGEIRGVNLFRASLVAFPEGEKMD 230
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 179 GURLRLHGYPVSSDVFKAFKQNGQFSCSENIQTDEIRGVNLFRASLIAFPEGEKIMD 238
QY 231 EAETESTKYLREALOKIPASSILSLEIRDVLEYGWHNTNLPRLRNRYMDVFGOHTKNKNA 290
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 239 EAEIFSTKYLKEALOKIPVSS-LsREIGDVLLEYGWHNTYLPRLRNRYIQVFQODTENTKS 297
QY 291 ---AEKLLELAKLEFNIFHSLQERELKHVSRRWKDGSPEMTFCRHRHVEYYALASCI AF 347
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 298 YKSKKLLELAKLEFNIFQSLQKRELESLVRWKESGFPMTFCRHRHVEYYTLASCI AF 357
QY 348 EPQHSQFRLGFTKMSHLITVLDWMYDVFQTVDELELFTATIKRWDPSAMECLPEYMKGVY 407
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 358 EPQHSQFRLGFAKTCHLTITVLDWMYDTFGTVDELELFTATMKRWDPSIDCLPEYMKGVY 417
QY 408 MNVYHTVNEMARVAEKAQGRDITLYARQAMEACFPDSYMOEAKWIATGYLPTFEYENLGK 467
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 418 IAVYDTVNEMAREAEAAQGRDITLYAREAMEAYIDSYMOEARWIAIGYLPSEFDEYENLGK 477
QY 468 VSSAHRPCALQPIITLDIPFPDHLKEVDFPSKLNLDICIILRLRGDTRCYKADRARGE 527
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 478 VSCGHRISALQPIITMDIPFPDHLKEVDFPSKLNLDIACAIIRLRGDTRCYKADRARGE 537
QY 528 ASSISCYMKDNPGLTTEEDALNHINEMIRDAIRELNWELLKPDNSVPITSKGAFDISRVM 587
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 538 ASSISCYMKDNPGVSEEDALDHINAMISDVIKGLNWELLKPDINVPISAKGAFDIARAF 597
QY 588 HHGCRYRDGYSFANVETKSLVMRTVIEPVPL 618
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 598 HYGYKYRDGYSVANVETKSLVTRTILLESVPL 628

```

RESULT 7
US-10-025-145A-4

```

: Sequence 4, Application US/10025145A
: Publication No. US20030175861A1
:
: GENERAL INFORMATION:
:
: APPLICANT: Croteau, Rodney B.
: APPLICANT: Bohlmann, Joerg
: APPLICANT: Steele, Christopher L.
: APPLICANT: Phillips, Michael A.
: TITLE OF INVENTION: Monoterpene Synthases from Grand Fir (Abies Grandis)
: FILE REFERENCE: WSUR118414
: CURRENT APPLICATION NUMBER: US/10/025,145A
: CURRENT FILING DATE: 2002-06-28
: PRIOR APPLICATION NUMBER: US 09/360,545
: PRIOR FILING DATE: 1999-07-26
: PRIOR APPLICATION NUMBER: PCT/US98/14528
: PRIOR FILING DATE: 1998-07-10
: PRIOR APPLICATION NUMBER: US 60/052,249
: PRIOR FILING DATE: 1997-07-11
: NUMBER OF SEQ ID NOS: 107
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 4

```


; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for windows Version 3.0
; SEQ ID NO 30
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Abies grandis
US-09-887-586A-30

Query Match 67.7%; Score 2200.5; DB 9; Length 627;
Best Local Similarity 68.1%; Pred. No. 1e-201;
Matches 427; Conservative 77; Mismatches 106; Indels 17; Gaps 7;

QY 1 MALSTPPLVSRCL-----SSSHEIKALRTIPTLGICRPGKSVASHINMCLTSVASTD 55
DB 1 MALVSISPLASKSCLRKSLISSIHEHKPPYRTIPNLGMRRGKSVTPSMSISLATAPDD 60
QY 56 SVQRRVGNYSNLWDDDFIQSLISTPYGAPDYRERADRLIGEVDIMFNKSLDGG--- 112
DB 61 GVQRRIGDYHSNIWDDDFIQSL-STPYGEPSPYQERAERLIVEVKKI-FNSMYLDDGRLMS 118
QY 113 --NDLQRLLLVDDVERLGIDRHFKEIKTALDYVNSYWNKEGICGGRSVTDLNSTAL 170
DB 119 SFNDLMQRLMIVDSVERLGIAHFKNEITSALDYVFRYWEENGICGGRDSIVTDLNSTAL 178
QY 171 GLRTLRLHGYTVSSDVLNVFKDKNGQFSSSTANIQIEGEIRGVNLFRASLVAFPGEKVM 230
DB 179 GFRTRLRLHGYTVSPEVLKAFQDQNGQFVCSPG-QTEGEIRSVNLRYASLIAFPGEKVM 237
QY 231 EAETPSTKYLRREALQKIPASSILSLEIRDVLEYGWHNTNLPRLAARNYMDVFGQHTK--N 287
DB 238 EAEIFSTRYLKEALQKIPVSA-LSQEIKFVMEYEGWHTNLPRLAARNYIDTLEKDTSAWLN 296
QY 288 KNAAEKLELAKLEFNIFHSLQERELKHVSRAWKDSGSPEMTFCRHRHVEYYALASCI 347
DB 297 KNAGKCLELAKLEFNIFNSLQOKELQYLLRWKESDLPKLTFAHRHVEFYTLASCI 356
QY 348 EPQHSGRFLGFTKMSHLITVLDNMYDVFGTVDELFTATIKRWDPESAMECLPEYMKGV 407
DB 357 DPKHSAPFLGFAKMGHLYTVLDDIYDTFGTIDLELFTSAIKRWNSSEIEHLPEYMKCV 416
QY 408 MMVYHTVNEMARVAEKAQGRDTLNYARQAWACFDSYMOEAKWIATGYLPTFEEYLENG 467
DB 417 MNVFETVNELTREAEKTQGRNTLNVYRKAWAAYFDSYMEBAKWSINGYLLPMFEEYHENG 476
QY 468 VSSAHRPCALQPIITLDIPFPDHILKEVDPPSKLNDLICILRLRGDTRCYKADRARGE 527
DB 477 VSSAYRVATLQPIITLNLAWLPDYILKGIDFSPRFNDLASSFLRLRGDTRCYKADRGE 536
QY 528 ASSISCTMKDNPGLTEEDALNHINFMIRDAIRELNWELLKPDNSVPITSKGAFDISR 587
DB 537 ASSISCTMKDNPGSTTEEDALNHINAMVNDI IKELNWE LLRSNDNIPMLAKGAFDITRAL 596
QY 588 HHGYRYRDGYSFANVETKSLVMRTVIE 614
DB 597 HHLTYIRDGFSVANKE TKLVMETLLE 623

RESULT 10
US-09-903-012-30
; Sequence 30, Application US/09903012
; Patent No. US20020094557A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20020094557A1, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903,012
; CURRENT FILING DATE: 2001-07-11

; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for windows Version 3.0
; SEQ ID NO 30
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Abies grandis
US-09-903-012-30

Query Match 67.7%; Score 2200.5; DB 9; Length 627;
Best Local Similarity 68.1%; Pred. No. 1e-201;
Matches 427; Conservative 77; Mismatches 106; Indels 17; Gaps 7;

QY 1 MALSTPPLVSRCL-----SSSHEIKALRTIPTLGICRPGKSVASHINMCLTSVASTD 55
DB 1 MALVSISPLASKSCLRKSLISSIHEHKPPYRTIPNLGMRRGKSVTPSMSISLATAPDD 60
QY 56 SVQRRVGNYSNLWDDDFIQSLISTPYGAPDYRERADRLIGEVDIMFNKSLDGG--- 112
DB 61 GVQRRIGDYHSNIWDDDFIQSL-STPYGEPSPYQERAERLIVEVKKI-FNSMYLDDGRLMS 118
QY 113 --NDLQRLLLVDDVERLGIDRHFKEIKTALDYVNSYWNKEGICGGRSVTDLNSTAL 170
DB 119 SFNDLMQRLMIVDSVERLGIAHFKNEITSALDYVFRYWEENGICGGRDSIVTDLNSTAL 178
QY 171 GLRTLRLHGYTVSSDVLNVFKDKNGQFSSSTANIQIEGEIRGVNLFRASLVAFPGEKVM 230
DB 179 GFRTRLRLHGYTVSPEVLKAFQDQNGQFVCSPG-QTEGEIRSVNLRYASLIAFPGEKVM 237
QY 231 EAETPSTKYLRREALQKIPASSILSLEIRDVLEYGWHNTNLPRLAARNYMDVFGQHTK--N 287
DB 238 EAEIFSTRYLKEALQKIPVSA-LSQEIKFVMEYEGWHTNLPRLAARNYIDTLEKDTSAWLN 296
QY 288 KNAAEKLELAKLEFNIFHSLQERELKHVSRAWKDSGSPEMTFCRHRHVEYYALASCI 347
DB 297 KNAGKCLELAKLEFNIFNSLQOKELQYLLRWKESDLPKLTFAHRHVEFYTLASCI 356
QY 348 EPQHSGRFLGFTKMSHLITVLDNMYDVFGTVDELFTATIKRWDPESAMECLPEYMKGV 407
DB 357 DPKHSAPFLGFAKMGHLYTVLDDIYDTFGTIDLELFTSAIKRWNSSEIEHLPEYMKCV 416
QY 408 MMVYHTVNEMARVAEKAQGRDTLNYARQAWACFDSYMOEAKWIATGYLPTFEEYLENG 467
DB 417 MNVFETVNELTREAEKTQGRNTLNVYRKAWAAYFDSYMEBAKWSINGYLLPMFEEYHENG 476
QY 468 VSSAHRPCALQPIITLDIPFPDHILKEVDPPSKLNDLICILRLRGDTRCYKADRARGE 527
DB 477 VSSAYRVATLQPIITLNLAWLPDYILKGIDFSPRFNDLASSFLRLRGDTRCYKADRGE 536
QY 528 ASSISCTMKDNPGLTEEDALNHINFMIRDAIRELNWELLKPDNSVPITSKGAFDISR 587
DB 537 ASSISCTMKDNPGSTTEEDALNHINAMVNDI IKELNWE LLRSNDNIPMLAKGAFDITRAL 596
QY 588 HHGYRYRDGYSFANVETKSLVMRTVIE 614
DB 597 HHLTYIRDGFSVANKE TKLVMETLLE 623

RESULT 11
US-09-900-797-30
; Sequence 30, Application US/09900797
; Publication No. US20030087406A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20030087406A1, Joseph P.
; APPLICANT: Starks, Courtney M.


```
RESULT 13
US-10-041-007-26
; Sequence 26, Application US/10041007
; Publication No. US20020164736A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seiichi P.T.
; APPLICANT: Schepmann, Hala G
; TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase
; FILE REFERENCE: P02081US1
; CURRENT APPLICATION NUMBER: US/10/041,007
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259,881
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Abies grandis
US-10-041-007-26
```

```
Query Match      67.7%; Score 2200.5; DB 13; Length 627;
Best Local Similarity 68.1%; Pred. No. 1e-201;
Matches 427; Conservative 77; Mismatches 106; Indels 17; Gaps 7;
```

```
QY      1 MALSTPLVSRSL-----SSSHEIKALRTIPTLGICRPGKSVASHINMCLTSVASTD 55
DB      1 MALVSISPLASKSCLRKSLISSIHEHKPPYRTIPNLGMRRRGKSVTPSMSISLATAAPDD 60

QY      56 SVQRRVGNHSLNWDDEFIQSLSTPYGADYRERADRLIGEYKDIMFNFKSLLEDG--- 112
DB      61 GVQRRIGDYHSNIWDDDFIQSL-STPYGEPSTYQERAERLIVEYKXI-FNSMYLDDGRLMS 118

QY      113 --NDLLORLLLVDDVERLGIDRHFKKEIKTALDYVNSYWNKEGIGCGRESVTDLNSTAL 170
DB      119 SFNDLMQRLMIVDSVERLGIAHFKEITSAIDYVFRYWEENGIGCGRDSIVTDLNSTAL 178

QY      171 GLRTLRLHGYTVSSDVLNVFKDKNGQFSSSTANIQIEGEIRGYVNLFRASLVAFPGKXMD 230
DB      179 GFRTLRLHGYTVSPVLKAFQDQNGQFVCSPG-QTEGEIRSVNLVYRASLIAFPGKXME 237

QY      231 EAETFSKYLRREALOKIPASSISLSLEIRDVLEYGWHNTLPRLEARNYMDVFGQHTK--N 287
DB      238 EAEIFSTRYLKEALOKIPVSA-LSQEIKFVMEYGMHTNLPRLERARNYIDTLEKDTSAWLN 296

QY      288 KNAAEKLELAKLEFNI FHSLOERELKHVSRWKMDSGSPEMTFCRHRHVEYYALASCI AF 347
DB      297 KNAGKLELAKLEFNI FNSLOQELQYLLRWKESDLPKLTFAHRHVEFYTLASCI AI 356

QY      348 EPQHSGRFLGFTKMSHLITVLDMYDVGFTVDELELFTATIKRWDPsameCLPEYMKGVY 407
DB      357 DPKHSAFRLGFAKCHLVTVLDIYDTFGTIDELFTSAIKRWNSSEIHLPEYMKCVY 416

QY      408 MMVYHTVNMARVAEKAQGRDTLNYARQAEACFDSYMOEAKWIATGYLPTFEEYLENGK 467
DB      417 MVMVFETVNELTREAEKTQGRNTLNYRKAMEAYFDSYMEBAKWIISNGYLPMEFEYHENGK 476

QY      468 VSSAHRPCALQPIITLDIPFPDHILKEVDPPSKLNDLICIILRLRGDTRCYKADRARGE 527
DB      477 VSSAYRVATLQPIITLNAWLPDYILKGIDFPSRFNDLASSFLRLRGDTRCYKADRARGE 536

QY      528 ASSISCYMKDNPGLTEEDALNHINFMIRDAIRELNWELKPDNSVPTSKKHAFDISRNV 587
DB      537 ASSISCYMKDNPGSTTEEDALNHINAMVNDI IKELNWELLRSDNIPMLAKKHAFDITRAL 596

QY      588 HHGYRRDGYSPANVETKSLVMRTVIE 614
DB      597 HHLIYTRDGSVANKE TKLVMETTLE 623
```

RESULT 14
US-10-025-145A-2
; Sequence 2, Application US/10025145A

```
; Publication No. US20030175861A1
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B.
; APPLICANT: Bohlmann, Joerg
; APPLICANT: Steele, Christopher L.
; APPLICANT: Phillips, Michael A.
; TITLE OF INVENTION: Monoterpene Synthases from Grand Fir (Abies Grandis)
; FILE REFERENCE: WSUR118414
; CURRENT APPLICATION NUMBER: US/10/025,145A
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 09/360,545
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: PCT/US98/14528
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: US 60/052,249
; PRIOR FILING DATE: 1997-07-11
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Abies Grandis
US-10-025-145A-2
```

```
Query Match      67.7%; Score 2200.5; DB 14; Length 627;
Best Local Similarity 68.1%; Pred. No. 1e-201;
Matches 427; Conservative 77; Mismatches 106; Indels 17; Gaps 7;
```

```
QY      1 MALSTPLVSRSL-----SSSHEIKALRTIPTLGICRPGKSVASHINMCLTSVASTD 55
DB      1 MALVSISPLASKSCLRKSLISSIHEHKPPYRTIPNLGMRRRGKSVTPSMSISLATAAPDD 60

QY      56 SVQRRVGNHSLNWDDEFIQSLSTPYGADYRERADRLIGEYKDIMFNFKSLLEDG--- 112
DB      61 GVQRRIGDYHSNIWDDDFIQSL-STPYGEPSTYQERAERLIVEYKXI-FNSMYLDDGRLMS 118

QY      113 --NDLLORLLLVDDVERLGIDRHFKKEIKTALDYVNSYWNKEGIGCGRESVTDLNSTAL 170
DB      119 SFNDLMQRLMIVDSVERLGIAHFKEITSAIDYVFRYWEENGIGCGRDSIVTDLNSTAL 178

QY      171 GLRTLRLHGYTVSSDVLNVFKDKNGQFSSSTANIQIEGEIRGYVNLFRASLVAFPGKXMD 230
DB      179 GFRTLRLHGYTVSPVLKAFQDQNGQFVCSPG-QTEGEIRSVNLVYRASLIAFPGKXME 237

QY      231 EAETFSKYLRREALOKIPASSISLSLEIRDVLEYGWHNTLPRLEARNYMDVFGQHTK--N 287
DB      238 EAEIFSTRYLKEALOKIPVSA-LSQEIKFVMEYGMHTNLPRLERARNYIDTLEKDTSAWLN 296

QY      288 KNAAEKLELAKLEFNI FHSLOERELKHVSRWKMDSGSPEMTFCRHRHVEYYALASCI AF 347
DB      297 KNAGKLELAKLEFNI FNSLOQELQYLLRWKESDLPKLTFAHRHVEFYTLASCI AI 356

QY      348 EPQHSGRFLGFTKMSHLITVLDMYDVGFTVDELELFTATIKRWDPsameCLPEYMKGVY 407
DB      357 DPKHSAFRLGFAKCHLVTVLDIYDTFGTIDELFTSAIKRWNSSEIHLPEYMKCVY 416

QY      408 MMVYHTVNMARVAEKAQGRDTLNYARQAEACFDSYMOEAKWIATGYLPTFEEYLENGK 467
DB      417 MVMVFETVNELTREAEKTQGRNTLNYRKAMEAYFDSYMEBAKWIISNGYLPMEFEYHENGK 476

QY      468 VSSAHRPCALQPIITLDIPFPDHILKEVDPPSKLNDLICIILRLRGDTRCYKADRARGE 527
DB      477 VSSAYRVATLQPIITLNAWLPDYILKGIDFPSRFNDLASSFLRLRGDTRCYKADRARGE 536

QY      528 ASSISCYMKDNPGLTEEDALNHINFMIRDAIRELNWELKPDNSVPTSKKHAFDISRNV 587
DB      537 ASSISCYMKDNPGSTTEEDALNHINAMVNDI IKELNWELLRSDNIPMLAKKHAFDITRAL 596

QY      588 HHGYRRDGYSPANVETKSLVMRTVIE 614
DB      597 HHLIYTRDGSVANKE TKLVMETTLE 623
```

RESULT 15

US-10-025-145A-32
; Sequence 32, Application US/10025145A
; Publication No. US20030175861A1
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B.
; APPLICANT: Bohlmann, Joerg
; APPLICANT: Steele, Christopher L.
; APPLICANT: Phillips, Michael A.
; TITLE OF INVENTION: Monoterpene Synthases from Grand Fir (Abies Grandis)
; FILE REFERENCE: WSUR118414
; CURRENT APPLICATION NUMBER: US/10/025,145A
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 09/360,545
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: PCT/US98/14528
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: US 60/052,249
; PRIOR FILING DATE: 1997-07-11
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Abies Grandis
US-10-025-145A-32

Query Match 67.6%; Score 2197.5; DB 14; Length 627;
Best Local Similarity 68.1%; Pred. No. 2e-201;
Matches 427; Conservative 77; Mismatches 106; Indels 17; Gaps 7;

QY 1 MALSTPLVSRSL-----SSSHEIKALRTIPTLGICRPGKSVASHINMCLTSVASTD 55
DB 1 MALVISISPLASKSCLRKSLISSIHEHKPPYRTIPLNGMRRRGKSVTPSMSISLATAAPDD 60
QY 56 SVQRRVGNTHSNLWDDDFIQSLISTPYGADYERADRLIGEVDIMFNPKSLLEDG--- 112
DB 61 GVORRIGDYHSNIWDDDFIQSL-STHYGSPSYQERAERLIVEVKI-FNSMYLDDGRLMS 118
QY 113 --NDLLQRLLLVDVERLIGIDRHFKKEIKTALDYVNSYWNKEGIGCGRESVTDLNSTAL 170
DB 119 SFNDLMQRLWIVDSVERLGIARHFKNELTSALDYVFRYWEENGIGCGRDSIVTDLNSTAL 178
QY 171 GLRTLRLHGYTVSSDVLNVFKDKNGQFSSSTANIQIEGEIRGVNLFRASLVAFPGEKVM 230
DB 179 GFRTLRLHGYTVSPVLKAFQDQNGQFVCSPG-QTEGEIRSVNLVYRASLIAFPGEKVM 237
QY 231 EAETFSKYREALOKIPASSILSLERDYLEYGMHTNLPRLLEARNYMDVFGQHTK--N 287
DB 238 EAETFSKYREALOKIPVSA-LSGEIKFMEYGMHTNLPRLLEARNYIDTLEKDTSAWLN 296
QY 288 KNAAEKLELAKLEFNIFHSLQERELKHSRWKWDGSGSPMTFCRHRHVEYYALASCI 347
DB 297 KNAGKLELAKLEFNIFNSLQOKELQYLLRWKESDLPKLTFAHRHVEFYTLASCI 356
QY 348 EPOHSGFRLGFTKMSHLITVLDMDYDVGTVDELELFTATIKRWDPASMECLPEYMKGV 407
DB 357 DPKHSAFRLGFAKCHLVTLDDYDTFGTIDELELFTSAIKRWNSSEIEHLPEYMKCV 416
QY 408 MMVYHTVEMARVAEKAQGRDTLNTYARQAEACFDSYMOEAKWIATGYLPTFEYLENGK 467
DB 417 MMVFETVNELTREAEKTOGRNTLNTYARQAEAYFDSYMEBAKWIISNGYLPTEFEYHENGK 476
QY 468 VSSAHRPCALQPIITLDIPFPDHILKEVDPPSKLNDLICITLRLRGDTRCYKADRARGE 527
DB 477 VSSAYRVATLQPIITLNLAWLPDYILKIDFPPSRFNDLASSFLRLRGDTRCYKADRARGE 536
QY 528 ASSISCYMKDNPGLTEEDALNHINFMIRDAIRELNMWELLPKDNSVPTTSKGAFDISRW 587
DB 537 ASCISCYMKDNPGSTEDALNHINAMVNDIIEKLNWELLRSDNIPMLAKGAFDITRAL 596
QY 588 HHGYYRQGYSFANVETKSLVMRTVIE 614

DB 597 HHLYYRDGFSVANKEKTKLVMEITLLE 623

Search completed: July 23, 2004, 09:09:33
Job time : 51 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2004, 08:55:51 ; Search time 58 Seconds
(without alignments)
3010.592 Million cell updates/sec

Title: US-10-025-145A-65

Perfect score: 3251

Sequence: 1 MALLITPLVSRSCLSSE.....FANVETKSLVMRTVIEPVPL 618

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|--------|-------------|--------|----|----------|--------------------|
| 1 | 3251 | 100.0 | 618 | 4 | AAB69390 | Aab69390 Grand fir |
| 2 | 2453 | 75.5 | 628 | 2 | AAW85701 | Aaw85701 Pinene gy |
| 3 | 2453 | 75.5 | 628 | 3 | AAV90837 | Aay90837 Grand fir |
| 4 | 2453 | 75.5 | 628 | 4 | AAB69371 | Aab69371 Grand fir |
| 5 | 2264 | 69.6 | 630 | 4 | AAB69391 | Aab69391 Grand fir |
| 6 | 2200.5 | 67.7 | 627 | 2 | AAW85700 | Aaw85700 Myrcene s |
| 7 | 2200.5 | 67.7 | 627 | 3 | AAV90842 | Aay90842 Grand fir |
| 8 | 2200.5 | 67.7 | 627 | 4 | AAB69370 | Aab69370 Grand fir |
| 9 | 2197.5 | 67.6 | 627 | 2 | AAW85710 | Aaw85710 Grand fir |
| 10 | 2197.5 | 67.6 | 627 | 4 | AAB69380 | Aab69380 Grand fir |
| 11 | 2197.5 | 67.6 | 627 | 5 | ABB79395 | Abb79395 Taxadiene |
| 12 | 2137 | 65.7 | 630 | 4 | AAB69393 | Aab69393 Grand fir |
| 13 | 2084.5 | 64.1 | 637 | 4 | AAB69392 | Aab69392 Grand fir |
| 14 | 2031.5 | 62.5 | 637 | 2 | AAW85702 | Aaw85702 Limonene |
| 15 | 2031.5 | 62.5 | 637 | 3 | AAV90859 | Aay90859 Grand fir |
| 16 | 2031.5 | 62.5 | 637 | 4 | AAB69372 | Aab69372 Grand fir |
| 17 | 1617.5 | 49.8 | 462 | 3 | AAB18115 | Aab18115 Pinus rad |
| 18 | 1611.5 | 49.6 | 462 | 3 | AAB18044 | Aab18044 Pinus rad |
| 19 | 1295.5 | 39.8 | 580 | 2 | AAV06571 | Aay06571 Delta-sel |
| 20 | 1295.5 | 39.8 | 581 | 2 | AAV06570 | Aay06570 Delta-sel |
| 21 | 1295.5 | 39.8 | 581 | 2 | AAV06563 | Aay06563 Grand fir |
| 22 | 1295.5 | 39.8 | 581 | 3 | AAV90854 | Aay90854 Grand fir |
| 23 | 1291.5 | 39.7 | 581 | 2 | AAV06569 | Aay06569 Delta-sel |
| 24 | 1267.5 | 39.0 | 344 | 2 | AAB18043 | Aab18043 Pinus rad |
| 25 | 1250.5 | 38.5 | 577 | 2 | AAW85704 | Aaw85704 Grand fir |

| | | | | | | |
|----|--------|------|-----|---|----------|--------------------|
| 26 | 1250.5 | 38.5 | 577 | 4 | AAB69374 | Aab69374 Grand fir |
| 27 | 1240.5 | 38.2 | 862 | 2 | AAW31655 | Aaw31655 Pacific Y |
| 28 | 1240.5 | 38.2 | 862 | 3 | AAV90852 | Aay90852 Yew taxad |
| 29 | 1240.5 | 38.2 | 862 | 5 | ABB79394 | Abb79394 Taxadiene |
| 30 | 1236.5 | 38.0 | 862 | 6 | ABU09782 | Abu09782 Pacific Y |
| 31 | 1231 | 37.9 | 593 | 2 | AAV06572 | Aay06572 Gamma-hum |
| 32 | 1231 | 37.9 | 593 | 2 | AAV06564 | Aay06564 Grand fir |
| 33 | 1231 | 37.9 | 593 | 3 | AAV90855 | Aay90855 Grand fir |
| 34 | 1230 | 37.8 | 593 | 2 | AAV06573 | Aay06573 Gamma-hum |
| 35 | 1230 | 37.8 | 593 | 2 | AAV06574 | Aay06574 Gamma-hum |
| 36 | 1188.5 | 36.6 | 817 | 2 | AAV06566 | Aay06566 Grand fir |
| 37 | 1188.5 | 36.6 | 817 | 5 | ABB79391 | Abb79391 Taxadiene |
| 38 | 1187 | 36.5 | 782 | 2 | AAW85703 | Aaw85703 Grand fir |
| 39 | 1187 | 36.5 | 782 | 3 | AAV90853 | Aay90853 Grand fir |
| 40 | 1187 | 36.5 | 782 | 4 | AAB69373 | Aab69373 Grand fir |
| 41 | 1187 | 36.5 | 782 | 5 | ABB79392 | Abb79392 Taxadiene |
| 42 | 1187 | 36.5 | 817 | 2 | AAV06567 | Aay06567 E-alpha-b |
| 43 | 1187 | 36.5 | 817 | 2 | AAV06568 | Aay06568 E-alpha-b |
| 44 | 1187 | 36.5 | 817 | 2 | AAV06562 | Aay06562 Grand fir |
| 45 | 1187 | 36.5 | 817 | 6 | ABU09781 | Abu09781 White fir |

ALIGNMENTS

RESULT 1
ID AAB69390 standard; protein; 618 AA.

XX AAB69390;

DT 30-APR-2001 (first entry)

DE Grand fir monoterpene synthase protein fragment SEQ ID NO: 65.

KW Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;

KW myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;

KW terpinolene synthase; insect resistance; nutrition.

OS Abies grandis.

XX WO200107565-A2.

PD 01-FEB-2001.

PF 24-JUL-2000; 2000WO-US020264.

PR 26-JUL-1999; 99US-00360545.

PI Steele CL, Bohlmann J, Croteu RB, Phillips MA;

DR WPI; 2001-182782/18.

DR N-PSDB; AAF73411.

PT New nucleic acid encoding monoterpene synthases, for increasing terpene
synthesis in plants, e.g. for increasing resistance to pests or for
treatment of cancer.

PS Claim 7; Page 150-151; 175pp; English.

XX The present invention provides the protein and coding sequences of
monoterpene synthases from the grand fir. These include (-)-camphene
synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-
limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase
and pinene synthase. The sequences can be used to produce transgenic
plants expressing high levels of the enzymes, resulting in levels which
are useful in protecting against and treating cancers, and to confer
insect resistance on plants

XX Sequence 618 AA;

SO

| | | | | | |
|-----------------------|-----|-----------------|---------------------------|-----------------|-----------------------------|
| Query Match | | 100.0%; | Score 3251; | DB 4; | Length 618; |
| Best Local Similarity | | 100.0%; | Pred. No. 2.7e-295; | | |
| Matches 618; | | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |
| Qy | 1 | MALLSITPLVSRSC | SSSHEIKALRRTIPTLGICRPGKSV | AHNSIMCLTSV | ASTDSVORR 60 |
| | | | | | |
| Db | 1 | MALLSITPLVSRSC | SSSHEIKALRRTIPTLGICRPGKSV | AHNSIMCLTSV | ASTDSVORR 60 |
| Qy | 61 | VGNHNSNLWDDDF | IQSLISTPYGAPDYRERADRLIGE | VKDIMEFNSLEDG | NDLQRL 120 |
| | | | | | |
| Db | 61 | VGNHNSNLWDDDF | IQSLISTPYGAPDYRERADRLIGE | VKDIMEFNSLEDG | NDLQRL 120 |
| Qy | 121 | LYDDVERLIGDRH | FKEIKTALDYVNSYWNKEGICG | GRESVVTDLNSTAL | GLRTLRLHG 180 |
| | | | | | |
| Db | 121 | LYDDVERLIGDRH | FKEIKTALDYVNSYWNKEGICG | GRESVVTDLNSTAL | GLRTLRLHG 180 |
| Qy | 181 | TVSSDVLVNFKD | NGQFSSSTANIQIEGEIRGVNL | FRASLVAFPEGEK | VMDEAETSTKYL 240 |
| | | | | | |
| Db | 181 | TVSSDVLVNFKD | NGQFSSSTANIQIEGEIRGVNL | FRASLVAFPEGEK | VMDEAETSTKYL 240 |
| Qy | 241 | REALQKIPASSIL | SLEIRDVLEYGWTNLPRL | EARNYMDVFGQHTK | NKNAAEKLELAKL 300 |
| | | | | | |
| Db | 241 | REALQKIPASSIL | SLEIRDVLEYGWTNLPRL | EARNYMDVFGQHTK | NKNAAEKLELAKL 300 |
| Qy | 301 | EFNIFHSIQEREL | KVSRWVKDSSPEMTFCRHRHVE | YYALASCIAP | EPQHSGRFGFTX 360 |
| | | | | | |
| Db | 301 | EFNIFHSIQEREL | KVSRWVKDSSPEMTFCRHRHVE | YYALASCIAP | EPQHSGRFGFTX 360 |
| Qy | 361 | MSHLITVLD | MYDVFQTVDELELFTATIKR | WDPSAMECLPEYMK | GVYMMVYHTVNEMARV 420 |
| | | | | | |
| Db | 361 | MSHLITVLD | MYDVFQTVDELELFTATIKR | WDPSAMECLPEYMK | GVYMMVYHTVNEMARV 420 |
| Qy | 421 | AEKQGRD | TLNYPARQAWACFPDSYMO | EAKWIATGYLPTFEE | YLENGKVSSAHRPCALQPI 480 |
| | | | | | |
| Db | 421 | AEKQGRD | TLNYPARQAWACFPDSYMO | EAKWIATGYLPTFEE | YLENGKVSSAHRPCALQPI 480 |
| Qy | 481 | LTLDIPFPD | HLKEVDFPSKLANDLICIL | RLRGDTRCYKAD | RAGEEASSISCYMKDNP 540 |
| | | | | | |
| Db | 481 | LTLDIPFPD | HLKEVDFPSKLANDLICIL | RLRGDTRCYKAD | RAGEEASSISCYMKDNP 540 |
| Qy | 541 | LTEEDALNH | INFMIRDAIRELNMEL | KPDNSVPIT | SKGAFDISRWVHGYRYRDGYSFA 600 |
| | | | | | |
| Db | 541 | LTEEDALNH | INFMIRDAIRELNMEL | KPDNSVPIT | SKGAFDISRWVHGYRYRDGYSFA 600 |
| Qy | 601 | NVETKSL | VMTVIEPVPL 618 | | |
| | | | | | |
| Db | 601 | NVETKSL | VMTVIEPVPL 618 | | |

| | | |
|----|---|--|
| XX | PI | Bohlmann J, Steele CL, Croteau RB; |
| XX | DR | WPI; 1999-120396/10. |
| XX | DR | N-PSDB; AAX08644. |
| XX | PT | New isolated gymnosperm monoterpene synthase DNA - obtained from Grand fir (Abies grandis), used to provide plants with modified production of monoterpenes, e.g. mycrene, limonene or pinene. |
| XX | PS | Claim 13; Page 77-79; 121pp; English. |
| CC | CC | Nucleotide sequences encoding mycrene synthase, limonene synthase and pinene synthase from Grand fir may be incorporated into any organism (e.g. intact plant, animal, microbe), or derived cell culture that produces geranyl diphosphate for the production of the aforementioned enzymes or their products. The sequences when expressed in transfected cells may also be used for the production or modification of flavour and aroma properties, improvement of defense capability, and the alteration of other ecological interactions mediated by mycrene, limonene, pinene, or their derivatives. In particular they can be used for the production of plant seeds for the extraction of oil or meal |
| CC | CC | Sequence 628 AA; |
| QY | Query Match | 75.5%; Score 2453; DB 2; Length 628; |
| QY | Best Local Similarity | 75.3%; Pred. No. 1.9e-220; |
| Db | Matches 475; Conservative 59; Mismatches 81; Indels 16; Gaps 6; | |
| QY | 1 | MALLSITPLVSRSC-----SSSHEIKALRRTIPTLGICRPGKSVASHINMCLTSVASTD 55 |
| Db | 1 | MALVSTAPLASKSCLHKSLSISTHELKALSRTIPALGMSRGRKSTIPSTISMSSTTVVTTDD 60 |
| QY | 56 | SVORRVGNHNSNLWDDDFIQSLISTPYGAPDYRERADRLIGEVDKIMEFNSLEDG--- 112 |
| Db | 61 | GVRRRMGDFHSNLWDDDFIQSL-PTAYEEKSYLERAEKLIGEVKN-MFNSMSLEDGELMS 118 |
| QY | 113 | --NDLLQRLLLVDDVERLIGDRHFKKEIKTALDYVNSYWNKEGICGRESVVTDLNSTAL 170 |
| Db | 119 | PLNDLIQRLMIVDSLRLGHRHFKKEIKSALDYVNSYWGENGICGRESVVTDLNSTAL 178 |
| QY | 171 | GLRTLRLHGYTVSSDVLNVFKDNGQFSSSTANIQIEGEIRGVNLFRASLVAFPEGEKVM 230 |
| Db | 179 | GLRTLRLHGYTVSSDVFKAFFKQNGQFSSCENIQTDEIRGVNLFRASLVAFPEGEKIMD 238 |
| QY | 231 | EAEFTSTKYLRALQKIPASSILSLEIRDVLEYGWHTNLPRLLEARNYMDVFGQHTKNKNA 290 |
| Db | 239 | EAEIFSTKYLKEALQKIPVSS-ISREIGDVLEYGWHTYLPRLLEARNYIQVFGQDTENTKS 297 |
| QY | 291 | ---AEKLELAKLEBNIHFSIQERELKVSRWVKDSSPEMTFCRHRHVEYYALASCIAP 347 |
| Db | 298 | YVKSKLLELAKLEFNIQSLQKRELESLVRWKESGPEMTFCRHRHVEYYTLASCIAP 357 |
| QY | 348 | EPQHSGFRLGFTKMSHLITVLDMYDVFQTVDELELFTATIKRWDPSAMECLPEYMKGYV 407 |
| Db | 358 | EPQHSGFRLGFAKTCHLITVLDMYDFTGTVDELELFTATMKRWDPSIDCLPEYMKGYV 417 |
| QY | 408 | KMYVHTVNEMARVAEKAQGRDTLNYPARQAWACFPDSYMOEAKWIATGYLPTFEEYLENGK 467 |
| Db | 418 | IAYVDTVNEMAREAEAAQGRDTLTYAREAWAYIDSYMOEARWIATGYLPSFDEYYENGK 477 |
| QY | 468 | VSSAHRPCALQPIITLTDIPFPDHLKEVDFPSKLANDLICILRLRGDTRCYKADRARGE 527 |
| Db | 478 | VSCGHRISALQPIITLMDIPFPDHLKEVDFPSKLANDLACAILRLRGDTRCYKADRARGE 537 |
| QY | 528 | ASSISCYMKDNPGLTEEDALNHINFMIRDAIRELNMELKPDNSVPITSKGAFDISRW 587 |
| Db | 538 | ASSISCYMKDNPVSEEDALDHINAMISDVIKGLNMELKPDINVPISAKGAFDIARAF 597 |
| QY | 588 | HHGYRRYRDGYSFANVETKSLVMTVIEPVPL 618 |
| Db | 598 | HHGYRRYRDGYSVANVETKSLVTTLLESVPL 628 |

RESULT 3
ID AAY90837 standard; protein; 628 AA.
XX AAY90837;
AC AAY90837;
XX 25-AUG-2000 (first entry)
DT
XX Grand fir pinene synthase protein sequence SEQ ID NO:20.
DE
XX
KW Synthase; protein co-ordinate data; active site; modification; terpenoid;
KW 3-dimensional coordinate; alpha carbon atom; plant; terpene synthase;
KW isoprenoid; breeding programme; fragrance; flavour; pheromone;
KW defensive agent; pigment; anticancer; steroid hormone;
KW signal transduction pathway; bile acid; affinity purification;
KW photoreceptor; enzymatic synthesis; nutrient supplement;
KW immunological reagent.
XX
OS Abies grandis.
XX
PN WO200017327-A2.
XX
PD 30-MAR-2000.
XX
PF 17-SEP-1999; 99WO-US021419.
XX
PR 18-SEP-1998; 98US-0100993P.
PR 22-APR-1999; 99US-0130628P.
PR 23-AUG-1999; 99US-0150262P.
XX
PA (KENT) UNIV KENTUCKY RES DEPT.
PA (SALK) SALK INST BIOLOGICAL STUDIES.
XX
PI Chappell J, Manna KR, Noel JP, Starks CM;
XX
XX WPI; 2000-292839/25.
DR N-PSDB; AAA38922.
XX
XX
PT Novel terpene synthase enzymes, useful for producing terpene
PT hydrocarbons, e.g. fragrances or anticancer agents, are derived from known
PT enzymes by specific amino acid alterations.
XX
PS Claim 102; Page 367-368; 450pp; English.
XX
CC The present invention describes an isolated terpene synthase (I)
CC comprising a region with at least 20% identity to region 265-535 of a 548
CC amino acid (aa) sequence (Ia), given in AAY90831. (I) contains nine alpha
CC -carbon atoms (alphaC) that have interatomic distances, between each
CC other, within tabulated ranges, have a centre point (within a sphere of
CC radius 2.3 Angstrom) within tabulated ranges, and have an ordered
CC arrangement of R groups (defining aa side chains), excluding specific
CC tabulated arrangements (tables given in the specification). (I)', and
CC related enzymes, are used to produce a wide range of terpenoids (e.g.
CC cyclic, acyclic, optionally hydroxylated), useful e.g. as fragrances,
CC flavours, pheromones, defensive agents, pigments, anticancer agents,
CC components of signal transduction pathways, precursors of steroid
CC hormones and bile acids, as photoreceptors and as co-factor side chains.
CC Some synthases with little or no catalytic activity (and nucleic acids
CC encoding them) are used as controls in the analysis of products formed by
CC enzymatic synthesis; as nutrient supplements; for affinity purification
CC of isoprenoids; or to develop immunological reagents or nucleic acids for
CC monitoring expression of terpene synthase or inheritance of the gene in
CC plant breeding programs. The new synthases may produce novel terpene
CC products. AAA38910 to AAA38938 and AAY90831 to AAY90859 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 628 AA;

Query Match 75.5%; Score 2453; DB 3; Length 628;
Best Local Similarity 75.3%; Pred. No. 1.9e-220;
Matches 475; Conservative 59; Mismatches 81; Indels 16; Gaps 6;

QY 1 MALSTITPLVSRSC-----SSSHEIKALRRTIPTLGICRPGKSVASHINMCLTSVASTD 55
DB 1 MALVSTAPLASKSCLSKSLISSTHELKALSRITPALGMSRGRKSIPTPSISMSSTVTVD 60
QY 56 SVQRRVGNHNSLWDDDFIQSLISTPYGAPDYRERADRLIGEVKDIMFNKSLDDG--- 112
DB 61 GVRRRMGDFHNSLWDDDFIQSL-PTAYEEKSYLERAEKDIGEVKN-MFNSMSLEDGELMS 118
QY 113 --NDLQRLLLVDVERLGIDRHFKKEIKTALDVYNISYWNKEIGCGRESVTDLNSTAL 170
DB 119 PLNDLIQRLWIVDSLERLGIHRHFKDEIKSALDVYISYWGENGIGCGRESVTDLNSTAL 178
QY 171 GLRTLRLHGYTVSSDVLNVFKDKNGQFSSSTANIQIEGEIRGVNLFRASLVAFPEKVM 230
DB 179 GLRTLRLHGYTVSSDVLNVFKDKNGQFSSSTANIQIEGEIRGVNLFRASLVAFPEKIM 238
QY 231 EAETFTKYLRALQKIPASSILSLRIVLYEGWHTNLPRLRARNYMDVFGQHTKNKA 290
DB 239 EAEIFSTKYLRALQKIPVSS-LSREIGDYLEYGMHTYLPRLRARNYIQVFGQDTEKTS 297
QY 291 ---AEKLLELAKLENIHFSLQERELKHSRWKDKSGSPEMTFCRHHVEYYALASCI 347
DB 298 YVSKSKLELAKLENIHFSLQERELKHSRWKDKSGSPEMTFCRHHVEYYTLASCI 357
QY 348 EPQHSGRFLGFTYMSHLITVLDMDYDVFGLVDELELFTATIKRWDPSAMECLPEYMKGV 407
DB 358 EPQHSGRFLGFTYMSHLITVLDMDYDVFGLVDELELFTATIKRWDPSAMECLPEYMKGV 417
QY 408 MMYHTVNEARVAEKAQGRDTLNYARQAEACFDSYMOEAKMIATGYLPTFEYLENGK 467
DB 418 IAVYDTVNEARVAEKAQGRDTLNYARQAEACFDSYMOEAKMIATGYLPTFEYLENGK 477
QY 468 VSSAHRPCALQPILTLDIPFDHILKEVDEPSPKNDLICILRLRGDTRCYKADRAGEE 527
DB 478 VSCGHRISALQPILTMDIPFDHILKEVDEPSPKNDLICILRLRGDTRCYKADRAGEE 537
QY 528 ASSISCYMKONPGLTEDALNHINFMIRDAIRELNWELLKPDNSVPITSKGAFDISR 587
DB 538 ASSISCYMKONPGVSEEDALDHINAMISDVYKGLNWELLKPDINVPISAKGAFDIARA 597
QY 588 HHGYYRDRGYSEANVETKSLVMRTVIEPVPL 618
DB 598 HYGYYRDRGYSEANVETKSLVMRTVIEPVPL 628

RESULT 4
AAB69371
ID AAB69371 standard; protein; 628 AA.
XX
AC AAB69371;
XX
DT 30-APR-2001 (first entry)
XX
DE Grand fir (-)-pinene synthase SEQ ID NO: 4.
XX
KW Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;
KW myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;
KW terpinolene synthase; insect resistance; nutrition.
XX
OS Abies grandis.
XX
PN WO200107565-A2.
XX
PD 01-FEB-2001.
XX
PF 24-JUL-2000; 2000WO-US020264.
XX
PR 26-JUL-1999; 99US-00360545.
XX
PA (UNIW) UNIV WASHINGTON STATE RES FOUND.
XX
PI Steele CL, Bohlmann J, Croten RB, Phillips MA;
XX

| | |
|----|--|
| DR | WPI; 2001-182782/18. |
| DR | N-PSDB; AAF73372. |
| XX | |
| PT | New nucleic acid encoding monoterpene synthases, for increasing terpene |
| PT | synthesis in plants, e.g. for increasing resistance to pests or for |
| PT | treatment of cancer. |
| XX | |
| PS | Claim 66; Page 110-112; 175pp; English. |
| XX | |
| CC | The present invention provides the protein and coding sequences of |
| CC | monoterpene synthases from the grand fir. These include (-)-camphene |
| CC | synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)- |
| CC | limonene, (-)-alpha-pinene synthase, limonene synthase, myrcene synthase |
| CC | and pinene synthase. The sequences can be used to produce transgenic |
| CC | plants expressing high levels of the enzymes, resulting in levels which |
| CC | are useful in protecting against and treating cancers, and to confer |
| CC | insect resistance on plants |
| XX | |
| SQ | Sequence 628 AA; |

| | | | | |
|---------------------------|-------|---------------------|------------|-------------|
| Query Match | 75.5% | Score 2453; | DB 4; | Length 628; |
| Best Local Similarity | 75.3% | Pred. No. 1.9e-220; | | |
| Matches 475; Conservative | 59; | Mismatches 81; | Indels 16; | Gaps 6; |

| | | | |
|----|-----|--|-----|
| QY | 1 | MALLSTPLVSRCL-----SSSEIKALRRTIPTLGI CRPGKSAVHSHINMCLTSVASTD | 55 |
| Db | 1 | MALVSTAPLASKSCLHKSLSISTTHELKALSRITIPALGMSRRGKSITPSPISMSSTTVTDD | 60 |
| QY | 56 | SVQRRVGNHYHSNLWDDDFIQSLISTPYGAPDYRERADRLIGEVDIMFNFSLDGG-- | 112 |
| Db | 61 | GVRRRMGDFHSNLWDDDVIOQL-PTAYEEKSYLERAEKLIGEYKN-MFNSMSLEDGELMS | 118 |
| QY | 113 | --NDLQRLLLVDDVERLGIDRHKKEIKTALDVNSYWNKEGICCGRESVTDLNSTAL | 170 |
| Db | 119 | PLNDLIQRLWIVDSLERTGIRHFKDEIKSALDVYSYWGENGICCGRESVTDLNSTAL | 178 |
| QY | 171 | GLRTLRLHGTYVSSDVLANVFKDNGQFSSSTANIQIEGEIRGVNLFRASLVAFPEKVM | 230 |
| Db | 179 | GLRTLRLHGYPVSSDVFKAFKQNGQFSCSENIQTDEEIRGVNLFRASLIAFPEKIMD | 238 |
| QY | 231 | EAETESTKYLRREALOKIPASSISLEIRDVLEYGWHTNLPRLEARNYMDVEGQHTKNKA | 290 |
| Db | 239 | EAEIFSTKYLKEALQKIPVSS-LSREIGDVLEYGWHTYLPRLEARNYIQVFQDTEENTKS | 297 |
| QY | 291 | ---AEKLELAKLEFNIFHSLQERELKHVSRWKDSGSPENTFCRRHVEYYALASCIAF | 347 |
| Db | 298 | YVSKKLELAKLEFNIFQSLQKRELSLVRWWKESGFPEMTCRRHVEYYTLASCIAF | 357 |
| QY | 348 | EPQSGFRLGFTKMSHLITVLDMYDVGTVDELELFTATIKRWDPSAMECLPEYMKGVY | 407 |
| Db | 358 | EPQSGFRLGFAKTCHLITVLDMYDTFGTVDELELFTATMKRWDPSIDCLPEYMKGVY | 417 |
| QY | 408 | MMVYHTVNEMARVAEKAQGRDTLNYARQAEACFDSYMQEAKMIATGYLPTFEEYLENGK | 467 |
| Db | 418 | IAYVDTVNEMAREAEAEAGRDITLYAREAMEAYIDSYMQEARMIATGYLPSFDEYYENGK | 477 |
| QY | 468 | VSSAHRPCALQPILTLDIPFPDHILKEVDFPSKLNDLICIILRLRGDTRCYKADRARGE | 527 |
| Db | 478 | VSCGHRISALQPILTMDIPFPDHILKEVDFPSKLNDLACAILRLRGDTRCYADRARGE | 537 |
| QY | 528 | ASSISCYMKDNPGLTBEDALNHINEMIRDAIRELNWELKPDNSVPITSKGAFDISRVM | 587 |
| Db | 538 | ASSISCYMKDNPGVSEEDALDHINAMISDVIKGLNWELKPDINVPISAKKHAFDIARAF | 597 |
| QY | 588 | HGGRYRDGYSFANVETKSLVMRTVIEPVL 618 | |
| Db | 598 | HYGYKRDGYSVANVETKSLVTRTLESVPL 628 | |

RESULT 5
AAB69391
ID AAB69391 standard; protein; 630 AA.
XX

| | |
|----|---|
| AC | AAB69391; |
| XX | |
| DT | 30-APR-2001 (first entry) |
| XX | |
| DE | Grand fir monoterpene synthase protein fragment SEQ ID NO: 67. |
| XX | |
| KW | Monoterpene synthase; grand fir; cancer; (-)-camphene synthase; |
| KW | myrcene synthase; (-)-limonene synthase; (-)-pinene synthase; |
| KW | terpinolene synthase; insect resistance; nutrition. |
| XX | |
| OS | Abies grandis. |
| XX | |
| PN | WC200107565-A2. |
| XX | |
| PD | 01-FEB-2001. |
| XX | |
| PF | 24-JUL-2000; 2000WO-US020264. |
| XX | |
| PR | 26-JUL-1999; 99US-00360545. |
| XX | |
| PA | (UNIW) UNIV WASHINGTON STATE RES FOUND. |
| XX | |
| PI | Steele CL, Bohlmann J, Croteau RB, Phillips MA; |
| XX | |
| DR | WPI; 2001-182782/18. |
| DP | N-PSNR. AAE73412 |

| | |
|----|---|
| XX | |
| PT | New nucleic acid encoding monoterpene synthases, for increasing terpene |
| PT | synthesis in plants, e.g. for increasing resistance to pests or for |
| PT | treatment of cancer. |
| XX | |
| PS | Claim 12; Page 154-156; 175pp; English. |

CC The present invention provides the protein and coding sequences of
CC monoterpene synthases from the grand fir. These include (-)-camphene
CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-
CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase
CC and pinene synthase. The sequences can be used to produce transgenic
CC plants expressing high levels of the enzymes, resulting in levels which
CC are useful in protecting against and treating cancers, and to confer
CC insect resistance on plants
SQ Sequence 630 AA;
XX

| | | | | |
|-----------------------|------------------|-------------------|------------|-------------|
| Query Match | 69.6%; | Score 2264; | DB 4; | Length 630; |
| Best Local Similarity | 68.3%; | Pred. No. 1e-202; | | |
| Matches 435; | Conservative 78; | Mismatches 98; | Indels 26; | Gaps 9; |

| | | | |
|----|-----|--|-----|
| QY | 1 | MALLSTPLVSRCL-----SSSHEIKALRRTIPTLGICRPCKSAHNSINMCLTSVAST | 54 |
| Dh | 1 | MALVSSAP--KSCILHKSILIRSTHIELKPLRRTIPTLGMCRGKSFTEPSVMSLTAVSD | 57 |
| QY | 55 | DSVQRVRGVNYSNLWDDDFIOSLISTPYGAPDYRERADRLIGEVDIMENFKLEDG-- | 112 |
| Dh | 58 | DGLQRIRIGDYHSNLWDDDFIOQL-STPYGEPSYRERAELIGEVE-MENSMPEDEGESM | 115 |
| QY | 113 | ---NDLLQRLLLVDDVERLGIDRHFKKEIKTALDYNVSYNWNEKGIGCGRESVTDLNSTA | 169 |
| Dh | 116 | SPLNDLIERLMWMDSVERLGIDRHFKKEIKSALDYVSYWNNEKGIGCGRDVFEPDVNSTA | 175 |
| QY | 170 | LGLRTLRLHGTYVSSDVLVNFKDNGQFSSSTANIQIEGEIRGYLNLFRASLVAFPGEKV | 229 |
| Dh | 176 | SGFRTLRLHGYSVSSEVLKVFDQNGQAFSPSTK-ERDIRTVNLRYASFIAFPGEKV | 234 |
| QY | 230 | DEAETESTKYLRREALOKIPASSISLEIRDVLEYGWHNTNLPRLERNYMDVFGOHT---- | 285 |
| Dh | 235 | EBAEIFSSRYLKEAVQKIPIVSS-ISQEIDYTTYLEYGWHNTMPRLETRNYLDVFGHPITSPWL | 293 |
| QY | 286 | KNKNA----AEKLLELAKEFNIFHSLQERELKHVSRMWKDGSGPEMTFCRRHYEYAL | 341 |
| Dh | 294 | KKKRTQYLDSEKLELAKLENIFHSLQÖKELOYLRSWWIHSGPELTFGRHHVEYYTL | 353 |
| QY | 342 | ASCIAPBPHSGFRLGFTKNSHLITVLDMYDVFGTVDELFLTATIKRMDSAMECLPE | 401 |

PR 23-AUG-1999; 99US-0150262P.
XX
PA (KENT) UNIV KENTUCKY RES DEPT.
PA (SALK) SALK INST BIOLOGICAL STUDIES.
XX
PI Chappell J, Manna KR, Noel JP, Starks CM;
XX
DR WPI; 2000-292839/25.
DR N-PSDB; AAA38927.
XX
PT Novel terpene synthase enzymes, useful for producing terpene
PT hydrocarbons, e.g. fragrances or antitumor agents, are derived from known
PT enzymes by specific amino acid alterations.
XX
PS Claim 117; Page 390-392; 450pp; English.
XX
CC The present invention describes an isolated terpene synthase (I)
CC comprising a region with at least 20% identity to region 265-535 of a 548
CC amino acid (aa) sequence (Ia), given in AAY90831. (I) contains nine alpha
CC -carbon atoms (alphaC) that have interatomic distances, between each
CC other, within tabulated ranges, have a centre point (within a sphere of
CC radius 2.3 Angstrom) within tabulated ranges, and have an ordered
CC arrangement of R groups (defining aa side chains), excluding specific
CC tabulated arrangements (tables given in the specification). (I), and
CC related enzymes, are used to produce a wide range of terpenoids (e.g.
CC cyclic, acyclic, optionally hydroxylated), useful e.g. as fragrances,
CC flavours, pheromones, defensive agents, pigments, antitumour agents,
CC components of signal transduction pathways, precursors of steroid
CC hormones and bile acids, as photoreceptors and as co-factor side chains.
CC Some synthases with little or no catalytic activity (and nucleic acids
CC encoding them) are used as controls in the analysis of products formed by
CC enzymatic synthesis; as nutrient supplements; for affinity purification
CC of isoprenoids; or to develop immunological reagents or nucleic acids for
CC monitoring expression of terpene synthase or inheritance of the gene in
CC plant breeding programs. The new synthases may produce novel terpene
CC products. AAA38910 to AAA38938 and AAY90831 to AAY90859 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 627 AA;

Query Match 67.7%; Score 2200.5; DB 3; Length 627;
Best Local Similarity 68.1%; Pred. No. 9.1e-197;
Matches 427; Conservative 77; Mismatches 106; Indels 17; Gaps 7;
QY 1 MALSTPTPLVSRSC-----SSSHEIKALRRTIPTLGICRPGKSAHSINMCLTSVASTD 55
DB 1 MALVSTISPLASKSCLRKSLISSIHEHKPPYRTIPNLGMRRRGKSVTPSMSISLATAAPDD 60
QY 56 SVQRRVGNVHSNLMWDDDFIQSLISTPYGAPDYRERADRLIGEYKDIMFNFKSLDGG--- 112
DB 61 GVQRRIGDYHSNIMWDDDFIQSL-STPYGSPSYQERARLLIVEVKKI-FNSMYLDDGRLMS 118
QY 113 --NDLQRLLLVDDVERLGDIDRHFKKEIKTALDDVNSYWNKEGICGGRSVTDLNSTAL 170
DB 119 SFNDLMQRLMIVDSEVERLGIAHFKEITTSALDYFRYWEENGICGGRDSIVTDLNSTAL 178
QY 171 GLRTLRHGTYVSSDVLNVFKDKNGQSSSTANIQIEGEIRGVNLNFRASLVAFPGKXVM 230
DB 179 GFRTLRHGTYVSPVLKAFQDQNGQVCSFG-QTEGEIRSVNLNLYRASLVIAFPGKXVM 237
QY 231 EAETFEPTYLREALQKIPASSISLEIRDVLEYGWHNTNLPRLAARNYMDVFGQHTK--N 287
DB 238 EAETFEPTYLKEALQKIPVSA-LSQETIKFVMEYGMHTNLPRLEARNYIDTLEKDTSAWLN 296
QY 288 KNAEKLLELAKLEFNIFHSLQERELKHVSRWMDSGSPEMTFCHRHVEYVALASCIAP 347
DB 297 KNA GKLLLELAKLEFNIFNSLQKELQYLLRWKESDLPKLTFAHRHVEFYTLASCIAP 356
QY 348 EPGHSGFRLGFTKMSHLITVLDWMYDVGTVDELLELFTATIKRWDPASAMECLPEYMKGVY 407
DB 357 DPKGSAFRLGFAKMCHLVTVLDDIYDTFTIDLELELFTSAIKRWNSSEIEHLPEYMKCVY 416
QY 408 MMVYHTVNMARVAEKAQGRDTLNYARQAEACFDSYMQEAKWIAATGYLPTFEEYLENGK 467

DB 417 MVVEFTVNELTREAEKTOGRNTLNVYRKAWAEAYFDSYMEAKWISNGYLPMPFEEYHENGK 476
QY 468 VSSAHRPCALQPILTLDIPFPDHLKEVDFPSKNDLICIILRLRGDTRCYKADRARGE 527
DB 477 VSSAYRVATLQPILTNLAMLPDYILKIGIDFPSRFNDLASSFRLRGDTRCYKADRGRGEE 536
QY 528 ASSISCYMKDNPGLTEEDALNHINEMIRDAIRELNWELKPDNSVPITSKKHAFDISRW 587
DB 537 ASSISCYMKDNPGSTEEEDALNHINAMVNDI IKELNWEELRSDNIPMLAKKHAFDITRAL 596
QY 588 HHGYYRVDGYSFANVETKSLVWRTVIE 614
DB 597 HHLIYYRDGFSVANKETKKLWETLLE 623

RESULT 8
AAB69370
ID AAB69370 standard; protein; 627 AA.
XX
AC AAB69370;
XX
DT 30-APR-2001 (first entry)
XX
DE Grand fir myrcene synthase SEQ ID NO: 2.
XX
KW Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;
KW myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;
KW terpinolene synthase; insect resistance; nutrition.
XX
OS Abies grandis.
XX
PN WO200107565-A2.
XX
PD 01-FEB-2001.
XX
PF 24-JUL-2000; 2000WO-US020264.
XX
PR 26-JUL-1999; 99US-00360545.
XX
PA (UNIW) UNIV WASHINGTON STATE RES FOUND.
XX
PI Steele CL, Bohlmann J, Croteu RB, Phillips MA;
XX
DR WPI; 2001-182782/18.
DR N-PSDB; AAF73371.
XX
PT New nucleic acid encoding monoterpene synthases, for increasing terpene
PT synthesis in plants, e.g. for increasing resistance to pests or for
PT treatment of cancer.
XX
PS Claim 58; Page 106-107; 175pp; English.
XX
CC The present invention provides the protein and coding sequences of
CC monoterpene synthases from the grand fir. These include (-)-camphene
CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-
CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase
CC and pinene synthase. The sequences can be used to produce transgenic
CC plants expressing high levels of the enzymes, resulting in levels which
CC are useful in protecting against and treating cancers, and to confer
CC insect resistance on plants
XX
SQ Sequence 627 AA;

Query Match 67.7%; Score 2200.5; DB 4; Length 627;
Best Local Similarity 68.1%; Pred. No. 9.1e-197;
Matches 427; Conservative 77; Mismatches 106; Indels 17; Gaps 7;
QY 1 MALSTPTPLVSRSC-----SSSHEIKALRRTIPTLGICRPGKSAHSINMCLTSVASTD 55
DB 1 MALVSTISPLASKSCLRKSLISSIHEHKPPYRTIPNLGMRRRGKSVTPSMSISLATAAPDD 60
QY 56 SVQRRVGNVHSNLMWDDDFIQSLISTPYGAPDYRERADRLIGEYKDIMFNFKSLDGG--- 112

Db 61 GVGRRIGDHSNIWDDDFIQSL-STPYGEPSYQERAERLIVEVKKI-FNSMYLDDGRLMS 118
Qy 113 --NDLIQRLLLVDDVERLGIDRHFKKEIKTALDYVNSYWNKEGIGGRESVTDLNSTAL 170
Db 119 SFNDLMQRLMIVDSVERLGIARHFKNEITSALDYVFRYWEENGIGGRDSIVTDLNSTAL 178
Qy 171 GLRTLRLHGYTVSSDVLNVFKDKNGQFSSSTANIQIEGEIRGVNLPRASLVAFPGEKVM 230
Db 179 GFRTRLRHGYTVSPEVLKAFQDQNGQFVCSPG-QTEGEIRSVNLRYASLIAFPGEKVM 237
Qy 231 EAETFSYKYLREALQKIPASSILSLERDYLEYGMHTNLPRLAARNYMDVFGQHTK--N 287
Db 238 EAEIFSTRYLKEALQKIPVSA-LSQEIKFVMEYGMHTNLPRLAARNYIDTLEKDTSAWLN 296
Qy 288 KNAAEKLELAKLEFNI FHSLOERELKHVSRWKSDSGSPMTFCRRHVEYYALASCI AF 347
Db 297 KNAGKLELAKLEFNI FNSLQCKELQYLLRWKESDLPKLTFAHRHVEFYTLASCI AI 356
Qy 348 EPQHSGRFLGFTKMSHLITVLDMDYDVGTVDELELFTATIKRWDSAMECLPEYMKGVY 407
Db 357 DPKHSARFLGFAKCHLVTLDDIYDTFGTIDELFTSAIKRNSSEIEHLPEYMKCVY 416
Qy 408 MMVYHTVEMARVAEKAQGRDTLVYARQAWACFDSYMOEAKWIAATGYLPTPEEYLENGK 467
Db 417 MVFETYNELTREAEKTQGRNTLVYRKAWAYFDSYMEBAKWISNGYLPMEFEYHENGK 476
Qy 468 VSSAHRPCALQPIITLDIPFPDHILKEVDFPSKNDLICITILRLRGDTRCYKADRARGE 527
Db 477 VSSAYRVATLQPIITLVNAMLDPYILKGIDFPSRFNDLASSFLRLRGDTRCYKADRARGE 536
Qy 528 ASSISCYMKDNPGLTEEDALNHINEMIRDAIRELNWELKPDNSVPTSKGHAFDISR VW 587
Db 537 ASCISCYMKDNPGSTTEEDALNHINAMVNDIITIKELNWELLRSDNIPMLAKGHAFDITRAL 596
Qy 588 HHGYRRDGYSFANVETKSLVMRTVIE 614
Db 597 HHLIYTRDGFVSANKETKCLVMETLLE 623

RESULT 9
AAW85710
ID AAW85710 standard; protein; 627 AA.
XX
AC AAW85710;
XX
DT 27-SEP-1999 (first entry)
XX
DE Grand fir monoterpene synthase clone AG3.48.
XX
KW Mycrene synthase; limonene synthase; pinene synthase; flavour;
KW monoterpene synthase; aroma; defense; plant seed; oil; meal; primer; PCR;
KW probe.
XX
OS Abies grandis.
XX
PN WO9902030-A1.
XX
PD 21-JAN-1999.
XX
PF 10-JUL-1998; 98WO-US014528.
XX
PR 11-JUL-1997; 97US-0052249P.
XX
PA (UNIW) UNIV WASHINGTON STATE RES FOUND.
XX
PI Bohlmann J, Steele CL, Croteau RB;
XX
DR WPI; 1999-120396/10.
XX
PT N-PSDB; AAX08663.
PT New isolated gymnosperm monoterpene synthase DNA - obtained from Grand
fir (Abies grandis), used to provide plants with modified production of

PT monoterpene, e.g. mycrene, limonene or pinene.
XX
PS Example 3; Page 107-109; 121pp; English.
XX
CC Nucleotide sequences encoding mycrene synthase, limonene synthase and
CC pinene synthase from Grand fir may be incorporated into any organism
CC (e.g. intact plant, animal, microbe), or derived cell culture that
CC produces geranyl diphosphate for the production of the aforementioned
CC enzymes or their products. The sequences when expressed in transfected
CC cells may also be used for the production or modification of flavour and
CC aroma properties, improvement of defense capability, and the alteration
CC of other ecological interactions mediated by mycrene, limonene, pinene,
CC or their derivatives. In particular they can be used for the production
CC of plant seeds for the extraction of oil or meal
XX
SQ Sequence 627 AA;

Query Match 67.6%; Score 2197.5; DB 2; Length 627;
Best Local Similarity 68.1%; Pred. No. 1.7e-196;
Matches 427; Conservative 77; Mismatches 106; Indels 17; Gaps 7;

Qy 1 MALSTPLVSRCL-----SSHEIKALRTIPTLGICRPGKVAHSINMCLTSVASTD 55
Db 1 MALVISISPLASKSCLRKSLISSIHEHKBPYRTIPNLGMRRRGKSVTPSMSISLATAPDD 60
Qy 56 SVQRRVGNVHSNIWDDDFIQSL-STPYGAPDYRERADRLIGEYKDIMFNKSLDEGG--- 112
Db 61 GVGRRIGDHSNIWDDDFIQSL-STHYGEPSYQERAERLIVEVKKI-FNSMYLDDGRLMS 118
Qy 113 --NDLIQRLLLVDDVERLGIDRHFKKEIKTALDYVNSYWNKEGIGGRESVTDLNSTAL 170
Db 119 SFNDLMQRLMIVDSVERLGIARHFKNEITSALDYVFRYWEENGIGGRDSIVTDLNSTAL 178
Qy 171 GLRTLRLHGYTVSSDVLNVFKDKNGQFSSSTANIQIEGEIRGVNLPRASLVAFPGEKVM 230
Db 179 GFRTRLRHGYTVSPEVLKAFQDQNGQFVCSPG-QTEGEIRSVNLRYASLIAFPGEKVM 237
Qy 231 EAETFSYKYLREALQKIPASSILSLERDYLEYGMHTNLPRLAARNYMDVFGQHTK--N 287
Db 238 EAEIFSTRYLKEALQKIPVSA-LSQEIKFVMEYGMHTNLPRLAARNYIDTLEKDTSAWLN 296
Qy 288 KNAAEKLELAKLEFNI FHSLOERELKHVSRWKSDSGSPMTFCRRHVEYYALASCI AF 347
Db 297 KNAGKLELAKLEFNI FNSLQCKELQYLLRWKESDLPKLTFAHRHVEFYTLASCI AI 356
Qy 348 EPQHSGRFLGFTKMSHLITVLDMDYDVGTVDELELFTATIKRWDSAMECLPEYMKGVY 407
Db 357 DPKHSARFLGFAKCHLVTLDDIYDTFGTIDELFTSAIKRNSSEIEHLPEYMKCVY 416
Qy 408 MMVYHTVEMARVAEKAQGRDTLVYARQAWACFDSYMOEAKWIAATGYLPTPEEYLENGK 467
Db 417 MVFETYNELTREAEKTQGRNTLVYRKAWAYFDSYMEBAKWISNGYLPMEFEYHENGK 476
Qy 468 VSSAHRPCALQPIITLDIPFPDHILKEVDFPSKNDLICITILRLRGDTRCYKADRARGE 527
Db 477 VSSAYRVATLQPIITLVNAMLDPYILKGIDFPSRFNDLASSFLRLRGDTRCYKADRARGE 536
Qy 528 ASSISCYMKDNPGLTEEDALNHINEMIRDAIRELNWELKPDNSVPTSKGHAFDISR VW 587
Db 537 ASCISCYMKDNPGSTTEEDALNHINAMVNDIITIKELNWELLRSDNIPMLAKGHAFDITRAL 596
Qy 588 HHGYRRDGYSFANVETKSLVMRTVIE 614
Db 597 HHLIYTRDGFVSANKETKCLVMETLLE 623

RESULT 10
AAB69380
ID AAB69380 standard; protein; 627 AA.
XX
AC AAB69380;
XX
DT 30-APR-2001 (first entry)

XX Grand fir monoterpene synthase protein fragment SEQ ID NO: 32.
DE
XX Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;
KW myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;
KW terpinolene synthase; insect resistance; nutrition.
XX
OS Abies grandis.
XX
PN WO200107565-A2.
XX
PD 01-FEB-2001.
XX
PF 24-JUL-2000; 2000WO-US020264.
XX
PR 26-JUL-1999; 99US-00360545.
XX
PA (UNIW) UNIV WASHINGTON STATE RES FOUND.
XX
PI Steele CL, Bohlmann J, Croteu RB, Phillips MA;
XX
PI
XX WPI; 2001-182782/18.
DR N-PSDB; AAF73391.
XX
XX New nucleic acid encoding monoterpene synthases, for increasing terpene
PT synthesis in plants, e.g. for increasing resistance to pests or for
PT treatment of cancer.
XX
PS Disclosure; Page 138-139; 175pp; English.
XX
CC The present invention provides the protein and coding sequences of
CC monoterpene synthases from the grand fir. These include (-)-camphene
CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-
CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase
CC and pinene synthase. The sequences can be used to produce transgenic
CC plants expressing high levels of the enzymes, resulting in levels which
CC are useful in protecting against and treating cancers, and to confer
CC insect resistance on plants
XX
SQ Sequence 627 AA;

Query Match 67.6%; Score 2197.5; DB 4; Length 627;
Best Local Similarity 68.1%; Pred. No. 1.7e-196;
Matches 427; Conservative 77; Mismatches 106; Indels 17; Gaps 7;

QY 1 MALISITPLVSRSC-----SSSHKIKALRTIPTLGICRPGKSAHNSIMCLTSVASTD 55
Db 1 MALVISISPLASKSCLRKSLISSIHEHKPPYRTIPNLGMRRRGKSVTPSMSISLATAPDD 60
QY 56 SVORRVGNHNSLWDDDFIQSLISTPYGAPDYRERADRLIGEVKDIMFNFKSLLEDG--- 112
Db 61 GVGRRIGDYHSNIWDDDFIQSL-STHYGEPSSYOERAERLIVEVKI-FNSMYLDDGRLMS 118
QY 113 --NDLLQRLLLVDVERLGIDRHEKKEIKTALDYNSYWNKIGCGRESVTDLNSTAL 170
Db 119 SFNDLMQRLWIVDSVERLGIAHFKEITSALDYVFRYWEENGIGCGRDSIVTDLNSTAL 178
QY 171 GLRTRLHGTYVSSDVLNVFKDKNGQFSSSTANIQIEGIRGVNLFRASLVAFPGEKVM 230
Db 179 GFRTRLRHGYTVSPVLLKAFQDQNGQFVCSPG-QTEGEIRSVNLVRSALIAFPGEKVM 237
QY 231 EAETFTSKYLREALQKIPASSISLEIRDVLEYGWHNTNLPRLAARNYMDVFGQHTK---N 287
Db 238 EAETFTSTRYLKEALQKIPVSA-LSGEIKFVMEYGMHTNLPRLAARNYIDTLEKDTSAWLN 296
QY 288 KNAAEKLLLELAKLEFNIFHSLQERELKHVSRWKKDSSPEMTFCRRHVEYYALASCI 347
Db 297 KNA GKLLLELAKLEFNIFNSLQOKELQYLLRWKESDLPKLTFAHRHVEFYTLASCI 356
QY 348 EPOHSGFRLGFTKMSHLITVLDMYDVFGTVDELELFTATIKRWDPSAMECLPEYMKGV 407
Db 357 DPKGSAFRLGFAKMCHLVTVLDDIYDTFGTIDELFTSAIKRWNSSIEHLP EYMKCVY 416

QY 408 NMVYHTVNEMARVAEKAQGRDITLNYARQAWACFDSYMOEAKMIATGYLPTFE EYL ENGK 467
Db 417 MVVFETVNELTREAEKTQGHNTLNVVRKAMEAYFDSYMEAKMISNGYLP TFE EYHENGK 476
QY 468 VSSAHRPCALQPILTLDIPEDHILKEVDPPSKLNDLICILRLRGDTRCYKADRARGE 527
Db 477 VSSAYRVATLQPILTLLNWLDPDIILKGIDPSPRFNDLASSFLRLRGDTRCYKADRGE 536
QY 528 ASGISCYMKDNPGLTEEDALNHINMIRDAIRELNLWELIKPDNSVPITSKHAFDISRYW 587
Db 537 ASCISCYMKDNPGST EEDALNHINAMVNDI IKELNLWELLSNDNI PMLAKHAFDITRAL 596
QY 588 HHGYRRDGYSPFANVETKSLVMRTVIE 614
Db 597 HHLYIYRDGFSVANKETKLVMEITLLE 623

RESULT 11
ABB79395
ID ABB79395 standard; protein; 627 AA.
XX
AC ABB79395;
XX
DT 13-AUG-2002 (first entry)
XX
DE Taxadiene synthase homologous protein sequence w85710.
XX
KW Taxane; taxane synthesis; taxadiene synthase; cytostatic; anticancer;
KW enzyme.
XX
OS Unidentified.
XX
PN WO200240694-A2.
XX
PD 23-MAY-2002.
XX
PF 16-NOV-2001; 2001WO-DK000763.
XX
PR 17-NOV-2000; 2000DK-00001730.
PR 29-NOV-2000; 2000US-0253843P.
XX
PA (NOVO) NOVOZYMES AS.
XX
PI Vind J;
XX
DR WPI; 2002-471624/50.
XX
PT Heterologous production of taxane analogs related compound useful as
PT anticancer agent involves cloning a full-length taxane synthesis pathway
PT from a taxan-producing organism into a taxane-resistant host cell.
XX
PS Example 3; Fig 1; 60pp; English.
XX
CC The present invention describes the heterologous expression of taxane
CC analogues, comprising cloning a DNA sequence comprising a taxane
CC synthesis pathway, making a DNA construct in which the DNA sequence is
CC under control of regulatory elements, introducing the DNA construct into
CC a host cell, growing the host cell to produce taxane analogues, and
CC recovering the required taxane from the culture medium. Also described:
CC (1) an isolated DNA sequence comprising the taxane synthesis pathway,
CC (preferably taxol synthesis pathway); (2) an expression vector comprising
CC the isolated DNA sequence; and (3) a host cell comprising a taxane
CC synthesis pathway derived from a taxane-producing organism, plant or
CC tree, the taxane synthesis pathway is foreign to the host cell. The
CC taxane analogues have cytostatic activity, and so can be used as
CC anticancer agents. The present sequence represents a taxadiene synthase
CC homologous protein, which is given in an example from the present
CC invention
XX
SQ Sequence 627 AA;

Query Match 67.6%; Score 2197.5; DB 5; Length 627;
Best Local Similarity 68.1%; Pred. No. 1.7e-196;

| | | | | | | | | | |
|-----------|---|---|-----|------------|------|--------|-----|------|----|
| Matches | 427; | Conservative | 77; | Mismatches | 106; | Indels | 17; | Gaps | 7; |
| QY | 1 | MALSTIPLVSRCL-----SSSHEIKALRRTIPTLGICRPGKSAHAINMCLTSVASTD | 55 | | | | | | |
| Db | 1 | MALVSIPLASKSCLRKSLISSIHEHKPPYRTIPNLGMRRGKSVTPSMSISLATAAPDD | 60 | | | | | | |
| QY | 56 | SVQRRVGNVHSNLWDDDFIQSLISTPYGAPDYRERADRLIGEVDIMFNKSLDGG-- | 112 | | | | | | |
| Db | 61 | GVQRRIGDYHSNIWDDDFIQSL-STHYGEPSYQERAERLIVEVKKI-FNSMYLDDGRIMS | 118 | | | | | | |
| QY | 113 | --NDLLQRLLLVDYVERLGIDRHFKKEIKTALDYVNSYWNKEGICGRESVTDLNSTAL | 170 | | | | | | |
| Db | 119 | SFNDLMQRLMIVDSVERLGIAHFKNIEITSALDYVERWYWEENIGIGGRDSIVTDLNSTAL | 178 | | | | | | |
| QY | 171 | GLRTRLRHGYTVSSDVLFVKDKNGQFSSSTANIQIEGEIRGVNLFRASLVAFPEKVM | 230 | | | | | | |
| Db | 179 | GFRTLRLHGTYVSPVLKAFQDQNGQFVCSPG-QTEGEIRSVNLNFRASLIAFPGEKVM | 237 | | | | | | |
| QY | 231 | EAEFTSTKYLRALQKIPASSILSLERDVLLEYGWHNLPRLEARNYMDVFGQHTK--N | 287 | | | | | | |
| Db | 238 | EAEIFSTRYLKEALQKIPVSA-LSQELKFMEYGMHTNLPRLERANYIDTLEKDTSAWLN | 296 | | | | | | |
| QY | 288 | KNAAEKLLLELAKLEFNI FHSLOERELKHVSRWKDSGSPMTFCRHRHVEYYALASCI | 347 | | | | | | |
| Db | 297 | KNAGKLLLELAKLEFNI FNSLQKELQYLRLRWKESDLPRLTFAHRHVEFYTLASCI | 356 | | | | | | |
| QY | 348 | EPQHSGRFLGFTKMSHLITVLDMDYDFGTVDELELFTATIKRWDPSAMECLPEYMKGV | 407 | | | | | | |
| Db | 357 | DPKHSAFRLGFAKMCHLVTLDDIYDTFGTIDELFTSAIKRWNSSEIHLPEYMKGV | 416 | | | | | | |
| QY | 408 | KMYVHTVNEMARVAEKAQGRDTLNVARQAEACFDSYMOEAKWIATGYLPTFEEYLENG | 467 | | | | | | |
| Db | 417 | MVVFETVNELTREAEKTQGRNTLVNRKAEAYFDSYMEAKWISNGYLLPTFEEYHENG | 476 | | | | | | |
| QY | 468 | VSSAHRPCALQPIITLDIPFPDHILKEVDFPSKLANDLICITLRLRGDTRCYKADRAGE | 527 | | | | | | |
| Db | 477 | VSSAYRVATLQPIITLNLAWLPDYILKGLDFPSRFNDLASSFLRLRGDTRCYKADRAGE | 536 | | | | | | |
| QY | 528 | ASSISCYMKDNPGLTEEDALNHINFMIRDAIRELNWELKPDNSVPITSKGHAFDISRW | 587 | | | | | | |
| Db | 537 | ASCISCYMKDNPGSTEEDALNHINAMVNDI IKELNWEILRSNDNIPMLAKKHAFDITRAL | 596 | | | | | | |
| QY | 588 | HHGYRRDGYSFANVETKSLVMRTVIE | 614 | | | | | | |
| Db | 597 | HHLYIYRDGFSVANKEVKLVMTLE | 623 | | | | | | |
| RESULT 12 | | | | | | | | | |
| ID | AAB69393 | standard; protein; 630 AA. | | | | | | | |
| AC | AAB69393; | | | | | | | | |
| DT | 30-APR-2001 | (first entry) | | | | | | | |
| DE | Grand fir monoterpene synthase SEQ ID NO: 78. | | | | | | | | |
| XX | Monoterpene synthase; grand fir; cancer; (-)-camphene synthase; | | | | | | | | |
| XX | myrcene synthase; (-)-limonene synthase; (-)-pinene synthase; | | | | | | | | |
| XX | terpinolene synthase; insect resistance; nutrition. | | | | | | | | |
| OS | Abies grandis. | | | | | | | | |
| XX | | | | | | | | | |
| PN | WO200107565-A2. | | | | | | | | |
| PD | 01-FEB-2001. | | | | | | | | |
| PF | 24-JUL-2000; 2000WO-US020264. | | | | | | | | |
| PR | 26-JUL-1999; 99US-00360545. | | | | | | | | |
| PA | (UNIW) UNIV WASHINGTON STATE RES FOUND. | | | | | | | | |

| | | | | |
|-----------------------|---|--|-------------|--------------|
| PI | Steele CL, | Bohlmann J, | Croteau RB, | Phillips MA; |
| XX | | | | |
| DR | WPI; 2001-182782/18. | | | |
| DR | N-PSDB; AAF73421. | | | |
| XX | | | | |
| PT | New nucleic acid encoding monoterpene synthases, for increasing terpene | | | |
| PT | synthesis in plants, e.g. for increasing resistance to pests or for | | | |
| PT | treatment of cancer. | | | |
| XX | | | | |
| PS | Claim 50; Page 166-167; 175pp; English. | | | |
| XX | | | | |
| CC | The present invention provides the protein and coding sequences of | | | |
| CC | monoterpene synthases from the grand fir. These include (-)-camphene | | | |
| CC | synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)- | | | |
| CC | limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase | | | |
| CC | and pinene synthase. The sequences can be used to produce transgenic | | | |
| CC | plants expressing high levels of the enzymes, resulting in levels which | | | |
| CC | are useful in protecting against and treating cancers, and to confer | | | |
| CC | insect resistance on plants | | | |
| XX | | | | |
| SQ | Sequence 630 AA; | | | |
| | | | | |
| Query Match | 65.7%; | Score 2137; | DB 4; | Length 630; |
| Best local Similarity | 67.4%; | Pred. No. 8.3e-191; | | |
| Matches 427; | Conservative 73; | Mismatches 114; | Indels 20; | Gaps 9 |
| QY | 1 | MALSTIPLVSRSL-----SSSEIKALRTIPTLGICRPGKSAHSINMCLTSVASTD | 55 | |
| DB | 1 | MALVSIPLSSKSVLHKSWIVSTYEHKAISRTIPNLGRLGRGKSTHSLRMSLSTAVSD | 60 | |
| QY | 56 | -SVQRRVGNVHSNLWDDDFIQSLISTPYGAPDYRERADRLIGEVDIMFNKSLDGG-- | 112 | |
| DB | 61 | HGVQRRIVEFHSNLWDDDFIQSL-STPYGAPSYRERADRLIVEYKGI-FTSISADEGLI | 118 | |
| QY | 113 | ---NDLLQRLLVDDVERLGIDRHFKKEIKTALDYVNSYWNKEGICGRESVTDLNSTA | 169 | |
| DB | 119 | TPLNDLIQRLMVDNVERLGIDRHFKKEIKALDYVSYWNKEGICGSDSGVADLNSTA | 178 | |
| QY | 170 | LGRLTRLHGTYVSSDVLFVKDK--KNGQFSSSTANIQIEGEIRGVNLFRASLVAFPGEK | 227 | |
| DB | 179 | LGFRILRLHGYSVSSDVLEHFKEEKEKGQFVCSA-IQTEBEIKSVNLFRASLIAFPGEK | 237 | |
| QY | 228 | VMDEAETPSTKYLRALQKIPASSILSLERDVLLEYGWHNLPRLEARNYMDVFGQHTKN | 287 | |
| DB | 238 | VMEAEIFSKIYLRALQNI | | |

ID AAB69392 standard; protein, 637 AA.
 AC AAB69392;
 XX
 DT 30-APR-2001 (first entry)
 XX
 DE Grand fir monoterpene synthase protein fragment SEQ ID NO: 69.
 XX
 KW Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;
 KW myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;
 KW terpinolene synthase; insect resistance; nutrition.
 XX
 OS Abies grandis.
 XX
 PN WO200107565-A2.
 PD 01-FEB-2001.
 XX
 PF 24-JUL-2000; 2000WO-US020264.
 XX
 PR 26-JUL-1999; 99US-00360545.
 XX
 PA (UNIW) UNIV WASHINGTON STATE RES FOUND.
 XX
 PI Steele CL, Bohlmann J, Croteau RB, Phillips MA;
 XX
 DR WPI: 2001-182782/18.
 DR N-PSDB; AAF73413.
 XX
 PT New nucleic acid encoding monoterpene synthases, for increasing terpene
 PT synthesis in plants, e.g. for increasing resistance to pests or for
 PT treatment of cancer.
 PS
 PS Claim 54; Page 159-161; 175pp; English.
 CC
 CC The present invention provides the protein and coding sequences of
 CC monoterpene synthases from the grand fir. These include (-)-camphene
 CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-
 CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase
 CC and pinene synthase. The sequences can be used to produce transgenic
 CC plants expressing high levels of the enzymes, resulting in levels which
 CC are useful in protecting against and treating cancers, and to confer
 CC insect resistance on plants
 CC
 XX
 XX Sequence 637 AA;
 SQ
 Query Match 64.1%; Score 2084.5; DB 4; Length 637;
 Best Local Similarity 64.9%; Pred. No. 7.1e-186;
 Matches 417; Conservative 80; Mismatches 115; Indels 31; Gaps 13;
 QY 1 MALLSITPL-VSRSC-----LSSSHEIKAL--RRTIPTLGICRPGKSAHNSIMCLTSTA 52
 DB 1 MALLSIVSLQVPKSCGLKSLISSNVQKALCISTAVPTLRRRRQKALV--INMKLTIVS 58
 QY 53 STDS-----VQRRVGNVHNSIMDDDFIQSLISTPYGAPDYREBRADRLIGEVDIMFN-- 105
 DB 59 HRDDNGGGVLQRRRIADHHPNLWEDDFIQSL-SSPYGGSSYSERAVTVEEVEKE-MFNSIP 116
 QY 106 --KSLEDGGNDLLQRLLLVDDVERLGIDRHFKKEIKTALDYNSYNEK-GIGCGRESVV 162
 DB 117 NNRELFQSQNDLLTRLWMVDSIERLGIDRHQNEIRVALDYYSYWEKEGIGCGRDTF 176
 QY 163 TDLNSTALGLRTLRLHGTVSSDVLNVFKDKNGQFSSTANIQIEGEI-RGVLNLFRASTV 221
 DB 177 PDLNSTALALRTLRLHGYNVSSDVLVEYFKDQGHFACPA-ILTEGQITRSVLNLYRASLV 235
 QY 222 AFGPEKVMDEAETFTSKYLREALQKIPASSILSLRIDVLEYGWHTNLPRLEARNYMDVF 281
 DB 236 AFGPEKVMEEAEIFSAASYLKEVLOKIPVSS-FSREIEYVLEYGWHTNLPRLEARNYIDVY 294
 QY 282 GQHTKNKN-----AAEKLELAKLIEFNIFHSLQERELKHVSRWWDKSGSPEMTFCHRHR 335
 DB 295 GQDSYESSNEMPYVNTQKLKLAKLIEFNIFHSLQOKELQYISRWWDKSSSHLFTTRHRH 354

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|----|-----|------------|----------|----------|----------|----------|----------|----------|----------|----------|------------|------|-------|--------|-----|-----|---|---|---|-----|---|---|---|---|---|---|---|---|---|---|---|-----|
| Qy | 336 | VEYYALASCI | AEFPQHS | GFRLGFTK | MSHLITVL | DDMYDV | FGTVDELE | LEFTATIK | RWDPSA | 395 | | | | | | | | | | | | | | | | | | | | | | |
| | | : : | : : | : : | : : | : : | : : | : : | : : | | | | | | | | | | | | | | | | | | | | | | | |
| Db | 355 | VEYYTMASCI | SMEPKHS | AFRLG | FVKTC | HLITVL | DDMYDT | FGTLD | LEQLFTTA | EKRWDLSE | 414 | | | | | | | | | | | | | | | | | | | | | |
| Qy | 396 | MECLPEYMK | GVYMMV | YHYVEN | EMARVA | EKAQGR | DTLNYARQ | AWACFP | DSYMQE | AKWIATGY | 455 | | | | | | | | | | | | | | | | | | | | | |
| | | : : | : | : | : | : | : | : | : | : | | | | | | | | | | | | | | | | | | | | | | |
| Db | 415 | TKCLPEYMK | AVYMDLYQ | CLNELAQ | EAEKTOGR | DTLNYIRN | AYESHF | DSFME | BAKWI | SSGY | 474 | | | | | | | | | | | | | | | | | | | | | |
| Qy | 456 | LPTEEYLE | NGKVS | SAHRPC | ALQILTL | DIPEPD | HLKEVD | FPSK | LNDLIC | ILRLRGDT | 515 | | | | | | | | | | | | | | | | | | | | | |
| | | : | : | : | : | : | : | : | : | : | | | | | | | | | | | | | | | | | | | | | | |
| Db | 475 | LPTEEYLN | KGKVS | SGSR | TATQIL | TL | DVPL | PNYILO | EIDYPS | RFNDL | ASSLRLRGDT | 534 | | | | | | | | | | | | | | | | | | | | |
| Qy | 516 | RCYKADR | RAGEE | ASSIS | CYMKD | PGLT | TEEDAL | NHIN | FIRDAI | RELN | WELLPK | DN | SV | PT | 575 | | | | | | | | | | | | | | | | | |
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | | | | | | | | | | | | | | | | | |
| Db | 535 | RCYKADR | RAGEE | ASAI | SCYMK | DHPG | ST | EE | DALN | HIN | MISDAI | RELN | WELLP | DKSPIS | | 594 | | | | | | | | | | | | | | | | |
| Qy | 576 | SKKHA | FDIS | RV | MHHG | RYR | DGYS | EFAN | VE | TKSL | V | M | R | T | V | IE | P | V | L | 618 | | | | | | | | | | | | |
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | | | | | | | | | | | | | |
| Db | 595 | SKKHA | FDIT | RA | FH | HL | YK | YR | DG | Y | T | V | A | S | S | E | T | K | N | L | V | M | K | T | V | L | E | P | V | A | L | 637 |

RESULT 14

AAW85702 ID AAW85702 standard; protein; 637 AA.

AAW85702; AC 27-SEP-1999 (first entry)

DE Limonene synthase of grand fir.

KW Myrcene synthase; limonene synthase; pinene synthase; flavour; aroma; defense; plant seed; oil; meal.

OS Abies grandis.

PN WO9902030-A1.

PD 21-JAN-1999.

PF 10-JUL-1998; 98WO-US014528.

PR 11-JUL-1997; 97US-0052249P.

PA (UNIW) UNIV WASHINGTON STATE RES FOUND.

PI Bohlmann J, Steele CL, Croteau RB;

DR WPI, 1999-120396/10.

XX N-PSDB; AAX08645.

PT New isolated gymnosperm monoterpene synthase DNA - obtained from Grand fir (Abies grandis), used to provide plants with modified production of monoterpenes, e.g. myrcene, limonene or pinene.

PS Claim 14; Page 82-84; 121pp; English.

CC Nucleotide sequences encoding myrcene synthase, limonene synthase and pinene synthase from Grand fir may be incorporated into any organism (e.g. intact plant, animal, microbe), or derived cell culture that produces geranyl diphosphate for the production of the aforementioned enzymes or their products. The sequences when expressed in transfected cells may also be used for the production or modification of flavour and aroma properties, improvement of defense capability, and the alteration of other ecological interactions mediated by myrcene, limonene, pinene, or their derivatives. In particular they can be used for the production of plant seeds for the extraction of oil or meal

XX Sequence 637 AA;

Query Match 62.5%; Score 2031.5; DB 2; Length 637;

Best Local Similarity 63.6%; Pred No. 6.6e-181;

| | | | | | | | | | |
|-----------|---|---|-----|------------|------|--------|-----|------|-----|
| Matches | 409; | Conservative | 84; | Mismatches | 119; | Indels | 31; | Gaps | 14; |
| QY | 1 | MALLSTITPL-VSRSC-----LSSSHEIKAL--RRTIPTLGICRPGKSAHNSIMCLTSVA | 52 | | | | | | |
| Db | 1 | MALLSTIVSLQVPKSCGLKSLISSNVQKALCISTAVPTLRMRROKALV--INMKLTIVS | 58 | | | | | | |
| QY | 53 | STDS-----VQRRVGNVNSNLWDDDFIQSLISTPYGAPDYRERADRLIGEVDIMFNF-- | 105 | | | | | | |
| Db | 59 | HRDNGGGVLRRIADHHPNLWEDDFIQSL-SSPYGSSYSERAEIVVEEVEKE-MFNSIP | 116 | | | | | | |
| QY | 106 | --KSLEDGNDLLQRLLLVDVERLIGDRHFKEIKTALDYVNSYWNK-GIGCGRESVV | 162 | | | | | | |
| Db | 117 | NNRELFGSQNDLLTRLMMVDSIERLIGIDRHQNEIRVALDYVYSYWEKEGIGCGRDSTF | 176 | | | | | | |
| QY | 163 | TDLNSTALGLRTLRLHGTYVSSDVLNVFKDKNGQFSSTANIQIEGEI-RGVNLFRASLV | 221 | | | | | | |
| Db | 177 | PDLNSTALALRTLRLHGVNVSDDVLEYFKDEKGFACPA-ILTEGQITRSVLNLYRASLV | 235 | | | | | | |
| QY | 222 | AFPGEKVMDEAETFTSTKYLRREALQKIPASSILSLERDVLLEYGWHNTNLPRLERANYMDF | 281 | | | | | | |
| Db | 236 | AFPGEKVMEEAEIIFSASYLKVKVLOKIPVSN-LSGEIEYVLEYGWHNTNLPRLERANYIEVY | 294 | | | | | | |
| QY | 282 | ---GQHTKNKNA--AEKLELAKLEFNIHFSLOERELKHVSRWKWDGSGSPMTFCRHRH | 335 | | | | | | |
| Db | 295 | EQSGYESLNEMPYMMKKLLQLAKLEFNIHFSLORELQISRWKESGSSQLTFRHRH | 354 | | | | | | |
| QY | 336 | VEYYALASCIAPFPOHSGFRLGFTKMSHLITVLDMDYDFGTVDLELEFTATIKRWDPGA | 395 | | | | | | |
| Db | 355 | VEYYTMAASCISMLPKHSAFRMEFVKVCHLVTVLDDIYDTFGTWNELQLFTDAIKRWDLST | 414 | | | | | | |
| QY | 396 | MECLPEYMKGVYMMVYHTVNEMARVAEKAQGRDTLVYARQAWACPDSYMGEAKWIATGY | 455 | | | | | | |
| Db | 415 | TRWLEPYMKGVYMDLYQCINEMVEBAEKTQGRDMLNYIQNAWEALFDTFMGEAKWISSSY | 474 | | | | | | |
| QY | 456 | LPTFEEXLENGKVSSAHRPCALQPIITLDIPERDHIKKEVDPSKNDLICITLRLRGDT | 515 | | | | | | |
| Db | 475 | LPTFEEXLKNKAKVSSGSRIATLQPIITLDVPLDPYILQEIIDYPSRFNELASSILRLRGDT | 534 | | | | | | |
| QY | 516 | RCYKADRARAGEEASSISCYMKDNPGLTEEDALNHINFMIRDAIRELWELLKPDNSVPIT | 575 | | | | | | |
| Db | 535 | RCYKADRARAGEEASAIISCYMKDHPGSIIEEDALNHINAMISDAIRELWELLRPDSKSPIS | 594 | | | | | | |
| QY | 576 | SKKGAFDISRVMHNGYRYRDGYSPANVETKSLVMRTVIEPVPL | 618 | | | | | | |
| Db | 595 | SKKGAFDITRAFHNVYKYRDGYTVSNNETKNLVMTVLEPLAL | 637 | | | | | | |
| RESULT 15 | | | | | | | | | |
| ID | AA90859 | standard; protein; 637 AA. | | | | | | | |
| AC | AA90859; | | | | | | | | |
| DT | 25-AUG-2000 | (first entry) | | | | | | | |
| DE | Grand fir limonene synthase protein sequence SEQ ID NO:58. | | | | | | | | |
| KW | Synthase; protein co-ordinate data; active site; modification; terpenoid; | | | | | | | | |
| KW | 3-dimensional coordinate; alpha carbon atom; plant; terpene synthase; | | | | | | | | |
| KW | isoprenoid; breeding programme; fragrance; flavour; pheromone; | | | | | | | | |
| KW | defensive agent; pigment; anticlinal; steroid hormone; | | | | | | | | |
| KW | signal transduction pathway; bile acid; affinity purification; | | | | | | | | |
| KW | photoreceptor; enzymatic synthesis; nutrient supplement; | | | | | | | | |
| KW | immunological reagent. | | | | | | | | |
| OS | Abies grandis. | | | | | | | | |
| PN | WO200017327-A2. | | | | | | | | |
| PD | 30-MAR-2000. | | | | | | | | |
| PF | 17-SEP-1999; 99WO-US021419. | | | | | | | | |
| XX | | | | | | | | | |

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|----|--------------|----------------|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|
| PR | 18-SEP-1998; | 98US-0100993P. | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|----|--------------|----------------|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|--|

[illegible]

Search completed: July 23, 2004, 09:02:26
Job time : 60 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2004, 09:00:27 ; Search time 21 Seconds
(without alignments)
2830.779 Million cell updates/sec

Title: US-10-025-145A-65
Perfect score: 3251
Sequence: 1 MALISITPLVSRSLSSSHE.....FANVETKSLVMTVIEPVPL 618

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|--------|--------------------|
| 1 | 724.5 | 22.3 | 599 | 2 | A48863 | limonene cyclase - |
| 2 | 717.5 | 22.1 | 554 | 2 | S68366 | (+)-delta-cadinene |
| 3 | 717.5 | 22.1 | 554 | 2 | S68365 | (+)-delta-cadinene |
| 4 | 689.5 | 21.2 | 591 | 2 | H84633 | probable limonene |
| 5 | 669.5 | 20.6 | 520 | 2 | A56118 | vetispiradiene syn |
| 6 | 656 | 20.2 | 600 | 2 | F71434 | probable limonene |
| 7 | 641.5 | 19.7 | 550 | 2 | T03714 | 5-epi-aristolochen |
| 8 | 632 | 19.4 | 559 | 2 | T08174 | sesquiterpene cycl |
| 9 | 615.5 | 18.9 | 548 | 2 | T06266 | germacrene C synth |
| 10 | 614.5 | 18.9 | 548 | 2 | T06265 | germacrene C synth |
| 11 | 586.5 | 18.0 | 1024 | 2 | G71434 | probable limonene |
| 12 | 569 | 17.5 | 632 | 2 | E96723 | hypothetical prote |
| 13 | 536 | 16.5 | 598 | 2 | H86460 | hypothetical prote |
| 14 | 504.5 | 15.5 | 785 | 2 | G96825 | hypothetical prote |
| 15 | 504.5 | 15.5 | 785 | 2 | T52059 | ent-kaurene syntha |
| 16 | 497.5 | 15.3 | 608 | 2 | G86443 | probable terpene s |
| 17 | 486.5 | 15.0 | 789 | 2 | T09672 | ent-kaurene syntha |
| 18 | 483 | 14.9 | 582 | 2 | C71424 | hypothetical prote |
| 19 | 481 | 14.8 | 530 | 2 | G96588 | hypothetical prote |
| 20 | 437.5 | 13.5 | 598 | 2 | T00509 | probable vetispira |
| 21 | 427.5 | 13.1 | 421 | 2 | C96642 | hypothetical prote |
| 22 | 426 | 13.1 | 598 | 2 | F96684 | probable terpene s |
| 23 | 425 | 13.1 | 350 | 2 | C56118 | vetispiradiene syn |
| 24 | 423.5 | 13.0 | 801 | 2 | T06783 | ent-kaurene syntha |
| 25 | 415.5 | 12.8 | 573 | 2 | T05328 | hypothetical prote |
| 26 | 408 | 12.5 | 802 | 2 | D85035 | ent-kaurene synthe |
| 27 | 406.5 | 12.5 | 612 | 2 | T05331 | hypothetical prote |
| 28 | 405 | 12.5 | 870 | 2 | A96637 | hypothetical prote |
| 29 | 404.5 | 12.4 | 823 | 2 | T02959 | kaurene synthase A |

| | | | | | | |
|----|-------|------|------|---|--------|--------------------|
| 30 | 404 | 12.4 | 383 | 2 | D71424 | hypothetical prote |
| 31 | 401 | 12.3 | 535 | 2 | T06285 | hypothetical prote |
| 32 | 393.5 | 12.1 | 598 | 2 | T05329 | hypothetical prote |
| 33 | 359.5 | 11.1 | 300 | 2 | B56118 | vetispiradiene syn |
| 34 | 320.5 | 9.9 | 471 | 2 | T06287 | hypothetical prote |
| 35 | 185.5 | 5.7 | 203 | 2 | H96525 | probable terpene c |
| 36 | 133 | 4.1 | 194 | 2 | T30554 | ubiquitin-protein |
| 37 | 125 | 3.8 | 1296 | 2 | I40645 | botulinum neurotox |
| 38 | 120.5 | 3.7 | 942 | 2 | B72015 | metalloproteinase, |
| 39 | 120.5 | 3.7 | 942 | 2 | C86610 | insulinase family/ |
| 40 | 120 | 3.7 | 834 | 2 | T19010 | hypothetical prote |
| 41 | 119.5 | 3.7 | 1077 | 2 | A97306 | superfamily II DNA |
| 42 | 117.5 | 3.6 | 1187 | 2 | JE0347 | hypothetical prote |
| 43 | 117.5 | 3.6 | 1493 | 2 | A38218 | GAP-associated pro |
| 44 | 116 | 3.6 | 456 | 2 | AG0199 | adenylosuccinate 1 |
| 45 | 116 | 3.6 | 576 | 2 | AC1384 | phosphomannomutase |

ALIGNMENTS

| | | | | | | |
|---|-----|---|-----|--|--|--|
| RESULT 1 | | | | | | |
| A48863 | | | | | | |
| limonene cyclase - spearmint | | | | | | |
| C;Species: Mentha spicata (spearmint) | | | | | | |
| C;Date: 12-May-1995 #sequence_revision 19-May-1995 #text_change 05-Nov-1999 | | | | | | |
| C;Accession: A48863 | | | | | | |
| R;Colby, S.M.; Alonso, W.R.; Katahira, E.J.; McGarvey, D.J.; Croteau, R. | | | | | | |
| J. Biol. Chem. 268, 23016-23024, 1993 | | | | | | |
| A;Title: 4S-limonene synthase from the oil glands of spearmint (Mentha spicata). cDNA 1st | | | | | | |
| A;Reference number: A48863; MUID:94043077; PMID:8226816 | | | | | | |
| A;Accession: A48863 | | | | | | |
| A;Status: preliminary | | | | | | |
| A;Molecule type: mRNA | | | | | | |
| A;Residues: 1-599 <COL> | | | | | | |
| A;Cross-references: GB:113459; NID:9410229; PIDN:AAC37366.1; PID:9410230 | | | | | | |
| C;Superfamily: vetispiradiene synthase 1 | | | | | | |
| Query Match | | | | | | |
| Best local Similarity 22.3%; Score 724.5; DB 2; Length 599; | | | | | | |
| Matches 197; Conservative 114; Mismatches 249; Indels 61; Gaps 16; | | | | | | |
| Qy | 13 | SCLSSHEIKALRRTIPTLGICRPKSVASHINMCLTSVASTDSVQRRVGNVHSLWDD | 72 | | | |
| Db | 20 | TCLQPSH-----FKSSPKLLSTNSSRSRLRVYCSSSGLT---ERRSGNYPSPRWDVN | 71 | | | |
| Qy | 73 | FIQSLSTPYGAPDYRE----RADRLIGEVDKIMFNFKSLDEGNDLLQRLLVDDVER | 127 | | | |
| Db | 72 | FIQSLLS-----DYKEDKHVIRASELVTVK-----MELEK-ETDQIRQLELIDDLQR | 118 | | | |
| Qy | 128 | LGIDRHFKRKIKTALD-----YVNSYNEKIGCGRESVVTDLNSTALGLRTLRLHG | 179 | | | |
| Db | 119 | MGLSDHFQNEFKELSSIYLDHHYKMPFPKE-----RDLYSTSLAFRLRLRHG | 168 | | | |
| Qy | 180 | YTVSSDVLNVFKDKNGQFSSTANIOEGEIRGVNLFRASLVAFPGKEKVMDEAETFTKY | 239 | | | |
| Db | 169 | FQVAQEVFDSFKNEGEFKES---LSDTRGLQLQYEASFLLTEGETTLESAREFATKF | 224 | | | |
| Qy | 240 | LRALQKIPASSILSLERDVLEYGHTNLRLLEARNYMDVFGQHTKNKNAEKLLELAK | 299 | | | |
| Db | 225 | LEEKVNEGVDGDLTLRIAYSLDPLHMRIRKPNAPWIE---WYRKRPDMNPVLELAI | 281 | | | |
| Qy | 300 | LEFNIFHSLOERELKHVSRWKDSSGE-MTECRHRHVEYYALASCIAPFQHSGRIGF | 358 | | | |
| Db | 282 | LDLNIYQAQFOELKESFRWVRNTGVEKLPFARDRLVECYFNNTGIIIPROHASARIM | 341 | | | |
| Qy | 359 | TKMSHLITVLDDMYDVFGTVDELELTATIKRWDPSPAMECLPEYMKGVMMVYHTVNEMA | 418 | | | |
| Db | 342 | GKVNALITVIDIYDVYGTLEBELQFTDLIRWDINSIDLPLYMQLCFLALNMFVDDTS | 401 | | | |
| Qy | 419 | RVAEKAQGRDTLNYARQAWACFDSYQAEAKWIATGYLPTFEYVLENGKVSSAHRPCALQ | 478 | | | |
| Db | 402 | YDVMEKEGVNVIYPLRQSWVDLADKYWEARWFYGGHKPSLEEYLEN-SWOSISGPCMLT | 460 | | | |

R./lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tailon, L. euss, D.; Niernan, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: H84633

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-591 <STO>

A;Cross-references: GB:AE002093; NID:g4115381; PIDN:AAD03382.1; GSPDB:GN00139

C;Genetics:

A;Gene: At2g24210

A;Map position: 2

C;Superfamily: vetispiradiene synthase 1

Query Match 21.2%; Score 689.5; DB 2; Length 591;
Best Local Similarity 29.3%; Pred. No. 1.2e-40;
Matches 182; Conservative 130; Mismatches 238; Indels 71; Gaps 19;

QY 23 ALRRITPTLIGCRPGKSAHSINMCL-----TSVASTDSVQRRVGNHNSLWDDDFIQSL 77
Db 16 ALRKTLR-----RPOSST-----CIIVTETTPCNKSPVQRRSANYQPSRWDHHLISV 64

QY 78 ISTPYGADYRERADRLIGEYKDIMNFKSLDGGNDLQRLLDVDERLIGIDRHFKKE 137
Db 65 ENKFAKDKRVRER-DLLEKEVR-----KMLNDEQKTYLDQLEFIDDLQKLGVSYHFEAE 117

QY 138 IKTALDYVNSYVNEKEIGCGRESVVDLNSTALGLRTLRLHGVTSSVDLVNFKDKNGQF 197
Db 118 IDNITL--TSSYKDR-----TNIQESDLHATALEFRLFRQHGVSSEDVDFVFMENCGKF 170

QY 198 SSTANIQIEGEIRGVNLFRASLVAFGEKMD-EAETFTKYLREALQKIPASSISLSE 256
Db 171 D-----RDDIYGLISLYEASYSSTKLDKNLQIFIRPFATQQLRDFVDTHSNEDFGSCD 223

QY 257 IRDV-----LEYGHTNLPLRLAARNYMDVFGQHTKNKNAEKLLEAKLEFNIFHSLQERE 312
Db 224 MVEIVVQALDMPYYQWMRLSTRWYIDYGRQNYKNLV--VVEPAKIDFNIVQAIHQEE 281

QY 313 LKHYSRWKWDG-SPEMTFCRHRHVEYALASCIAPFEPQHSQFRLGFTKMSHLITVLDW 371
Db 282 LKNVSSWMWETGLGKQLYFARDRIVENYFWTIGQIQEPQGYVRQMTKINALTTIDDI 341

QY 372 YDVGTVDELELFTATIKRWDPASMECLPEYMGVYMMVHTVNMARVAEKAQGRDTLN 431
Db 342 YDIYGTLEELQLFTVAFENWDINRLDEPEYMRLCFLVIYNEVNSIACEILRTKNINVIP 401

QY 432 YARQAMEACFDSYMOEAKWIATGYLPTFEYYLENGKVSSA-----HRPCALQPILTLDI 485
Db 402 FLKKSMTDVSKAYLVEAKYKSGHKPNLEEYMQNARISISSPTIFVHFYCVFSDQLSIQV 461

QY 486 PFPDHLKEVDFFPSKLDNLIC--ILRLRGDTRCYKADRRARGEASSISCYMKDNPGLTE 543
Db 462 -----LETLSQHQQNVVRCSSSVFRLANDLVTSPELARQDVCKSIQCYMSET-GASE 513

QY 544 EDALNHNFMIRDAIRELNWELKPDNSVPITSKKHAFA-----DISRVMHGYYRYRDGY- 597
Db 514 DKARSHVROMINDLWDEMYEKAAHSSSI-----LHDMFETVINLARMSCQCMYQYGDGHC 569

QY 598 SFANVETKSLVMRTVIEPVPL 618
Db 570 SPEKAKIVDRVMSLLENPIPL 590

RESULT 5

A56118

vetispiradiene synthase 1 - Hyoscyamus muticus (fragment)

C;Species: Hyoscyamus muticus

C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 29-Sep-1999

C;Accession: A56118

R;Back, K.; Chappel, J.

J. Biol. Chem. 270, 7375-7381, 1995

A;Title: Cloning and bacterial expression of a sesquiterpene cyclase from Hyoscyamus muti

A;Reference number: A56118; MUID:95221394; PMID:7706281

A;Accession: A56118

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-520 <BAC>

A;Cross-references: GB:U20108; NID:g763422; PIDN:AAA86337.1; PID:g763423

C;Superfamily: vetispiradiene synthase 1

Query Match 20.6%; Score 669.5; DB 2; Length 520;
Best Local Similarity 31.2%; Pred. No. 2.5e-39;
Matches 161; Conservative 111; Mismatches 211; Indels 33; Gaps 13;

QY 112 GNDLQRLLLVDVYERLIGIDRHFKKEIKTALDYV--NSYVNEKEIGCGRESVVDLNST 168
Db 29 GTTLTEKLNLDIIFERLGIAVHFKEQIEDMLDIYRADPYF-----EAHEYNDLNTS 80

QY 169 ALGLRTLRLHGTYVSSVDLVNFKDKNGQFSSSTANIQIEGEIRGVNLFRASLVAFPEKV 228
Db 81 SVQFRLRQHGYNVSPNIFSRFQDANGKFES---LRSDIRGLNLNLYEASHVTRHKEDI 136

QY 229 MDEAETSTKYLRALQKIPASSISLSLEIRDVLEYGHTNLPLRLAARNYMDVFGQHTKNK 288
Db 137 LEELAVSVGHLESAPHL--KSPLSKVTHALEQSLHKSIPRYEIRYFISY-EEEEFK 193

QY 289 NAAEKLLEAKLEFNIFHSLQERELKHYSRWKMD-SGSPMTFCRHRHVEYALASCIAP 347
Db 194 N--DLLRFAKLDYNLQMLHKEHSEVSRRWKDLDFVTTLPYARDRAVECYFTWGVYA 251

QY 348 EPQHSQFRLGFTKMSHLITVLDWYDVFGTVDELELFTATIKRWDPASMECLPEYMGVY 407
Db 252 EPQYSGARVMAKTAMISIVDFTDAYGIVKELEVYTDALQRMDISQIDRLPEYMKISY 311

QY 408 MMVHTVNMARVAEKAQGRDTLVYARQAMEACFDSYMOEAKWIATGYLPTFEYYLENGK 467
Db 312 KALLDLYDYEKELSKDGRSDVVHYAKERMKEIVGNFYIEGKMFIEGYMPSVSEYLSNAL 371

QY 468 VSSAHRPCALQPILTLDIFPFDHLKEVDFFPSKL--NDLICILRLRGDTRCYKADRRAG 525
Db 372 ATSTYVLLTTSYLGKMSATKEHEWLATNPKILEANATLC---RVVDIATYEVEKGRG 428

QY 526 EEASISCYMKDNPGLTEEDALNHNFMIRDAIRELNWELKPDNSVPITSK--KHAFDI 583
Db 429 QIATGIECYMRDY-GVSTEVAMEKQEMADIAMKDVNEEILRP---TPVSSEILTRLNL 484

QY 584 SRVMHGYRY-RDGYSFANVETKSLVMRTVIEPVPL 618
Db 485 ARIDVYTKHNQDGYTHPEKVLKPHIALLVDSIDI 520

RESULT 6

F71434

probable limonene cyclase ; Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

A;Variety: Columbia

C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 20-Jun-2000

C;Accession: F71434

R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk

P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terry, N.; Giele

avanagh, T.; Hempel, S.; Kotter, P.; Eutian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.

Nature 391, 485-488, 1998

A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech,

erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Reehman, S.; Ansc

C.; Chalwatzis, N.

A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal

A;Reference number: A71400; MUID:98121113; PMID:9461215

A;Accession: F71434

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-600 <BEV>

A;Cross-references: GB:Z97341; NID:g2244991; PID:g2245028

C;Genetics:

A;Map position: 4COP9-4G3845

C;Superfamily: vetispiradiene synthase 1

Query Match 20.2%; Score 656; DB 2; Length 600;
Best Local Similarity 29.4%; Pred. No. 2.7e-38;
Matches 182; Conservative 122; Mismatches 246; Indels 68; Gaps 19;

| | | | |
|----|-----|---|-----|
| QY | 26 | RTIPTLGICRPGKSVASHSINMCLTSAVSTDSVQRRVGNVHSLNMDDFIQSLSTPYGAP | 85 |
| DB | 26 | RTLATLEL-----ELCHSLSDAKNHCORNERNRHGESPS---QPERLSLID-----K | 72 |
| QY | 86 | DYRERADRLLIG---EVKDIMFNFKSLDEGNDLL--QRLLVDDVERLGIDRHFKKEIK | 139 |
| DB | 73 | NVRNRLLTMSGGVLKYKQDM--RKEVETAEKAILFKKELEWIDSLQRLGISYHKHEIH | 130 |
| QY | 140 | TALDVVNSYWNKEGIGCGRESVVTDLNSTALGLRTLRLHGTVSSDVLNVFKDNGQFSS | 199 |
| DB | 131 | DILRKIHQHG-----IERETQDLHATSLLEFILLRQHGFVSDADFVFISETGEFRK | 184 |
| QY | 200 | TANIQIEGEIRGVNLFRASLVAFPGKVMDEAETSTKYLRREALOKIPASSILSL--- | 256 |
| DB | 185 | T---LHSDIKGLSLYEASYSFMSDFKLKETRIYANKRLSEFVAE--SSKTICREDET | 238 |
| QY | 257 | -----IRDVLEYGWHNTLPRLEARNYMDVFGQHTKNKNAEKLLELAKLEFNIFHSLQER | 311 |
| DB | 239 | YILEMVKRALETPTYHWSIRLLEARNYINVY--EKHEMNPLLEFPAIDFNMLQANHGE | 295 |
| QY | 312 | ELKHSRWKDSG-SPEMTFCRHRVEXYALASCIAFEPQHSGRFGFTKMSHLITVLD | 370 |
| DB | 296 | ELKLIS-----STGLMKQLDFVRDRITSESYFWTIGIFYEPEFKYCKRILTKIFMLIVIMD | 351 |
| QY | 371 | MYDVFQTVDELELTATIKRWDPSPAMECLPEYMKGVMMVYHTVNEMARVAEKAQGRDTL | 430 |
| DB | 352 | IYDIYGLTELELEFTNVVEKWDVNHVERLLPNYMRMCFLLYNEINQIGYDVLKDKGLNVI | 411 |
| QY | 431 | NYARQWAEACFDSYMOEAKWIATGYLPTFEYYLENGKVSSAHRPCALOPIITLDIPFPDH | 490 |
| DB | 412 | PYLKQYWTDLFKFTLTESKWKYTGKPSFEEMYQNGVISSSVPTILLHLFSVLSDHISDQ | 471 |
| QY | 491 | ILKEVDFPSKLANDLI--CIILRLRGDTRCYKADRAGEEASISCYMKDNPGLTEEDAL | 547 |
| DB | 472 | TLTLD--DSKNHSVVRSCATILRLANDLATSTEEMARGDSPKSVOCYMETRA--SEEAR | 527 |
| QY | 548 | NHINFMIRDAIRELNMELKPD-----NSVPITSKGAFDISRVHMGYRRDGY-SFA | 600 |
| DB | 528 | RHMQSMISD-----SWDIINSDLKTAHTSSSLPRGFLAAANLNRVVQCITRRHGDGHSPE | 582 |
| QY | 601 | NVETKSLVMRTVIEPVPL 618 | |
| DB | 583 | KTKTVDYIQSVLFNPPVPL 600 | |

RESULT 7
T03714

5-epi-aristolochene synthase - common tobacco
N;Alternate names: sesquiterpene cyclase
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 29-Sep-1999
C;Accession: T03714
R;Facchini, P.J.; Chappell, J.
Proc. Natl. Acad. Sci. U.S.A. 89, 11088-11092, 1992
A;Title: Gene family for an elicitor-induced sesquiterpene cyclase in tobacco.
A;Reference number: Z15024; MUID:93066390; PMID:1438319
A;Accession: T03714
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-550 <FAC>
A;Cross-references: EMBL:L04680; NID:g170342; PIDN:AAA19216.1; PID:g505588
A;Experimental source: strain NK326
C;Genetics:
A;Introns: 37/3; 126/1; 251/2; 324/2; 370/3; 452/3
C;Function:
A;Description: mediates the conversion of the isoprenoid intermediate farnesyl diphospha
C;Superfamily: vetispiradiene synthase 1

Query Match 19.7%; Score 641.5; DB 2; Length 550;
Best Local Similarity 28.4%; Pred. No. 2.5e-37;
Matches 167; Conservative 124; Mismatches 245; Indels 51; Gaps 15;

| | | | |
|----|-----|---|-----|
| QY | 46 | MCLTSVAS-TDSVQRRVGNVHSLNMDDF-----IQSLSTPYGAPDYRERADRLLIGEYKD | 100 |
| DB | 1 | MASAAVANYEEETVRPADFSPLMGDQFLSFSIDNQVAEKY---IYAQIEALKEQTRRS | 57 |
| QY | 101 | IMFNFKSLEDGNDLLQRLLVDDVERLGIDRHFKKEIKTALDVVNSYWNKEGIGCGRES | 160 |
| DB | 58 | MLL-----ATGRKLADTLNLIDIERLGISYHFEKEIDEILDQIYN-----QNS | 101 |
| QY | 161 | VVTDLNSTALGLRTLRLHGTVSSDVLNVFKDNGQFSSSTANIQIEGEIRGVNLFRASL | 220 |
| DB | 102 | NCNDLCTSAIQFRLRQHGPNISPEIFSKFQDENGKFKES---LASDVLGLNLTYASH | 157 |
| QY | 221 | VAFPGKVMDEAETSTKYLRREALOKIPASSILSLERDVLEYGWHNTLPRLEARNYMDV | 280 |
| DB | 158 | VRTHADDILEDALAFSTIHLESAAPHL--KSPLRQVTHALEQCLHKGVPRVETRFIIS | 215 |
| QY | 281 | FGQHTKNKNAAEKLLLELAKLEFNIFHSLQERLKHVSRWKCD-SGSPMTFCRHRVEXY | 339 |
| DB | 216 | IYDKQSKN--NVLIRFAKDFENLLQMLHKQELAQVSRWKDLDFTVTLTPYARDRVCEY | 273 |
| QY | 340 | ALASCIAFEPQHSGRFGFTKMSHLITVLDMDYDVFQTVDELELTATIKRWDPSPAMECL | 399 |
| DB | 274 | FWALGVYFEPQYSQARVMLVKTISMISIVDDTFDAYGYVKELEAYTDAIQRWIDINEIDRL | 333 |
| QY | 400 | PEYMKGVMMVYHTVNEMARVAEKAQGRDTLNYARQWAEACFDSYMOEAKWIATGYLPTF | 459 |
| DB | 334 | PDYMKISYKAILDLYKDYKEKLSSAGRSHIVCHAIERMAEVRVRYNVVESTWFIEGYMPV | 393 |
| QY | 460 | EEYLENGKVSSAHRPCALOPIITLDIPFPDHILKEVDFP-----SKLANDLICILRLRGD | 514 |
| DB | 394 | SEYLSNALATTYYTYLATTSYIGM-----KSATEQDFEWSKNPKILEASVITICRAIDD | 447 |
| QY | 515 | TRCYKADRAGEEASISCYMKDNPGLTEEDALNHINFMIRDAIRELNMELKPDNSVPI | 574 |
| DB | 448 | TATYVEKSRGQIATGIECCWRDY-GISTKEAMAKFQNMETAWKDINEGLRP--TPV | 503 |
| QY | 575 | TSK--KHAFDISRVMHHGYRVR-DGYSFANVETKSLVMRTVIEPVPL 618 | |
| DB | 504 | STEFILPILNLARIVEVYTHNLDGYTHPEKVLKPHIINLVDISIKI 550 | |

RESULT 8
T08174

sesquiterpene cyclase (EC 2.5.1.-) - pepper
C;Species: Capsicum annuum (pepper)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: T08174
R;Back, K.; Shin, D.H.; He, S.
Plant Cell Physiol. 39, 899-904, 1998
A;Title: Cloning and bacterial expression of sesquiterpene cyclase, a key branch point en
A;Reference number: Z16395; MUID:99033462; PMID:9816674
A;Accession: T08174
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-559 <BAC>
A;Cross-references: EMBL:AF061285; NID:g3108342; PIDN:AAC61260.1; PID:g3108343
C;Function:
A;Pathway: the synthesis of phytoalexin capsidiol
A;Note: unduced by UV
C;Superfamily: vetispiradiene synthase 1
C;Keywords: isoprenoid biosynthesis; transferase

Query Match 19.4%; Score 632; DB 2; Length 559;
Best Local Similarity 30.0%; Pred. No. 1.2e-36;
Matches 173; Conservative 112; Mismatches 238; Indels 54; Gaps 18;

| | | | |
|----|----|---|-----|
| QY | 55 | DSVQRRVGNVHSLNMDDF-----IQSLSTPYGAPDYRERADRLLIGEVDIMFNFKS-LE | 109 |
| | | : : : : : : : : : | |

Db 16 EEIRPVADSPSLMGDRFLSFSIDNOVETKYAQ-----EIEPLKEQTRSMML 63
Qy 110 DGGNDLQRLLLVDVERLGIDRHFKKEIKTALDYV-NSYWNEKIGCGRESVTDLNST 168
Db 64 ASGRKLTSETNLIDVIERLGIAHYHFEKEIDELDRYNNNSNPEG-----DYNNEDLCTC 118
Qy 169 ALGLRTLRLHGTVSSDVLNVFKDKNGQFSSSTANIQIEGIRGVNLPRASLVAFPGEKV 228
Db 119 RLQFRLRLQHGYNISLKI FSKFLDNGRLKES---LASDVLGLSLSYEASHVSHGED 174
Qy 229 MDEAETPSTKYLRREALQKIPASSILSLERDYLEYGMHTNLPRLRARNYMDVFGQHTKN 288
Db 175 LEDALAFSTHLESATPHLEYP--LKEQVRHALEQSLHKGIPRIEIQFISSVYDKQA 232
Qy 289 NAAEKLLELAKLEFNIFHSLQERELKHVSRWKDSGSP-MTFCRHRHYEYALASCI 347
Db 233 N-DVLLRFAKLDYNMLQMLHKQELAEVSRWKDLNFVNTLPYARDRVCEYFWALGVY 290
Qy 348 EPQHSGRFGFTKMSHLITVLDMDYDFGTVDLELELTATIKRWDPSAMECLPEYMKGV 407
Db 291 EPQYSGARWMLVKTIAMISIVDDTYDAYGYDELAITYDVIQRWDIKEIDSLPDYMK--- 347
Qy 408 MMVYHTVNEMARVAEKAQGRD---TLNVARQAMEACFDSYMOEAKWATGYLPTFEEYL 463
Db 348 -ISYKALLDLYKDYEKEMSRDGRSHVYVYAKERLKLKLVKSYNIEAKPTEGHMPASEYL 406
Qy 464 ENGKVSAAHRCALQPILTLDIPFPDHLKEVDFP--SKLNDLI--CI-ILRLRGDTRCY 518
Db 407 RNAFVTTYYYLATTSYLGW-----KYAKEQOFEWLSKNPKILEGCVTICRVIDDIATY 460
Qy 519 KADRARGEASSISCYMKDNPGLTEEDALNHINMIRDAIRELNWELLKPDNSVPITSK 578
Db 461 EVEKNRGQSTGIECYMRDYSVSTKE-AMAKFQEMGESGWKDINEGMLRP-TPIMEFLS 518
Qy 579 HAFDISRWVHGXYR-RDGYSFANVETKSLVMTVIE 614
Db 519 RILNLARLVDTYKGNEDGYTHPEKVIKPHIAMVVD 555

RESULT 9
T06266
germacrene C synthase - tomato
C:Species: Lycopersicon esculentum (tomato)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-May-2000
C:Accession: T06266
R:Colby, S.M.; Crook, J.; Dowdle-Rizzo, B.; Lemaux, P.G.; Croteau, R.
Proc. Natl. Acad. Sci. U.S.A. 95, 2216-2221, 1998
A:Title: Germacrene C synthase from Lycopersicon esculentum cv. VFNT Cherry tomato: cDNA
A:Reference number: Z15576; MUID:98151492; PMID:9482865
A:Accession: T06266
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-548 <COL>
A:Cross-references: EMBL:AF035631; NID:g2967688; PIDN:AAC39432.1; PID:g2967689
A:Experimental source: cultivar VFNT
C:Superfamily: vetispiradiene synthase 1

Query Match 18.9%; Score 615.5; DB 2; Length 548;
Best Local Similarity 27.0%; Pred. No. 1.7e-35;
Matches 159; Conservative 136; Mismatches 229; Indels 65; Gaps 16;
Qy 52 ASTDSVQRVGNVYHSNLWDDFI-----QSLISTPYGADYRERADRLIGEVDIMF 103
Db 3 ASSADKCRPLANFHPVSWGYNHFLSYTHEITNQEKVE---VDEYKETIRKMLVETCD--- 55
Qy 104 NFKSLEDGNDLLQRLLLVDVERLGIDRHFKKEIKTALDYV--NSYWNEKIGCGRES 160
Db 56 -----NSTQKLVLIDAMQRLGVAYHFDNEIETSIQNI F DASSKQNDND----- 98
Qy 161 VVTDLNS TALGLRTLRLHGTVSSDVLNVFKDKNGQFSSSTANIQIEGIRGVNLFRASL 220
Db 99 --NNLYVVS LRFRLVRQOGHYMSSDVFKQFTNQDGKFET---LTNDVQGLLSLYEASH 152

Qy 221 VAFPEKVMDEAFPESTKYLRREALQKIP-ASSILSLERDYLEYGMHTNLPRLRARNYMD 279
Db 153 LRVNREEILEEALFTTTHLESIVSNLSNNNSLKEVGEALQTPIRMTLPRMGARKYIS 212
Qy 280 VFGQHTQNQAAEK-LLELAKLEFNIFHSLQERELKHVSRWKCD-SGSPENTFCRHRVE 337
Db 213 IY---ENNDAHHLILKFAKLD FNMLOKFPHQRELSDLTRWKKDLDFANKYPYARDRLVE 268
Qy 338 YYALASCIAEFQHSGRFGFTKMSHLITVLDMDYDFGTVDLELELTATIKRWDPSAME 397
Db 269 CYFWILGVYFEPKYSRARKMTKVLNLTSTIIDTFDAYATFDELVT FNDALIQWDANAID 328
Qy 398 CLPEYMKGVYMMVYHTVNEMARVAEKAQGRDTLNYARQAMEACFDSYMOEAKWI-ATGYL 456
Db 329 SIQPYMRPAQALLDIYSEMEQVLSKEGLDRVYAKNEMKCLVRAYFKETQWLNDCH 388
Qy 457 PTFEEYLENGKVSAAHRCALQPILTLDIPFPDHLKEVDFPSKNDLI-----CIILRL 511
Db 389 PKYEEQVENATVSAGY-----MMISTCLVGIEEFISHETFEWLMNESVIVRASAL 443
Qy 512 RGDTRCYKADRAFGEEASSISCYMKDNPGLTEEDALNHINFM--IRDAIRELNWELLKPD 569
Db 444 MNDIVGHEDEGEFGHVASLIECYMKDYGASKOE--TYIKFLKEVTNAWKDINKQFSRP- 499
Qy 570 NSVPITSKKAFLISRVMHNGYRDRDGYSFANVETKSLVMTVIEPVPL 618
Db 500 TEVPMFVLERYNLTRVADTLYKEKDYSTAKGKLKMNIPILIESYKI 548

RESULT 10
T06265
germacrene C synthase, epidermal - tomato
C:Species: Lycopersicon esculentum (tomato)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-May-2000
C:Accession: T06265
R:Colby, S.M.; Crook, J.; Dowdle-Rizzo, B.; Lemaux, P.G.; Croteau, R.
Proc. Natl. Acad. Sci. U.S.A. 95, 2216-2221, 1998
A:Title: Germacrene C synthase from Lycopersicon esculentum cv. VFNT Cherry tomato: cDNA
A:Reference number: Z15576; MUID:98151492; PMID:9482865
A:Accession: T06265
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-548 <COL>
A:Cross-references: EMBL:AF035630; NID:g2967686; PIDN:AAC39431.1; PID:g2967687
A:Experimental source: cultivar VFNT
C:Superfamily: vetispiradiene synthase 1

Query Match 18.9%; Score 614.5; DB 2; Length 548;
Best Local Similarity 26.8%; Pred. No. 2e-35;
Matches 158; Conservative 137; Mismatches 229; Indels 65; Gaps 16;
Qy 52 ASTDSVQRVGNVYHSNLWDDFI-----QSLISTPYGADYRERADRLIGEVDIMF 103
Db 3 ASSADKCRPLANFHPVSWGYNHFLSYTHEITNQEKVE---VDEYKETIRKMLVETCD--- 55
Qy 104 NFKSLEDGNDLLQRLLLVDVERLGIDRHFKKEIKTALDYV--NSYWNEKIGCGRES 160
Db 56 -----NSTQKLVLIDAMQRLGVAYHFDNEIETSIQNI F DASSKQNDND----- 98
Qy 161 VVTDLNS TALGLRTLRLHGTVSSDVLNVFKDKNGQFSSSTANIQIEGIRGVNLFRASL 220
Db 99 --NNLYVVS LRFRLVRQOGHYMSSDVFKQFTNQDGKFET---LTNDVQGLLSLYEASH 152
Qy 221 VAFPEKVMDEAFPESTKYLRREALQKIP-ASSILSLERDYLEYGMHTNLPRLRARNYMD 279
Db 153 LRVNREEILEEALFTTTHLESIVSNLSNNNSLKEVGEALQTPIRMTLPRMGARKYIS 212
Qy 280 VFGQHTKNKNAJEK-LLELAKLEFNIFHSLQERELKHVSRWKCD-SGSPENTFCRHRVE 337
Db 213 IY---ENNDALHHLILKFAKLD FNMLOKFGHRELSDLTRWKKDLDFANKYPYARDRLVE 268
Qy 338 YYALASCIAEFQHSGRFGFTKMSHLITVLDMDYDFGTVDLELELTATIKRWDPSAME 397

D_b 269 CYFWILGVFEFPKYSNRARKMTKVLNLTISIIDDTFDAYATFDELVTFNDAIQRPWDANAID 328
Q_y 398 CLPEYMKGVMMYYHTVNMENARVAEKAQGRTLNARQAWEACFDSYMGEAKWI-ATGYL 456
D_b 329 SIQPYMRPAYQALDIYSEMEQVLSKEGKLDRVYYAKNEMKKLVRAYFFKETQWLNDCDHI 388
Q_y 457 PTFEYLENGKVSSAHRPCALOPILTLDIPFPDHILKEVDPPSKINDLI-----CIIRL 511
D_b 389 PKYEQVENAIVSAGY----MISTTCLVGIEEFISHETFEWLMNESVIVASALIARA 443
Q_y 512 RGDTRCYKADRRARGEESISICYMKDNPGLTTEEDALNHINFM--IRDAIRELWELLKPD 569
D_b 444 MNDIVGHEDEQERGHVASLIECYMKDYGASKQE---TYIKFLKEVTNAWKDINKQFFRP- 499
Q_y 570 NSVPITSKHAFDISRWHHGYYRDRGYSFANVETKSLVMKTVIPVPL 618
D_b 500 TEVPMFVLERVNLNLRVADTLTYEKDDTYTNAGKGLKNMINSIILIESVKI 548

RESULT 11
G71434
probable limonene cyclase - Arabidopsis thaliana
C;/Species: Arabidopsis thaliana (mouse-ear cress)
A;/Variety: Columbia
C;/Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 05-Dec-1998
C;/Accession: G71434
R;/Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk
P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weltzienegger, T.; Pohl, T.M.; Terryn, N.; Giel
avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.
Nature 391, 485-488, 1998
A;/Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech
erhoff, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans
C.; Chalwatzis, N.
A;/Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal
A;/Reference number: A71400; MWID:9812113; PMID:9461215
A;/Accession: G71434
A;/Status: preliminary; nucleic acid sequence not shown; translation not shown
A;/Molecule type: DNA
A;/Residues: 1-1024 <BEV>
A;/Cross-references: GB:Z97341; NID:g2244991; PID:e327011; PID:g2245029
C;/Genetics:
A;/Map position: 4COP9-4G3845

```

Query Match      18.0%; Score 586.5; DB 2; Length 1024;
Best Local Similarity 30.2%; Pred. No. 4.8e-33;
Matches 163; Conservative 109; Mismatches 195; Indels 73; Gaps 17;

QY      86 DYERADRLIGEVKDIMENFKSLEDGNDLLQRLLYVDVERLGIDRHFKKEIKTALDYV 145
      ||| | | | : : : | | | : | | : | | : | | | |
DB      5 DNERVTLLKQEVSKML-----NETEGLLEQLLELDTLQRLGVSYHFEQELIKTLLNV 57

QY      146 NSYWNEKGIGCGRESVVT---DLNSTALGLRTLRLHGYTVSSDVLNVFKDKNGQFSSTA 201
      : | : : : : | | | | | | | |
DB      58 ----HVKNVRAHKNRIDRNKMGDLYATALEFLLRQH-----DV-----FDGNI 97

QY      202 NIQIEG-EIRGYLNLFFASLVAFPGEKVMDEAETSTKYLR--EALQKIPASSILSLEI 257
      : : : : | | : | : : : : : : : | | | : : : :
DB      98 GVDLDKDKIKGILSLYEASYLSTRIDTKLKEISYYTTKRLRKFEVVKNETKSYTLRRMV 157

QY      258 RDVLEYGMHTNLPRLRNRYMDVFGQ-HTKNKNAAEKLELAKLEFNI FHSLOERELKHV 316
      || : | : | | | | : : : | : | | | | | | : : : | :
DB      158 IHALEMPYHRRVGRLEAKRYIEVYGERHDN---PILLELAKLDENFVQAHQDELKSL 213

QY      317 SRWKKDSG-SPEMTFCRRHREVEYYALASCIAPFEPQHSGRLLGFTKMSHLITVLDMYDVF 375
      ||| : | : : | | | | | | | : : : : | : | | : : :
DB      214 SSWWSKTGLTKHLDPFVADRITEGYFSSVGVMYEPEFA YHRQMLTKVFM LITTDIYDIY 273

QY      376 GTVDELELFTATIKRWDSAMECLPEYMKGVMMYYHTVNEMARVAEKAQGRPTLNYARQ 435
      || : | | : | | : : : | | | | : : : : : : : : : :
DB      274 GTLEELQLFITTIWEKWDVNRLEELPNYMKLCFLCLVNEINQIGYFVLRDKGFNVIPLYKE 333

QY      436 AWEACFDSYMQEAKWIATGYLPTFEEYLENGKVVSA-----HRPCALQPILTLDI--PF 487
      : | : : : | | | : | | | | | : : : : | : | | | :

```

| | | | |
|----------------|-----|---|-----|
| D _b | 334 | SWADMCCTFLKEAKWKSGYKPEEFEEYMONGMISSSVPTILHLFCULSD-QTLDILGSY | 392 |
| O _y | 488 | PDHILKEVDFPSKLANDLICILRLRGD-----TRCYKADRARGEASISCYMKD | 537 |
| D _b | 393 | NHSVRS-----SATILRLANDLATSSVSHGFTTYNTEELARGDITMKSVCQCHME | 442 |
| O _y | 538 | NGGLTEEDALNHINFMIRDAIRELWELLKPDNSVPITSKGAFDISRWHHGYRKYRDGY | 597 |
| D _b | 443 | T-GASEAESRAYIOGIIIGVAMDLINE--KSCRLHQGFLEAANLGVAQCYYOYGDEH | 499 |

RESULT 12
 E96723
 hypothetical protein F20P5.19 [imported] - *Arabidopsis thaliana*
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
 C;Accession: E96723
 R;Theologias, A.; Ecker, J.R.; Palm, C.U.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maizl, R.; Marzali,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: E96723
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-632 <STO>
 A;Cross-references: GB:AE005173; NID:g2194130; PIDN:AAB61105.1; GSPDB:GN00141
 C;Genetics:
 A;Gene: F20P5.19
 A;Map position: 1
 C;Superfamily: vetispiradiene synthase 1

| Query Match | 17.5%; Score 569; DB 2; Length 632; |
|--|---|
| Best Local Similarity | 26.5%; Pred. No. 4e-32; |
| Matches 174; Conservative 120; Mismatches 276; Indels 86; Gaps 18; | |
| Qy 10 | VSRSCLSSSHEIKALRTIPTLIGRPGKSAHSINMCLTSVASTDSVQRRV 61 |
| Db 16 | LSRLCWRNLNSSSYHYPLKSSLSFSRQSPKLCIVRATTNPTDDNSTRSF 68 |
| Qy 62 | GNHNSNLWDDFIQSLISTPYGAPDYRERADRLIGEVKDIMENFKSLDGGNDLQRL 119 |
| Db 69 | TPHPSPSLWGHFLSASVNOTEMDDLWRQIEALKPIV-NAMLLPCNGADAKKIT 120 |
| Qy 120 | LLVDVERLGIDRHFKKEIKTALDVNSYNEKIGCGRESVTDLNSTALGLRTLRLHG 179 |
| Db 121 | CFIHTLVSLGVSYHFEKEIVEFLKDAFENIEDMIIDCKEDDLYTVSIIIFRVRLYG 176 |
| Qy 180 | YTVSSDYNVEKDKNGQFSSTANIQIEGIRGLNLFRA 218 |
| Db 177 | HYITPELHITISYFFELIHTCMCVDFENRFKGGDGNFKKCLNDDVRGMLSFEYA 232 |
| Qy 219 | SLVAFPGKVMDEAETESTKYLRALQKIPASSILSLBIRDVLEYGWHNTLPRLEARN 276 |
| Db 233 | SHFGTTEDILEEAMSFQKHLEFLVGEKAKHYPHITKLIQALYIPQNFNLEILVARE 292 |
| Qy 277 | YMDVFGQHTKKNNAEKLLELAKLEFNIHLSLOERELKHVSRWKDSGSPEMTFCHR 334 |
| Db 293 | YIDFYELETDHNEMLLKLAKLNFRPLQLOIQLDKTLITWKELDLVSKIPLYFRER 349 |
| Qy 335 | HVEYYALASCLAEPOHSGFRLGFTKNSHLITVLDMDYDVGIVDELELFTATIKRWDP 394 |
| Db 350 | LAEPYFMATGIYEPQYSARIMLAKSIILVDIVNTFDVYGTIDEVKSILVQAIERWSD 409 |
| Qy 395 | AMECLPEYMKGYVMVYHTVNEMARVAEKAQGRDTLNYARQAMEAFDSYMOEAKMIATG 454 |
| Db 410 | AVDVLDPDYLVKVFRTTFDLFKELBEEYVSSEARSFTMQAYAEQLRIIMKGYLQEAEMWSNRG 469 |

[illegible]

RESULT 13

H866460
hypothetical protein F14M2.13 - *Arabidopsis thaliana*
C/Species: *Arabidopsis thaliana* (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C/Accession: H866460
R/Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hultzar, L.
Nature 408, 816-820, 2000
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A/Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A/Reference number: A86141; MUID:21016719; PMID:11130712

A/Accession: H86460
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-598 <STO>
A/Cross-references: GB:AE005172; NID:g9665095; PIDD:AA97286.1; GSPDB:GN00141
C/Genetics:
A/Map position: 1
C/Superfamily: velispiradiene synthase 1

| Query Match | 16.5% | Score 536 | DB 2 | Length 598 |
|-----------------------|------------------|---|-----------|------------|
| Best Local Similarity | 27.4% | Pred. No. 7.8e-30 | | |
| Matches 162 | Conservative 123 | Mismatches 254 | Indels 52 | Gaps 17 |
| QY | 44 | INMCLTSVASTDSVQRRVGNVHS--NLWDDDFIQSLISTPYGAPDYRERADRLIGEVDKI | 101 | |
| DB | 44 | LNLGVKACSKTSGVSSRPLPHSAPDLMGDHL-----SVPTENSEFDLTLEIEESI | 95 | |
| QY | 102 | MENFKS-LEDGGNDLQRLLVDDVERLGIDRHFKKEIKTALDY----VNSYWEKGIGC | 156 | |
| DB | 96 | KPKVRNMLMSSHKTDEKERICLIHLICLGTPHYFEKEIEIEILEQAFRKLDMLFTDE--- | 151 | |
| QY | 157 | GRESVTDLNLSTALGLRTLRLHGTVSSDVLNVFKDKNGQFSSTANIQIEGEIRGLNLF | 216 | |
| DB | 152 | -----DDELTAIMFEVFRLLGKHICSDVDFDRFKVDAKFKE---HLVSDVRGMQLY | 201 | |
| QY | 217 | RASLVAFPGEKVMDEAETPSTKYLRAL--QKIPASSILSLEIRVLEYGWHNTNLPRLA | 274 | |
| DB | 202 | EAHLATPFETILDEALSF-TRYHLESLAGQOATAPHI-SRHILNALYKPRFLKMEIIAA | 259 | |
| QY | 275 | RNYMDVFGQHTKNKNAAEKLELAKLEFNI FHSLQERELKHSRWKDSGSP-EMTFCRH | 333 | |
| DB | 260 | REYIHFY----QKEGHDETLKFAKLNFNFCQLHYVRELKTLTKWKDIDLPLYKLPYIRD | 315 | |
| QY | 334 | RHVEYYALASCIAFEPQHSGRFLGFTKMSHLITVLDDMYDVFGTYDELELFTATIKRWD | 393 | |
| DB | 316 | RLLETFIGVMAYLLEPHYSLGRITATKVSQVIVVMDTCDAYGTFSSEVRSLLIDSLERWD | 375 | |
| QY | 394 | SAMECLPEYMKGVMMVYHTVENARVAEKAQGR---DTLNYARQAEACFDSYMOEA | 448 | |
| DB | 376 | GAIDKLPSCLRIVIQSIIVETMEDIER-EMKPRGRSSSVQDTVEIEIKIMGRA---YAEIS | 430 | |
| QY | 449 | KWIATGYLPTFEEYLENGKVSASHRPCALQPILTLDIPFPDHILKEVDFPSKNDLICII | 508 | |

Db 431 .KMARAGHAVPTEDDYIELGLDSSGICRFAMYSFISMEDCEEQNQTAMFKSKPKMLRALSVI 490

Qy 509 LRLRGDTRCYKADIARGEEAASSISCTYMKDNPGLTEEDALNHINFMIRDALRELNWELLKP 568

Db 491 FRLINDIAGFEEEMRRGEVAVGVANCYVKOH-NVTKELAVREIKMKIRDNYKIMMEEFLLTI 549

Qy 569 DN-SVPIITSKKAHEDISRVMTHGYYRRDGYSPANVETKSLVMRTVIEPVL 618

Db 550 KSYSRPILVR--CFNIVRLVNLYYEEGDNFTNPNGKLDLITSLFFHPLPL 598

RESULT 14

G96825
hypothetical protein T8K14.12 [imported] - *Arabidopsis thaliana*
C/Species: *Arabidopsis thaliana* (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C/Accession: G96825
R/Theologian, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A/Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A/Reference number: A86141 | MUID:21016719 | PMID:11130712

A/Accession: G96825
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-785 <STO>
A/Cross-references: GB:AE005173; NID:g4835764; PIDN:AAD30231.1; GSPDB:GN001411
C/Genetics:
A/Gene: T8K14.12
A/Map position: 1

| Query Match | 15.5%; | Score 504.5; | DB 2; | Length 785; | |
|-----------------------|-------------------|--|------------------------------------|----------------------------------|-----|
| Best Local Similarity | 28.8%; | Pred. No. 2e-27; | | | |
| Matches 152; | Conservative 105; | Mismatches 230; | Indels 41; | Gaps 15; | |
| QY | 114 | DLQRLLVDDVERLGIDRHFKEIKTALDYVNSYWNKGI | CGRESVTDLNSTALGLR | 173 | |
| Db | 270 | DQYARLSIIIVTLSELGIDRDFKEIKSILDETYRWLR | -----GDEEICLDLATCALAFR | 324 | |
| QY | 174 | TLRLHGYTVSSDVLNVPKDKNGQFSSSTANQIEGEIR | ---GVNLFRASLVAFPEGEKVD | 230 | |
| Db | 325 | LLLAHGVDVSYDPLKPFABESG-FSDT--- | LEGVYKNTFSVLELFKAA-QSYPHESALK | 378 | |
| QY | 231 | EAETSTKYLREALQKIPASSI---LSLEIRDVLEYGWH | TNLPRLLEARNYMDVFGQHTK | 286 | |
| Db | 379 | KQCCWTKQYLEMELSSWVKTSVRDKYLKKEVEDALAF | PSASLSERSDHRRKI-LNGSAVE | 437 | |
| QY | 267 | NKNAAE-----KLLELAKLEFNI | FHSLQERELKHVSRWKDKSGSPENTFCRRH | 335 | |
| Db | 438 | NTRVTKTSYRLINICTSDILKLAVD | DFNFCQSIHREEMERLDRIVENRLQELKFAROKL | 497 | |
| QY | 336 | VEYYALASCIAPQPHSGFRIGFTKMSHLITVLD | MYDVFGTVDELELFTATIKRWDPSA | 395 | |
| Db | 498 | AYCYFSGAATLPSPELSDARISWAKGV | LTTVVDFFDVGSGKEELENLHLVEKWDLNG | 557 | |
| QY | 396 | M-ECLPEYMKGYMMVYHTVNEMARVAEKAQGR | DTLNYARQAEACFDSYMQEAKWIATG | 454 | |
| Db | 558 | VPEYSSEHVEIIFSVLRDITILETGDKAF | TYQGRNVTHHIVKIWLDLKSMLEAEWSSDK | 617 | |
| QY | 455 | YLTFEEYLENGKVSSAHRPCALQIL | TLDPFPDPHILKEVDFP--SKNDLICILRLR | 512 | |
| Db | 618 | STPSLEDYMENAYISFALGPVL | PATYLI | GPPLPE---KTVDSHQYNQLYKVLVSTWGRLL | 674 |
| QY | 513 | GDTRCYKADRRAGEASSISCYMK-DN | PGLTEEDALNHINFMIRDAIR | ELNWLKPDNS | 571 |
| Db | 675 | NDIQGFKRESAEG-KLNAVSLMKHERD | NRSKVEIIESMKGLAEKRREELHKL | VLEEGKS | 733 |

```

QY      572 VPITSKHAF-DISRVWHGYYRDKGYSFANVETKSLVMRTVIEPVVL 618
      | | | : : | | | : : | | | : | | |
DB      734 VVPRECKEAFLLKMSKVLNLFYRKDDG--FTSNDLMSLVKSVIYEVS 779

```

RESULT 15

T52059
ent-kaurene synthase (EC 2.5.1.-) [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
C;Accession: T52059
R;Yamaguchi, S.; Sun, T.; Kawaide, H.; Kamiya, Y.
Plant Physiol. 116, 1271-1278, 1998
A;Title: The GA2 locus of Arabidopsis thaliana encodes ent-kaurene synthase of gibberellin biosynthesis
A;Reference number: Z25926; MUID:98205064; PMID:9536043
A;Accession: T52059
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-785 <YAM>
A;Cross-references: EMBL:AF034774; PIDN:AAC39443.1
C;Genetics:
A;Gene: GA2
C;Keywords: transferase

| | | | | |
|-----------------------|-------------------|------------------|------------|-------------|
| Query Match | 15.5%; | Score 504.5; | DB 2; | Length 785; |
| Best Local Similarity | 28.8%; | Pred. No. 2e-27; | | |
| Matches 152; | Conservative 105; | Mismatches 230; | Indels 41; | Gaps 15; |

QY 114 DULÖRLLLVDDVERLIGIDRHFKEIKTALDYANSYWEKIGICGRESVVTDLNSTALGLR 173
 Db 270 DÖYARLSIIIVTESIGIDRDFKEIKSILDEYRYWLR----GDEEICLDLALCALAFR 324
 QY 174 TLRHGYTVSSDVLVNFVKDNGÖFSSSTANIÖIEGEIR--GVLNLFRASTVAFPEGEKVM 230
 Db 325 LLLAHGYDVSYPDKPFAEESG-FSDT---LEGYVKNTPSVLELFKAA-ÖSYPHESALK 378
 QY 231 EAETFSTKYLREALÖKIPASSI---LSLEIRDVLEYGWHNTNLPRLPEARNYMDFGÖHTK 286
 Db 379 KÖCCWTKÖYLEMELSSWVKTSVRDKYLKKEVEDALAFPSYASLERSDHRKJ-LNGSAVE 437
 QY 287 NKNAAE-----KLELAKLEFNI FHSIÖERELKHVS RWMKDSGSPENTFCRHRH 335
 Db 438 NTRVTKTSYRLHNICTSDILKLAVDDFNFCÖSIHREMERLDRWIVENRLÖELKFAÖKL 497
 QY 336 VEYVALASCIAPFÖHSGFRLGFTKMSHLITVLDDMYDVFCTVDELELFTATIKRWDP 395
 Db 498 AYCYFSGAATLFSPELSDARISWAKGVLTTVDDFFDVGGSKEBELNLIHLVEKMDLNG 557
 QY 396 M-ECLPEYMKGVMMVYHTVNEMARVAEKAÖGRDTLNYARÖAMEACFDSYMOEAKMIATG 454
 Db 558 VPEYSEHVEIIFSVLRDTILLETGDKAFYÖGRVTHIIVKIWLDLKMSMLREAEWSSDK 617
 QY 455 YLPTFEERYLNGKVSSAHRPCALÖPILTLDPFPDHLKEVDFP-SKLNLCIILRLR 512
 Db 618 STPSLEDYMENAYISFALGPVILPATYLLIGPLPE--KTVDSHÖYNÖLYKLVSTMGRLL 674
 QY 513 GÖTRCYKADRARGEASISCYMK-DNPGLTÖEDALNHINFMIRDAIRELWELLKPDNS 571
 Db 675 NDIÖGFKRESAEG-KLNAVSLMHKHERDNRSKEVIESMKGLAEKRREELHLVLBEKGS 733
 QY 572 VPITSKRHAF-DISRYVHHGYRRDGYSPANVETKSLVMRTVIEPVPL 618
 Db 734 VVPRECKEAFLLKMSKYLNLFRYKDDG--FTSNDLMSLVKSIVIEPVSL 779

```
Search completed: July 23, 2004, 09:04:15
Job time : 23 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: ~ July 23, 2004, 08:56:41 ; Search time 13 Seconds
(without alignment)
2475.335 Million cell updates/sec

Title: US-10-025-145A-65

Perfect score: 3251
Sequence: 1 MALLSITPLVSRSLSSHE.....FANVETKSLVMTVIEPVPL 618

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1 | 2453 | 75.5 | 628 | 1 | TSD1_ABIGR |
| 2 | 2200.5 | 67.7 | 627 | 1 | TSD2_ABIGR |
| 3 | 2031.5 | 62.5 | 637 | 1 | TSD3_ABIGR |
| 4 | 1240.5 | 38.2 | 862 | 1 | TASY_TAXBR |
| 5 | 1238.5 | 38.1 | 862 | 1 | TASY_TAXBA |
| 6 | 1209.5 | 37.2 | 862 | 1 | TASY_TAXCH |
| 7 | 717.5 | 22.1 | 554 | 1 | DCS1_GOSAR |
| 8 | 717.5 | 22.1 | 554 | 1 | DCS2_GOSAR |
| 9 | 701.5 | 21.6 | 554 | 1 | DCS4_GOSAR |
| 10 | 699.5 | 21.5 | 555 | 1 | DCS3_GOSAR |
| 11 | 692.5 | 21.3 | 554 | 1 | DCS1_GOSHI |
| 12 | 667 | 20.5 | 601 | 1 | CASS_RICCO |
| 13 | 644.5 | 19.8 | 548 | 1 | SEAS_TOBAC |
| 14 | 133 | 4.1 | 1941 | 1 | UBR1_KLULA |
| 15 | 125 | 3.8 | 1295 | 1 | BXA2_CLOBO |
| 16 | 117.5 | 3.6 | 1513 | 1 | GRLF_RAT |
| 17 | 114 | 3.5 | 456 | 1 | PUR8_ECOLI |
| 18 | 111.5 | 3.4 | 602 | 1 | LEPA_HELPY |
| 19 | 110 | 3.4 | 2875 | 1 | RREP_TSWV1 |
| 20 | 109.5 | 3.4 | 1513 | 1 | GRLF_HUMAN |
| 21 | 108.5 | 3.3 | 570 | 1 | EZRA_BACAA |
| 22 | 108.5 | 3.3 | 1061 | 1 | EX5C_BUCAP |
| 23 | 107 | 3.3 | 815 | 1 | CC53_YEAST |
| 24 | 105.5 | 3.2 | 428 | 1 | SYS_PASNU |
| 25 | 105.5 | 3.2 | 898 | 1 | YMW6_YEAST |
| 26 | 105.5 | 3.2 | 1026 | 1 | MY1B_DROME |
| 27 | 105 | 3.2 | 1790 | 1 | VIT_ANTGR |
| 28 | 104.5 | 3.2 | 510 | 1 | CHLB_PINTH |
| 29 | 104.5 | 3.2 | 570 | 1 | EZRA_BACCR |
| 30 | 104.5 | 3.2 | 1500 | 1 | GRLF_CANFA |
| 31 | 104 | 3.2 | 1510 | 1 | MUXB_HAEIN |
| 32 | 103.5 | 3.2 | 598 | 1 | SYD_LACPL |
| 33 | 103.5 | 3.2 | 822 | 1 | V2A_BMV |

| | | | | | | |
|----|-------|-----|------|---|------------|--------------------|
| 34 | 103 | 3.2 | 666 | 1 | NEBU_HUMAN | P20929 homo sapien |
| 35 | 102.5 | 3.2 | 567 | 1 | YE28_METJA | Q58823 methanococ |
| 36 | 102.5 | 3.2 | 1085 | 1 | CASR_BOVIN | P35384 bos taurus |
| 37 | 102.5 | 3.2 | 2364 | 1 | SPCO_HUMAN | Q01082 homo sapien |
| 38 | 102 | 3.1 | 593 | 1 | SYD_THERTN | Q8rai7 thermoaner |
| 39 | 102 | 3.1 | 700 | 1 | LSHR_RAT | P16235 ratus norv |
| 40 | 102 | 3.1 | 4036 | 1 | RRLP_DUGBV | Q66431 dugbe virus |
| 41 | 101.5 | 3.1 | 693 | 1 | IF2_OCEIH | Q8equ1 oceanobacil |
| 42 | 101.5 | 3.1 | 820 | 1 | SUS2_TULGE | Q41607 tulipa gese |
| 43 | 101 | 3.1 | 1277 | 1 | IF3X_YEAST | Q03690 saccharomyc |
| 44 | 100.5 | 3.1 | 419 | 1 | YE87_SCHPO | O14303 schizosacch |
| 45 | 100.5 | 3.1 | 519 | 1 | YMP4_YEAST | Q04347 saccharomyc |

ALIGNMENTS

RESULT 1
TSD1_ABIGR
ID TSD1_ABIGR STANDARD: PRT; 628 AA.
AC 024475;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Pinene synthase, chloroplast precursor (EC 4.2.3.14) (Beta-geraniolene synthase) ((-)-(1S,5S)-pinene synthase).
DE Ag3.18.
OS Abies grandis (Grand fir).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.
OX NCBI_TaxID=46611;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX MEDLINE=97413772; PubMed=9268308;
RA Bohlmann J., Steele C.L., Croteau R.;
RT "Monoterpene synthases from grand fir (Abies grandis). cDNA isolation, characterization, and functional expression of myrcene synthase, (-)-(4S)-limonene synthase, and (-)-(1S,5S)-pinene synthase.";
RT J. Biol. Chem. 272:21784-21792(1997).
RL
CC -1- FUNCTION: Involved in defensive oleoresin formation in conifers in response to insect attack or other injury. Involved in monoterpene (C10) olefins biosynthesis. A mixture of alpha-and beta-pinene is produced by this enzyme.
CC -1- CATALYTIC ACTIVITY: Geranyl diphosphate = pinene + diphosphate.
CC -1- COFACTOR: Manganese and potassium.
CC -1- PATHWAY: Oleoresinosis.
CC -1- SUBCELLULAR LOCATION: Chloroplast.
CC -1- INDUCTION: By wounding.
CC -1- SIMILARITY: Belongs to the terpene synthase family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL; U87909; AAB710E5.1; -.
DR HSSP; Q40577; SEAT.
DR InterPro; IPR008930; Terp_cyc_toroid.
DR InterPro; IPR001906; Terp_synth-like.
DR InterPro; IPR005630; Terpene_synth_C.
DR InterPro; IPR008949; Terpenoid_synth.
DR Pfam; PF01397; Terpene_synth; 1.
DR Pfam; PF03936; Terpene_synth_C; 1.
KW lyase; Manganese; Transf. synth. C; 1.
KW TRANSIT
FT CHAIN 1 ?
FT ACT_SITE 524 628 PINENE SYNTHASE.
FT ACT_SITE 601 601 BY SIMILARITY.
FT ACT_SITE 605 605 BY SIMILARITY.
SQ SEQUENCE 628 AA; 71505 MW; 23DBB78BF3C8072C CRC64;

Query Match 75.5%; Score 2453; DB 1; Length 628;
Best Local Similarity 75.3%; Pred. No. 3e-158;
Matches 475; Conservative 59; Mismatches 81; Indels 16; Gaps 6;

| | | | |
|----|-----|--|-----|
| QY | 1 | MALISITPLVSRSL-----SSSHEIKALRRTIPTLGICRPGKSVASHINMCLTSVASTD | 55 |
| DB | 1 | MALVSTAPLASKSCLHKSLSISTHELKALSRITPALGMSRGRKSITPSSISMSSTVTVD | 60 |
| QY | 56 | SVQRVGNVHNSLWDDDFIQSLISTPYGAPDYRERADRLIGEYKDIMFNKSLDEGG--- | 112 |
| DB | 61 | GVRRMGDFHNSLWDDVIOQL-PTAYEKSYLERAEKLIGEYKN-MFNSMSLEDGELMS | 118 |
| QY | 113 | --NDLLQRLLLVDVERLGIDRHFKEIKTALDYNSYWNKEGICGGRSVTDLNSTAL | 170 |
| DB | 119 | PLNDLQRLWIVDSLERLGIDRHFKEIKSALDYNSYWNKEGICGGRSVTDLNSTAL | 178 |
| QY | 171 | GLRTRLHGTYVSSDVLANVFKDKNGQFSSTANIQIEGEIRGVNLFRASLVAFPGEXVMD | 230 |
| DB | 179 | GLRTRLHGYPVSSDVFAFKFGQNGQFSCSENIQTDEIRGVNLFRASLVAFPGEXIMD | 238 |
| QY | 231 | EAETPSTKYLRREALQKIPASSILSLERDVLEYGWHNTNLRLEARNYMDVFGQHTKNKA | 290 |
| DB | 239 | EAETPSTKYLRREALQKIPVSS-LSREIGDVLEYGWHNTNLRLEARNYIQVFGQDTEINTKS | 297 |
| QY | 291 | --AEKLLLELAKLEFNIHSLQERELKAVSRWVKDSCSPMTFCRHRHVEYYALASCIAP | 347 |
| DB | 298 | YVKSCKLLELAKLEFNIHSLQERELKAVSRWVKDSCSPMTFCRHRHVEYYTLASCIAP | 357 |
| QY | 348 | EPQSGFRLGFTKMSHLITVLDMDYVFGTVDELELFTATIKRWDPSAMECLPEYMKGVY | 407 |
| DB | 358 | EPQSGFRLGFTKMSHLITVLDMDYVFGTVDELELFTATIKRWDPSIDCLPEYMKGVY | 417 |
| QY | 408 | MMVYHTVNEMARVAEKAQGRDTLNYARQAWACFDSYMOEAKWIATGYLPTFEEYLENGK | 467 |
| DB | 418 | IAVYDTVNEMAREAEAAQGRDTLTAREAWAYIDSYMGEARWATATGYLPSFDEYENGK | 477 |
| QY | 468 | VSSAHRPCALQPIITLDIPFPDHLKEVDFPSK.LNDLICIILRLRGDTRCYKADRARGEE | 527 |
| DB | 478 | VSCGHRISALQPIITLDIPFPDHLKEVDFPSK.LNDLICALRLRGDTRCYKADRARGEE | 537 |
| QY | 528 | ASSISCYMKDNPGLTTEEDALNHINFMIRDAIRELNWELKPDNSVPITSKGHAFDISRW | 587 |
| DB | 538 | ASSISCYMKDNPGVSEEDALDHINAMISDVIKGLNWELKPDINVPISAKGHAFDIARAF | 597 |
| QY | 588 | HGGRYRDGYSFANVETKSLVMRTVIEPVPL 618 | |
| DB | 598 | HGGRYRDGYSVANVETKSLVTRILLESVPL 628 | |

RESULT 2
TSD2_ABIGR STANDARD; PRT; 627 AA.
ID TSD2_ABIGR
AC O24474;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Myrcene synthase, chloroplast precursor (EC 4.2.3.15).
GN AG2.2.
OS Abies grandis (Grand fir).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.
OX NCBI_TaxID=46611;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RA MEDLINE=97413772; Pubmed=9268308;
RX Bohlmann J., Steele C.L., Croteau R.;
RT "Monoterpene synthases from grand fir (Abies grandis). cDNA isolation,
RT characterization, and functional expression of myrcene synthase, (-)-
RT (4S)-limonene synthase, and (-)-(1S,5S)-pinene synthase.";
RL J. Biol. Chem. 272:21784-21792(1997).
CC -!- FUNCTION: Involved in defensive oleoresin formation in conifers in
CC response to insect attack or other injury. Involved in monoterpene

CC (C10) olefins biosynthesis.
CC -!- CATALYTIC ACTIVITY: Geranyl diphosphate = myrcene + diphosphate.
CC -!- COFACTOR: Manganese and potassium.
CC -!- PATHWAY: Oleoresinosis.
CC -!- SUBCELLULAR LOCATION: Chloroplast.
CC -!- INDUCTION: By wounding.
CC -!- SIMILARITY: Belongs to the terpene synthase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U87908; AAB71084.1; -.
CC HSSP; Q40577; SEAS.
CC DR InterPro; IPR008930; Terp_cyc_toroid.
CC DR InterPro; IPR001906; Terp_synth-like.
CC DR InterPro; IPR005630; Terpene_synth_C.
CC DR InterPro; IPR008949; Terpene_synth.
CC DR Pfam; PF01397; Terpene_synth; 1.
CC DR Pfam; PF03936; Terpene_synth_C; 1.
CC DR Lyase; Manganese; Transit peptide; Chloroplast.
CC KW TRANSIT 1 ? CHLOROPLAST (POTENTIAL).
CC FT CHAIN ? 627 MYRCENE SYNTHASE.
FT ACT_SITE 523 523 BY SIMILARITY.
FT ACT_SITE 600 600 BY SIMILARITY.
FT ACT_SITE 604 604 BY SIMILARITY.
SQ SEQUENCE 627 AA; 72478 MW; 2E0DA492E0C971FD CRC64;

Query Match 67.7%; Score 2200.5; DB 1; Length 627;
Best Local Similarity 68.1%; Pred. No. 3.4e-141;
Matches 427; Conservative 77; Mismatches 106; Indels 17; Gaps 7;

| | | | |
|----|-----|---|-----|
| QY | 1 | MALISITPLVSRSL-----SSSHEIKALRRTIPTLGICRPGKSVASHINMCLTSVASTD | 55 |
| DB | 1 | MALVISIPLASKSCLRKSLSIHHEKPPRYRTIPNLGMRGRKSVTPSMSISLATAPDD | 60 |
| QY | 56 | SVQRVGNVHNSLWDDDFIQSLISTPYGAPDYRERADRLIGEYKDIMFNKSLDEGG--- | 112 |
| DB | 61 | GVQRRIGDYHSNIWDDFIQSL-STPYGEPYQERAERLIVEVKI-FNSMYLDDGRMS | 118 |
| QY | 113 | --NDLLQRLLLVDVERLGIDRHFKEIKTALDYNSYWNKEGICGGRSVTDLNSTAL | 170 |
| DB | 119 | SFNDLMQRLWIVDSVERLGIDRHFKEIKETSALDYVFRYWEENGICGGRDSIVTDLNSTAL | 178 |
| QY | 171 | GLRTRLHGTYVSSDVLANVFKDKNGQFSSTANIQIEGEIRGVNLFRASLVAFPGEXVMD | 230 |
| DB | 179 | GFRTRLHGTYVSEVLKAFQDQNGQFVCSPG-QTEGEIRSVNLFRASLVAFPGEXVME | 237 |
| QY | 231 | EAETPSTKYLRREALQKIPASSILSLERDVLEYGWHNTNLRLEARNYMDVFGQHTK--N | 287 |
| DB | 238 | EAETPSTRYLKEALQKIPVSA-LSQEIKFVMEYGWHNTNLRLEARNYIDTLEKDTSAMLN | 296 |
| QY | 288 | KNAAEKLLLELAKLEFNIHSLQERELKAVSRWVKDSCSPMTFCRHRHVEYYALASCIAP | 347 |
| DB | 297 | KNAGKLLLELAKLEFNIHSLQERELQYLLRWKESDLPKLTFAHRHVEYYTLASCIAP | 356 |
| QY | 348 | EPQSGFRLGFTKMSHLITVLDMDYVFGTVDELELFTATIKRWDPSAMECLPEYMKGVY | 407 |
| DB | 357 | DPKHSAPRLGFAKCHLVTVLDIYDTFGTIDELFTSAIKRWNSSSEIHLPEYMKGVY | 416 |
| QY | 408 | MMVYHTVNEMARVAEKAQGRDTLNYARQAWACFDSYMOEAKWIATGYLPTFEEYLENGK | 467 |
| DB | 417 | MMVFEYVNELTREAEKTQGRNTLNVYRKAWAYFDSYMEAKWISNGYLPMEFEEYHENGK | 476 |
| QY | 468 | VSSAHRPCALQPIITLDIPFPDHLKEVDFPSK.LNDLICIILRLRGDTRCYKADRARGEE | 527 |
| DB | 477 | VSSAYRVATLQPIITLNAWLPDYILKGIDFPSRFNDLASSFLRLRGDTRCYKADRARGEE | 536 |
| QY | 528 | ASSISCYMKDNPGLTTEEDALNHINFMIRDAIRELNWELKPDNSVPITSKGHAFDISRW | 587 |

Db 537 ASCISCYMKDNPSTEDALNHINAMNDIIKELNWEILRSNDIEMLAKKHAFDITRAL 596
Qy 588 HGGYRRDGYSPANVETKSLVMRTVIE 614
Db 597 HHLTYIRDDGFSVANKEKTKLVMETLLE 623

RESULT 3

TSD3_ABIGR
ID_TSD3_ABIGR STANDARD; PRT; 637 AA.
AC 022340;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE (-)-(4S)-limonene synthase, chloroplast precursor (EC 4.2.3.16).
GN AG10.
OS Abies grandis (Grand fir).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.
OX NCBI_TaxId=46611;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX MEDLINE=97413772; PubMed=9268308;
RA Bohlmann J., Steele C.L., Croteau R.;
RT "Monoterpene synthases from grand fir (Abies grandis). cDNA isolation,
RT characterization, and functional expression of myrcene synthase, (-)-
RT (4S)-limonene synthase, and (-)-(1S,5S)-pinene synthase.";
RL J. Biol. Chem. 272:21784-21792(1997).
CC -1- FUNCTION: Involved in defensive oleoresin formation in conifers in
CC response to insect attack or other injury. Involved in monoterpene
CC (C10) olefin biosynthesis.
CC -1- CATALYTIC ACTIVITY: Geranyl diphosphate = limonene + diphosphate.
CC -1- COFACTOR: Manganese and potassium.
CC -1- PATHWAY: Oleoresinosis.
CC -1- SUBCELLULAR LOCATION: Chloroplast.
CC -1- INDUCTION: By wounding.
CC -1- SIMILARITY: Belongs to the terpene synthase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC
DR EMBL; AF006193; AAB70907.1; -.
DR InterPro: IPR008930; Terp_cyc_toroid.
DR InterPro: IPR001906; Terp_synth-like.
DR InterPro: IPR005630; Terpene synth_C.
DR InterPro: IPR008949; Terpenoid_synth.
DR Pfam; PF01397; Terpene_synth; 1.
DR Pfam; PF03936; Terpene_synth_C; 1.
DR Lyase; Manganese; Transit peptide; Chloroplast.
KM TRANSIT 1 ? CHLOROPLAST (POTENTIAL).
FT CHAIN ? 637 (-)-(4S)-LIMONENE SYNTHASE.
FT ACT_SITE 533 533 BY SIMILARITY.
FT ACT_SITE 610 610 BY SIMILARITY.
FT ACT_SITE 614 614 BY SIMILARITY.
SQ SEQUENCE 637 AA; 73477 MW; 8E80CD9DDE86898 CRC64;

Query Match 62.5%; Score 2031.5; DB 1; Length 637;
Best Local Similarity 63.6%; Pred. No. 9.2e-130;
Matches 409; Conservative 84; Mismatches 119; Indels 31; Gaps 14;

Qy 1 MALISITPL-VSRSC-----LSSSHRIKAL--RTIPTLGICRPGKSAHVSIMMCLTVA 52
Db 1 MALISIVSLQVPKSCGLKSLISSNVQALCISTAVPTLRMRROKALV--INMCLTIVS 58
Qy 53 STDS-----VQRRVGNHNSNLWDDFIQSLISTPYGAPDYRERADRLIGEVDIMFNF-- 105
Db 59 HRDNGCGVLQRRADHHPNLWEDDFIQSL-SSPYGSSYSERAEVVEVKE-MFNSIP 116

Qy 106 --KSLEDGNDLLQRLLLVDDVERLGDIDRHFKKEIKTALDYVNSYNNEK-GIGCGRESV 162
Db 117 NNRELFPSONDLLITRLMVDISIERLGDIDRHQONEIRVALDYVSYWKEKEGIGCGRSTF 176
Qy 163 TDLNSTALGLRTLRLHGTYVSSDYLVNFKDKNGQFSSSTANIQIEEI-RGVNLFRASLV 221
Db 177 PDLNSTALALRTLRLHGYNVSSDYLVLEYFKDEKGFACPA-ILTEGOITRSVLNLYRASLV 235
Qy 222 AFPGEKVMDEAETITSTKYLREALQKIPASSILSLERDVLLEYGWTNLPRLERARNYMDVF 281
Db 236 AFPGEKVMDEAEIISASYLKKVLOKIPVSN-LSGEIEYVLEYGWTNLPRLERARNYIEVY 294
Qy 282 ---GQHTKNKNA--AEKLELAKLEFNIHSLQERELKHVSRWKDSSPEMTECRHRH 335
Db 295 EQSGYESLNEMPYNMKKLLQAKLEFNIHSLQRLRELQISIRWKESGSSQLTFRHRH 354
Qy 336 VEYVALASCIAPFPOHSGFRLGFTKSHLITVLDMDYDFGTVDELELFTATIKRWDP 395
Db 355 VEYITMASCTISMLPKHSAFRMEFVKVCHLVTVLDIDYDTFGTMELOLFTDAIKRWDLS 414
Qy 396 MECLPEYMKGVMMVYHTVNEMARVAEKAQGRDTLNYARQAEACFDSYMOEAKWIATGY 455
Db 415 TRWLPXYMKGVYMDLYQCINEMVEAEKIQGRDMLNLIQNAWEALFDTFQEAKWISSY 474
Qy 456 LPTFEEYLENGKVSSAHRPCALQPIITLDIPEPDHILKEVDFPSKNDLICIILRLRGDT 515
Db 475 LPTFEEYLNKAKVSSGSRIATLQPIITLDVPLPDYILOEIDVPSRFNELASSILRLRGDT 534
Qy 516 RCYKADRRAGEEASSISCYMKDNPGLTEEDALNHINFMIRDAIRELWELLKPDNSVPIT 575
Db 535 RCYKADRRAGEEASSISCYMKDHPGSTEEDALNHINAMISDAIRELWELLRPDSKSPIS 594
Qy 576 SKGHAFDISRVWHGGRYRDGYSPANVETKSLVMRTVIEPVPL 618
Db 595 SKGHAFDITRAFHVHYKRYRDGYTVSNNETKNLVMTVLEPLAL 637

RESULT 4

TASY_TAXBR
ID_TASY_TAXBR STANDARD; PRT; 862 AA.
AC Q41594; Q94FV8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Taxadiene synthase (EC 4.2.3.17) (Taxa-4(5), 11(12)-diene synthase).
GN TDC1.
OS Taxus brevifolia (Pacific yew).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Taxaceae; Taxus.
OX NCBI_TaxId=46220;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96199163; PubMed=8621577;
RA Wildung M.R., Croteau R.B.;
RT "A cDNA clone for taxadiene synthase, the diterpene cyclase that
RT catalyzes the committed step of taxol biosynthesis.";
RL J. Biol. Chem. 271:9201-9204(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21297238; PubMed=11404343;
RA Trapp S.C., Croteau R.B.;
RT "Genomic organization of plant terpene synthases and molecular
RT evolutionary implications.";
RL Genetics 158:811-832(2001).
CC -1- FUNCTION: Catalyzes the cyclization of the ubiquitous isoprenoid
CC intermediate geranylgeranyl diphosphate to taxa-4,11-diene, the
CC parent olefin with a taxane skeleton.
CC -1- CATALYTIC ACTIVITY: Geranylgeranyl diphosphate = taxa-4,11-diene +
CC diphosphate.
CC -1- PATHWAY: Taxol biosynthesis; first step.
CC -1- SIMILARITY: Belongs to the terpene synthase family.
CC -----

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL; U48796; AAC49310.1; -.
CC EMBL; AF326519; AAK83566.1; -.
DR HSSP; Q40577; SEAU.
DR InterPro; IPR008930; Terp_cyc_toroid.
DR InterPro; IPR001906; Terp_synth-like.
DR InterPro; IPR005630; Terpene synth C.
DR InterPro; IPR008949; Terpenoid_synth.
DR Pfam; PF01397; Terpene_synth; 1.
DR Pfam; PF03936; Terpene_synth_C; 1.
KW Taxol biosynthesis; lyase.
FT ACT_SITE 758 758 BY SIMILARITY.
FT ACT_SITE 835 835 BY SIMILARITY.
FT ACT_SITE 839 839 BY SIMILARITY.
FT CONFLICT 148 148 L -> V (IN REF. 2).
FT CONFLICT 767 767 A -> V (IN REF. 2).
SQ SEQUENCE 862 AA; 98303 MW; 9141B59780CD79A1 CRC64;

Query Match 38.2%; Score 1240.5; DB 1; Length 862;
Best Local Similarity 42.6%; Pred. No. 3.9e-76;
Matches 269; Conservative 109; Mismatches 205; Indels 49; Gaps 10;

QY 23 ALRRTIPTLGICRPG-----KVAHSINMCLTSV-ASTDSVQRRVGNYSNL-----W-- 69
DB 240 ALLQKAKALGINLPYDLPFIKYLSTTRRRLTDVSAADNIPANMLNLEGLLEVIDWNK 299
QY 70 -----DDDFIQSLISTPYGAPDYRERADRLIGEVDIMFNFKSLEDGN-----D 114
DB 300 IMRFQSKDGSFLSSPASTACVLMN-----TGDEKCFITLNNLLDKFGGCVPCMYSID 351
QY 115 LLQRLLLVDVERLGIDRHFKKEIKTALDVNSYWNKEGIGCGRESVTDLNTALGLRT 174
DB 352 LLERLSLVDNIEHLGIGRHFKEIKGALDYVYRHWSEKIGIGWGRDLSLPDLNTALGLRT 411
QY 175 LRLHGTVSSDVLNVFKDKNGQFSSSTANIQIEGEIRGVNLFRASLVAEPGEKVMDEAET 234
DB 412 LRMHGTVSSDVLNVFKDKNGQFSSAG-QTHVELRSVNLFRASDLAFPERAMDARK 470
QY 235 FSTKYLRAL-QKIPASSILSLERIDVLEYGWHTNLPRLRARNYMDVEGQ-----H 284
DB 471 FAEPYLRALATKISTNTKLFKEIYVEYEPWMSIPRLRARSYIDSYDDNYVMQRTLY 530
QY 285 TKKNKAAEKLLELAKLEFNIHSLQERELKHSRWKDKSGSPMTFCRHRHVEYYALASC 344
DB 531 RMPISLNSKCLELAKLDENIVQSLHQEELKLTTRWKESGMADINFTRRVAEY--FSS 588
QY 345 IAFEPQSGFRLGFTKMSHLITVLDNMYDVGTVDELELFTATIKRWDPSPAMECLPEYMK 404
DB 589 ATFEPEYSATRIAFTKIGCLQVLFDMADIFATLDELKSFTEGVKRWDTSLHEIPECMQ 648
QY 405 GVVNMVYHTVNMARVAEKAQGRDPTLYARQAWACFDSYMOEAKWIATGYLPTFEELYE 464
DB 649 TCFKWPFKLMEEVNNDVVKQGRDMLAHIRKPMELFYNCYGEREWLEAGYIPTFEELYK 708
QY 465 NGKVSAAHRPCALQPIITLDIPFPDHILKEVDFPSKLDNLICILRLRGDTRCYKADRAR 524
DB 709 TYAISVGLGPTLQPIILMGELVKDDVVEKVVHPSNMFELVLSWRLLTNDTKTYQAEKAR 768
QY 525 GEEASSISCYMKDNPGLTEEDALNINFMIRDAIRELNMELKPDNSVPTSKEHAFDIS 584
DB 769 GQQAAGIACYMKDNPGATEEDAICIKRVVDRAKESFEYFKPSNDIPMGCKSFIFNLR 828
QY 585 RVWHGYYRRDGYSPANVETKSLVMRTVIEPV 616
DB 829 LCVQIFYKFIIDGYGIANEIKDYIRKYIDPI 860

RESULT 5
TASY TAXBA STANDARD; PRT; 862 AA.
AC Q93YA3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Taxadiene synthase (EC 4.2.3.17) (Taxa-4(5),11(12)-diene synthase).
GN TDC1 OR TASY.
OS Taxus baccata (English yew).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Taxaceae; Taxus.
OX NCBI_TaxID=25629;
RN [1]
RP SEQUENCE FROM N.A.
RA Goerhardt B.;
RL Thesis (2001), Technische Universitaet Berlin, Germany.

CC -!- FUNCTION: Catalyzes the cyclization of the ubiquitous isoprenoid intermediate geranylgeranyl diphosphate to taxa-4,11-diene, the parent olefin with a taxane skeleton.
CC -!- CATALYTIC ACTIVITY: Geranylgeranyl diphosphate = taxa-4,11-diene + diphosphate.
CC -!- PATHWAY: Taxol biosynthesis; first step.
CC -!- SIMILARITY: Belongs to the terpene synthase family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR EMBL; AJ320538; CAC42773.1; -.
DR InterPro; IPR008930; Terp_cyc_toroid.
DR InterPro; IPR001906; Terp_synth-like.
DR InterPro; IPR005630; Terpene synth C.
DR InterPro; IPR008949; Terpenoid_synth.
DR Pfam; PF01397; Terpene_synth; 1.
DR Pfam; PF03936; Terpene_synth_C; 1.
KW Taxol biosynthesis; lyase.
FT ACT_SITE 758 758 BY SIMILARITY.
FT ACT_SITE 835 835 BY SIMILARITY.
FT ACT_SITE 839 839 BY SIMILARITY.
SQ SEQUENCE 862 AA; 98048 MW; B37835AFDC1DEFE CRC64;

Query Match 38.1%; Score 1238.5; DB 1; Length 862;
Best Local Similarity 42.4%; Pred. No. 5.3e-76;
Matches 273; Conservative 110; Mismatches 206; Indels 55; Gaps 13;

QY 15 LSSSHEI--KALRRTIPTLGICRPG-----KVAHSINMCLTSV-ASTDSVQRRVGNYS 66
DB 230 LSPDFEIIFFPALQKAKALGINLPYDLPFIKSLSTRRRLTDVSAADNIPANMLNLE 289
QY 67 NL-----W-----DDDFIQSLISTP--YGAPDYRERADRLIGEVD-----IM 102
DB 290 GLEEVIDWNKIMRFQSKDGSFLSSPASTACVLMNTGD--EKCFITLNNLLDKFGGCVPCM 347
QY 103 FNFKSLEDGNDLLQRLLLVDVERLGIDRHFKKEIKTALDVNSYWNKEGIGCGRESVY 162
DB 348 YSL-----DLLERLSLVDNIEHLGIGRHFKEIKVALDYVYRHWSEKIGIGWGRDLSV 399
QY 163 TDLNSTALGIRTLRLHGTVSSDVLNVFKDKNGQFSSSTANIQIEGEIRGVNLFRASLVA 222
DB 400 PDLNTTALGLRTLRTHGVDYSSDVLNVFKDKNGQFSSAG-QTHVELRSVNLFRASDLA 458
QY 223 FPGEKVMDAETPSTKYLRAL-QKIPASSILSLERIDVLEYGWHTNLPRLRARNYMDVF 281
DB 459 FPDEGAMDARKFAEPYLRDALATKISTNTKLFKEIYVEYEPWMSIPRLRARSYIDSY 518
QY 282 GQ-----HTKNKNAAEKLLELAKLEFNIHSLQERELKHSRWKDKSGSPMTFCR 332


```
Db 519 DDDYVWRKTLYRMPSLNSKCLLAKLDENIVQSLHQEELKLTTRWKEGSMADINFTR 578
Qy 333 HRHVEYYALASCIAPFEPQHSFRLGFTKMSHLITVLDMDYDFGTVDELEFTATIKRWD 392
Db 579 HRVAEVY--FSSATFEPEYSATRIAFKIGCLOVLFDDMADIFATLDELKSFTEGVKRW 636
Qy 393 PSAMECLPEYMKGYMMVYHTVNEMARVAEKAQGRDTLNYARQAWACFDSYMOEAKWIA 452
Db 637 TSLHIEIPECMQTCFKVMFKLMEEVNNDVVKVQGRDMLAHIRKPMELYNFCYQEREWLE 696
Qy 453 TGYLPTFEELYENGKVSASAHPCALQPIITLDIPFPDHILKEVDFPSKNDLICITLRLR 512
Db 697 AGYIPTFEELYKTYAISVGLGPCTLOPILMGLVKDDVVEKVKHYPSPMELVSLSWRLT 756
Qy 513 GDTRCYKADRARGEASSISCYMKDNPGLTEEDALNHINFMIRDAIRELWELLKPDNSV 572
Db 757 NDTKTYQAEKARGQOASGIACYMKDNPGLATEEDAIKHICRVVDRALKKASFEYFKPSNDI 816
Qy 573 PITSKKHAFDISRVMHGYRYRDGYSFANVETKSLVMRTVIEPV 616
Db 817 PMGCKSFIFNLRLCVQIFYKPIDGYGIANEEIKDYIRKVYIDPI 860
```

```
RESULT 6
TASY_TAXCH STANDARD; PRT; 862 AA.
ID TASY_TAXCH
AC Q9FT37;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Taxadiene synthase (EC 4.2.3.17) (Taxa-4(5),11(12)-diene synthase).
GN TDC1.
OS Taxus chinensis (Chinese yew).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Taxaceae; Taxus.
OX NCBI_TaxID=29808;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Callus;
RA Wang W., Shi Q., Ouyang T., Zhu P., Cheng K.;
RT "Cloning, expression, and characterization of taxadiene synthase, a
RL diterpene cyclase from Taxus chinensis.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Catalyzes the cyclization of the ubiquitous isoprenoid
CC intermediate geranylgeranyl diphosphate to taxa-4,11-diene, the
CC parent olefin with a taxane skeleton.
CC -1- CATALYTIC ACTIVITY: Geranylgeranyl diphosphate = taxa-4,11-diene +
CC diphosphate.
CC -1- PATHWAY: Taxol biosynthesis; first step.
CC -1- SIMILARITY: Belongs to the terpene synthase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AY007207; AAC02257.1; -.
DR HSSP; Q40577; SEAU.
DR InterPro; IPR008930; Terp_cyc_toroid.
DR InterPro; IPR001906; Terp_synth-like.
DR InterPro; IPR005630; Terpene_synth_C.
DR InterPro; IPR008949; Terpenoid_synth.
DR Pfam; PF01397; Terpene_synth; 1.
DR Pfam; PF03936; Terpene_synth_C; 1.
DR Taxol biosynthesis; Lyase.
KW ACT_SITE 758 758 BY SIMILARITY.
FT ACT_SITE 835 835 BY SIMILARITY.
FT ACT_SITE 839 839 BY SIMILARITY.
SQ SEQUENCE 862 AA; 98069 MM; 3A597BAF722BF679 CRC64;
```

Query Match 37.2%; Score 1209.5; DB 1; Length 862;
Best Local Similarity 41.9%; Pred. No. 4.9e-74;
Matches 270; Conservative 110; Mismatches 209; Indels 55; Gaps 12;

```
Qy 15 LSSSHEI--KALREFITPLGICRPG-----KVAHSINMCLTSV-ASTDSVQRVGNYS 66
Db 230 LSPDFEITFPALLCKAKALGINLPYDLPIFKYLTSTREARLTDSAAADNIPANMLNLE 289
Qy 67 NL-----W-----DDDFIOSLSTFYGAPDYRERADRLIGEVDIMFNFKS---LE 109
Db 290 GLEEVMDWKIMRFQSKDGSFLSSPAST-----ACVLMNTGDEKCFITLNNLVK 339
Qy 110 DGG-----NDLQRLLLVDVERLGIIDHFKEIKTALDYVNSYWNKIGCGRESV 162
Db 340 FGGCVPCWYSIDLIERLSVDNIEHLGIGHFKOEIKVALDYVYRHSERIGWGRDSL 399
Qy 163 TDLNSTALGLRTFLHGYTVSSDVLNVFKDKNGQFSSTANIQIEGIRGVNLFRASLVA 222
Db 400 PDLNTTALGLRTFLTHGYDVSSDVLNPFKDNENGRFSSAG-QTHVELRSVILFRASDLA 458
Qy 223 FPEGKVMDEAFETGTYKLRAL-QKIPASSILSLERDVLLEYGWHFNLRLRNMDVF 281
Db 459 FPDEGAMDARKEFAEPLRDALATKISTNTKLFKEIEYVEYEPWMSIPRSEARSYDSY 518
Qy 282 GQ-----HTYKNAAEKLELAKLEFNIHSLQERELKHSRWKDSGSPENTFCR 332
Db 519 DDDYVWRKTLYRMPSLNSKCLLAKLDENIVQSLHQEELKLTTRWKEGSMADINFTR 578
Qy 333 HRHVEYYALASCIAPFEPQHSFRLGFTKMSHLITVLDMDYDFGTVDELEFTATIKRWD 392
Db 579 HRVAEVY--FSSATFEPEYSATRIAFKIGCLOVLFDDMADIFATLDELKSFTEGVKRW 636
Qy 393 PSAMECLPEYMKGYMMVYHTVNEMARVAEKAQGRDTLNYARQAWACFDSYMOEAKWIA 452
Db 637 TSLHIEIPECMQTCFKVMFKLIEEVNNDVVKVQGRDMLAHIRKPMELYNFCYQEREWLD 696
Qy 453 TGYLPTFEELYENGKVSASAHPCALQPIITLDIPFPDHILKEVDFPSKNDLICITLRLR 512
Db 697 AGYIPTFEELYKTYAISVGLGPCTLOPILMGLVKDDVVEKVKHYPSPMELVSLSWRLT 756
Qy 513 GDTRCYKADRARGEASSISCYMKDNPGLTEEDALNHINFMIRDAIRELWELLKPDNSV 572
Db 757 NDTKTYQAEKARGQOASGIACYMKDNPGLATEEDAIKHICRVVDRALKKASFEYFKPSNDI 816
Qy 573 PITSKKHAFDISRVMHGYRYRDGYSFANVETKSLVMRTVIEPV 616
Db 817 PMGCKSFIFNLRLCVQIFYKPIDGYGIANEEIKDYIRKVYIDPI 860
```

```
RESULT 7
DCS1_GOSAR STANDARD; PRT; 554 AA.
ID DCS1_GOSAR
AC Q39761;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE (+)-delta-cadinene synthase isozyme XCl (EC 4.2.3.13) (D-cadinene
DE synthase).
OS Gossypium arboreum (Tree cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=29729;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nanking;
RX MEDLINE=96132653; PubMed=8554317;
RA Chen X.-Y., Chen Y., Heinstein P., Davison V.J.;
RT "Cloning, expression, and characterization of (+)-delta-cadinene
RT synthase: a catalyst for cotton phytoalexin biosynthesis.";
RL Arch. Biochem. Biophys. 324:255-266(1995).
CC -1- FUNCTION: Responsible for the cyclization of trans,trans-farnesyl
CC diphosphate (FPP) to (+)-delta cadinene.
```

-!- CATALYTIC ACTIVITY: 2-trans,6-trans-farnesyl diphosphate = (+) -
CC delta-cadinene + diphosphate.
CC -!- PATHWAY: Phytoalexins gossypol and lacinilene C biosynthesis;
CC first (committed) step.
CC -!- SIMILARITY: Belongs to the terpene synthase family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL; U23206; AAA93064.1; -.
DR PIR; S68365; S68365.
DR HSSP; Q40577; SEAU.
DR InterPro; IPR008930; Terp_cyc toroid.
DR InterPro; IPR001906; Terp_synth-like.
DR InterPro; IPR005630; Terpene synth_C.
DR InterPro; IPR008949; Terpenoid synth.
DR Pfam; PF01397; Terpene_synth; 1.
DR Pfam; PF03936; Terpene_synth_C; 1.
KM lyase; Multigene family.
FT ACT_SITE 451 451 BY SIMILARITY.
FT ACT_SITE 527 527 BY SIMILARITY.
FT ACT_SITE 531 531 BY SIMILARITY.
SQ SEQUENCE 554 AA; 64137 MW; 59D6922DEDF9DCAF CRC64;

Query Match 22.1%; Score 717.5; DB 1; Length 554;
Best Local Similarity 31.8%; Pred. No. 4.7e-41;
Matches 183; Conservative 107; Mismatches 243; Indels 43; Gaps 14;

QY 51 VASTDSVQRRVGNHNSLWDDDFIQSLISTPYGAPD-----YRBRADRLIGEYKDIMFN 104
Db 14 LSSNKDEMRPKADFQPSIWGDLFL-----NCPDKNIDAETEKHHQQLKEEVR----- 60
QY 105 FKSLEDEGNDLLQRLLLVDVERLGIDRHFKKEIKTALDVNSYVNEKGIGCGRESVTTD 164
Db 61 -KMIVAPMANSTQKLAFIDSVQRLGVSYHFTKEIEDEL- -NITYH-----NND AEND 110
QY 165 INSTALGLRTLRLHGTYVSSDVLANVFKDKNGQFSSTANIQIEGEIRGVNLFRASLVAFP 224
Db 111 LYTTSIRFRLLRHGVNSCDVENKFKDEQGNFKSS----VTSVGRGLLELYQASYLRVH 166
QY 225 GEKVMDEAETFTSKYLREALQKIPASSILSLSEIRDVLEYGWHNTNLPRL EARNYMDVFGQH 284
Db 167 GEDILDEAISTTTHLSLAVASL--DHP LSEEVSHALKQSIIRGLPRVEARHYLSVY-QD 223
QY 285 TKKNKAAEKLELAKLEFNIFHSLQERELKHVSRWKCD-SGSPENTFCRHRHVEYYALAS 343
Db 224 IESHNKA--LLEFAKIDFNMLQFLHRKELSEICRWKDKLDFQRKLPRYARDRVEGYFWIS 281
QY 344 CIAFEPQHSQFRIGFTKMSHLITVLDWYDVFQTVDELFTATIKRWDPSAMECLPEYM 403
Db 282 GGVYFEPQYSLGRKMLTKVIAMASIVDDTYDSYATYBELIPYTNAIERWDIKCID EIPBYM 341
QY 404 KGVYMMVYHTVNMARVAEKAQGRDTLNYARQAMEACFDSYMQEAKMIATGYLPTFE EYL 463
Db 342 KPSYKALLDVEEMVQLVAEHGRQYVEYAKNAMIRLAQSYLVEAKWTLQNYKPSFE EFK 401
QY 464 ENGKVSAAHRPCALQPI LTL-DIPFDHILKEVDFP SKLNDLICILRLRGDTRCYKADR 522
Db 402 ANALPTCGYAMLAITSFVGMGDIPTPETFKMAASDP-KIIQASTIICRFMDDVAEHKFKH 460
QY 523 ARGEEASSISCYMKDNGLTTEEDALNHNFMIRDAIRELNWELLPD NSVPTSCKHAPD 582
Db 461 RREDDCSAIECYMEBY-GVTAQEAAYDFNKHVESAWKDLNQEF LKP-TEMPTEVLNRSLN 518
QY 583 ISRVVHGGYRYRDGYSFANVETKSLVMTVIEPVP L 618
Db 519 LARVMDVLYREGDYTYVGKAAKGITSLIEPIAL 554

RESULT 8
DCS2_GOSAR
ID DCS2_GOSAR STANDARD; PRT; 554 AA.
AC Q39760;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE (+)-delta-cadinene synthase isozyme XC14 (EC 4.2.3.13) (D-cadinene synthase).
OS Gossypium arboreum (Tree cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=29729;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nanking;
RX MEDLINE=96132653; PubMed=8554317;
RA Chen X.-Y., Chen Y., Heinstein P., Davisson V.J.;
RT "Cloning, expression, and characterization of (+)-delta-cadinene
RT synthase: a catalyst for cotton phytoalexin biosynthesis.";
RL Arch. Biochem. Biophys. 324:255-266(1995).
CC -!- FUNCTION: Responsible for the cyclization of trans,trans-farnesyl
CC diphosphate (FPP) to (+)-delta cadinene.
CC -!- CATALYTIC ACTIVITY: 2-trans,6-trans-farnesyl diphosphate = (+) -
CC delta-cadinene + diphosphate.
CC -!- PATHWAY: Phytoalexins gossypol and lacinilene C biosynthesis;
CC first (committed) step.
CC -!- SIMILARITY: Belongs to the terpene synthase family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL; U23205; AAA93065.1; -.
DR PIR; S68366; S68366.
DR HSSP; Q40577; SEAU.
DR InterPro; IPR008930; Terp_cyc toroid.
DR InterPro; IPR001906; Terp_synth-like.
DR InterPro; IPR005630; Terpene synth_C.
DR InterPro; IPR008949; Terpenoid synth.
DR Pfam; PF01397; Terpene_synth; 1.
DR Pfam; PF03936; Terpene_synth_C; 1.
KM lyase; Multigene family.
FT ACT_SITE 451 451 BY SIMILARITY.
FT ACT_SITE 527 527 BY SIMILARITY.
FT ACT_SITE 531 531 BY SIMILARITY.
SQ SEQUENCE 554 AA; 64158 MW; A88974665E0F6B2B CRC64;

Query Match 22.1%; Score 717.5; DB 1; Length 554;
Best Local Similarity 31.9%; Pred. No. 4.7e-41;
Matches 184; Conservative 108; Mismatches 241; Indels 43; Gaps 14;

QY 51 VASTDSVQRRVGNHNSLWDDDFIQSLISTPYGAPD-----YRBRADRLIGEYKDIMFN 104
Db 14 LSSNKDEMRPKADFQPSIWGDLFL-----NCPDKNIDAETEKHHQQLKEEVR----- 60
QY 105 FKSLEDEGNDLLQRLLLVDVERLGIDRHFKKEIKTALDVNSYVNEKGIGCGRESVTTD 164
Db 61 -KMIVAPMANSTQKLAFIDSVQRLGVSYHFTKEIEDEL- -NITYH-----NND AEND 110
QY 165 INSTALGLRTLRLHGTYVSSDVLANVFKDKNGQFSSTANIQIEGEIRGVNLFRASLVAFP 224
Db 111 LYTTSIRFRLLRHGVNSCDVENKFKDEQGNFKSS----VTSVGRGLLELYQASYLRVH 166
QY 225 GEKVMDEAETFTSKYLREALQKIPASSILSLSEIRDVLEYGWHNTNLPRL EARNYMDVFGQH 284
Db 167 GEDILDEAISTTTHLSLAVASLDYP--LSEEVSHALKQSIIRGLPRVEARHYLSVY-QD 223

QY 285 TKKNAAEKLELAKLEFNIHFSLOERELKHVSRWKD-SGSPMTFCRHRHVEYALAS 343
Db 224 IESHN--KVLLEPAKIDFNWQVLHRKELSEISRWKDLDFQRKLPYARDRVEGYFWIS 281
QY 344 CIAEPQHSQFRLGFTKMSHLITVLDMDYDVGTVDELELFTATIKRWDPSAMECLPEYM 403
Db 282 GYVEPEQYSLGRKMLTKVIAMASIVDDTYDSYATYELIPYTKAIERWDIKCIDELPEYM 341
QY 404 KGVYMWVYHTVNEMARVAEKAQGRDITLVYARQAMEACFDSYMOEAKWIATGYLPTFEYL 463
Db 342 KPSYKALLDVEEMEQLVAKHGROYVEYAKNAMIRLAQSYLVEARWTLQNYKPSFEFEK 401
QY 464 ENGVSSAHRPCALQPIITL-DIPFPDHILKEVDFPSKLNLCITILRLRGDTRCYKADR 522
Db 402 ANALEPTCYAMLAITSFVGMGDIPTPETFKWAANDP-KIIQASTICRFMDVAEHKFKH 460
QY 523 ARGEAASSISCYMKDNPGLTEEDALNHINFMIRDAIRELNWELLKPDNSVPITSKHAFD 582
Db 461 RREDDCSAIECYMEY-GVTAQEAAYDFVFNKHVESAWKDVNKEFLKP-TEMPTEVLNRSLN 518
QY 583 ISRYWHGYYRDRGYSFANVETKSLVMTVIEPVPL 618
Db 519 LARVMDVLYREGDYTYVGKAAKGITSLIEPVAL 554

RESULT 9
DCS4_GOSAR STANDARD; PRT; 554 AA.
AC 049853;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE (+)-delta-cadinene synthase isozyme C2 (EC 4.2.3.13) (D-cadinene synthase).
GN CAD1-C2.
OS Gossypium arboreum (Tree cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Malvales; Malvaceae; Malvaceae; Gossypium.
OC NCBI_TaxID=29729;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nanking;
RA Meng Y., Jia J., Liu C., Liang W., Zhou X., Heinsteins P., Chen X.-Y.; Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RL -1- FUNCTION: Responsible for the cyclization of trans,trans-farnesyl diphosphate (FPP) to (+)-delta-cadinene.
CC -1- CATALYTIC ACTIVITY: 2-trans,6-trans-farnesyl diphosphate = (+)-delta-cadinene + diphosphate.
CC -1- PATHWAY: Phytoalexins gossypol and lacinilene C biosynthesis; first (committed) step.
CC -1- SIMILARITY: Belongs to the terpene synthase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Y16432; CAA76223.1; --
DR HSSP; Q40577; SEAU.
DR InterPro; IPR008930; Terp_cyc_toroid.
DR InterPro; IPR001906; Terp_synth-like.
DR InterPro; IPR005630; Terpene_synth_C.
DR InterPro; IPR008949; Terpenoid_synth.
DR Pfam; PF01397; Terpene_synth; 1.
DR Pfam; PF03936; Terpene_synth_C; 1.
KW lyase; Multigene family.
FT ACT_SITE 451 451 BY SIMILARITY.
FT ACT_SITE 527 527 BY SIMILARITY.

FT ACT SITE 531 531 BY SIMILARITY.
SQ SEQUENCE 554 AA; 64117 MW; 35DD66D3E838AAC CRC64;
Query Match 21.6%; Score 701.5; DB 1; Length 554;
Best Local Similarity 31.5%; Pred. No. 5.6e-40;
Matches 179; Conservative 108; Mismatches 238; Indels 43; Gaps 14;
QY 59 RRVGNHNSLWDDFIQSLISTPYCAPD-----YERADRLLGEVKDIMENFKSLEDGG 112
Db 22 RPKADFPQSIWGDIFL-----NCPDKNIDAGTEKRHQQLKEVR-----KMIVAPM 67
QY 113 NDLLQRLLLVDVIRLIGIDRHFKKEIKTALDYVNSYWNKEGIGGRESVVTDLNSTALGL 172
Db 68 ANSTQKLAFIDSVQRLGVSYHFTKEIDELE--NIYHN-----NNDALNDLYTSLRF 118
QY 173 RTLRHGTVSSDYLVNFKQKNGQSSSTANQIEGEIRGVNLFRASLVAFPGKVMDEA 232
Db 119 RLIREHGVNSCDYFNKFKDEQGNFKSS---VTSVQGLLELYQASYLVRHGEDILDEA 174
QY 233 ETESTKYIREALQKIPASSISLEIRDVLEYGWHNTLPRLEARNYMDVFGQHTKKNAAE 292
Db 175 ISFTTHSLAVSGL--DHPLSEEVSHALKQSIIRGLPRVEARHYLSVY-QDIESHNKA- 230
QY 293 KLEELAKLEENIFHSLQERELKHVSRWKD-SGSPMTFCRHRHVEYALASCIAPFEPQ 351
Db 231 -LLEPAKIDFNMLQFLHRKELSEICRWKDLDFQRKLPYARDRVEGYFWISGVYFEPQ 289
QY 352 SGFRLGFTKMSHLITVLDMDYDVGTVDELELFTATIKRWDPSAMECLPEYMKGVYMWVY 411
Db 290 SLGRKMLTKVIAMASIVDDTYDSYATYELLIPYTKAIERWDIKCIDELPEYMKPSYKALL 349
QY 412 HTVNEMARVAEKAQGRDITLVYARQAMEACFDSYMOEAKWIATGYLPTFEYLLNGKVSSA 471
Db 350 DVYKEMEQVAEHGROYVEYAKNAMIRLAQSYLVEARWTLQNYKPSFEFEKANALPTCG 409
QY 472 HRPICALQPIITL-DIPFPDHILKEVDFPSKLNLCITILRLRGDTRCYKADRARGEASS 530
Db 410 YAMLAITSFVGMGDIPTPETFKWAANDP-KIIQASTICRFMDVAEHKFKHREDDCSA 468
QY 531 ISCYMKDNPGLTEEDALNHINFMIRDAIRELNWELLKPDNSVPITSKHAFDISRVWHG 590
Db 469 IECYMEY-GVSAQEAAYDFVFNKHVESAWKDVNOEFQKP-TEMPTEVLNRSNLARVMDVL 526
QY 591 YRYRDGYSFANVETKSLVMTVIEPVPL 618
Db 527 YREGDYTYVGKAAKGITSLIEPVAL 554

RESULT 10
DCS3_GOSAR STANDARD; PRT; 555 AA.
AC Q43714;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE (+)-delta-cadinene synthase isozyme A (EC 4.2.3.13) (D-cadinene synthase).
GN CAD1-A.
OS Gossypium arboreum (Tree cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Malvales; Malvaceae; Malvaceae; Gossypium.
OC NCBI_TaxID=29729;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nanking;
RX MEDLINE=97060798; PubMed=8904844;
RA Chen X.-Y., Wang M., Chen Y., Davison V.J., Heinsteins P.; "Cloning and heterologous expression of a second (+)-delta-cadinene synthase from Gossypium arboreum."; J. Nat. Prod. 59:944-951 (1996).
RT -1- FUNCTION: Responsible for the cyclization of trans,trans-farnesyl diphosphate (FPP) to (+)-delta-cadinene.
CC


```
CC -1- CATALYTIC ACTIVITY: 2-trans,6-trans-farnesyl diphosphate = (+)-
CC delta-cadinene + diphosphate.
CC -1- PATHWAY: Phytoalexins gossypol and lacinilene C biosynthesis;
CC first (committed) step.
CC -1- SIMILARITY: Belongs to the terpene synthase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X96429; CAA65289.1; -.
DR EMBL; U27535; AAB41259.1; -.
DR HSSP; Q40577; SEAT.
DR InterPro; IPR008930; Terp_cyc_toroid.
DR InterPro; IPR001906; Terp_synth-like.
DR InterPro; IPR005630; Terpene synth_C.
DR InterPro; IPR008949; Terpenoid_synth.
DR Pfam; PF01397; Terpene_synth; 1.
DR Pfam; PF03936; Terpene_synth_C; 1.
KW Lyase; Multigene family.
FT ACT_SITE 452 452 BY SIMILARITY.
FT ACT_SITE 528 528 BY SIMILARITY.
FT ACT_SITE 532 532 BY SIMILARITY.
SQ SEQUENCE 555 AA; 64103 MW; 7060CAFD9D99412F9 CRC64;

Query Match 21.5%; Score 699.5; DB 1; Length 555;
Best Local Similarity 31.5%; Pred. No. 7.7e-40;
Matches 181; Conservative 104; Mismatches 241; Indels 49; Gaps 14;

QY 56 SVQRRVGNVYNSNLWDDDFIQSLISTPYGAPD-----YRERADRLIGEVDIMFN 105
DB 18 SENRPKADFHPIGWDMFI-----CPDIDDATELQYEE-----LKAQVR----- 59

QY 106 KSLIEDGNDLLQRLLLVDVERLGIDRHFKKEIKTALDYVNSYWNKEIGCGRESVVTDL 165
DB 60 KMIWEYVDDSNQKLPFIDAVQRLGVSYHFEKEIJELENIYRDTN-----NNDADTDL 112

QY 166 NSTALGLRTLRLHGTVSSDVLNVFKDKNGQFSSTANIQIEGIRGVNLFRASLVAFP 225
DB 113 YTTALRRLLRHHGFDISCDAFNKFDEAGNFKAS----LTSVQGLLELYEASYNRVHG 168

QY 226 EKVMDEATPSTKYLRALOKIPASSILSLIEIRDVLEYGMHTNLPRLAARNYMDVFGQHT 285
DB 169 EDILDEAISTTQTLALPTL--HHPLSEQVGHALKQSIIRGLPRVEARNFISIT-QL 225

QY 286 KMKNAAEKLELAKLEFNIFHSLQERELKHVSRWKCD-SGSPETFCRHRHVEYALASC 344
DB 226 ESHN--KSLLOFAKIDFNLQLLHRKELSEICRWKXLDLFTRKLPARDRVVEGYFWIMG 283

QY 345 IAFEPQSGFRLGFTKMSHLITVLDMYDVGTVDELELFTATIKRWDPSAMECLPEYMK 404
DB 284 VYFEPQYSLGRKMLTKVIAMASIVDDTYSYATYDELIPYTNAIERWDIKCMNQLPNYMK 343

QY 405 GVVYMMVYHTVNEMARVAEKAQGRD--TLNYARQAEACFDSYMQEAKWIATGYLPTFE EYL 463
DB 344 ISYKALLNVYEEMQQLLAN-QGRQRYVEYAKKAMIRLVQAYLLLEAKWTHQNYKPTFE EFR 402

QY 464 ENGVSAHRCALQPIRLTLDIPFPDHLKEVDFPSKLANDLICITLRLRGDTRCYKADRA 523
DB 403 DNALPTSGYMLAITAFVGMGEVITPETFKMAASDPKTIKASTICRFMDIAEHKFNHR 462

QY 524 RGEASASISCYMKDNPGLTEBDALNHNFMIRDAIRELNMWELKPDNSVPTSKHAFDI 583
DB 463 REDDCSAIECYMKQY-GVTAQEAAYNEFNKHIESSWKDVNEEFKLP-TEMPPTVLCRSLNL 520

QY 584 SRVWHGYYRYRDGYSFANVETKSLVMTVIEPVL 618
DB 521 ARVMDVLYREGDGYTHVGKAKAGGITSLLIDPIQI 555
```

```
RESULT 11
DCS1_GOSHI
ID DCS1 GOSHI STANDARD; PRT; 554 AA.
AC P93665;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE (+)-delta-cadinene synthase (EC 4.2.3.13) (D-cadinene synthase).
GN CDN1.
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=3635;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Westburn M;
RA Davis E.M., Chen Y.-S., Essenberg M., Pierce M.L.;
RT "cDNA sequence of a (+)-delta-cadinene synthase gene induced in
RT Gossypium hirsutum L. by bacterial infection.";
RL (In) Plant Gene Register PGR98-040.
RN [2]
RP PARTIAL SEQUENCE, AND CHARACTERIZATION.
RX MEDLINE=96351891; PubMed=8728715;
RA Davis E.M., Tsuji J., Davis G.D., Pierce M.L., Essenberg M.;
RT "Purification of (+)-delta-cadinene synthase, a sesquiterpene cyclase
RT from bacteria-inoculated cotton foliar tissue.";
RL Phytochemistry 41:1047-1055(1996).
CC -1- FUNCTION: Responsible for the cyclization of trans,trans-farnesyl
CC diphosphate (FPP) to (+)-delta cadinene.
CC -1- CATALYTIC ACTIVITY: 2-trans,6-trans-farnesyl diphosphate = (+)-
CC delta-cadinene + diphosphate.
CC -1- PATHWAY: Phytoalexins gossypol and lacinilene C biosynthesis;
CC first (committed) step.
CC -1- INDUCTION: By bacterial infection.
CC -1- SIMILARITY: Belongs to the terpene synthase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U88318; AAC12784.1; -.
DR HSSP; Q40577; SEAU.
DR InterPro; IPR008930; Terp_cyc_toroid.
DR InterPro; IPR001906; Terp_synth-like.
DR InterPro; IPR005630; Terpene synth_C.
DR InterPro; IPR008949; Terpenoid_synth.
DR Pfam; PF01397; Terpene_synth; 1.
DR Pfam; PF03936; Terpene_synth_C; 1.
KW Lyase.
FT ACT_SITE 451 451 BY SIMILARITY.
FT ACT_SITE 527 527 BY SIMILARITY.
FT ACT_SITE 531 531 BY SIMILARITY.
SQ SEQUENCE 554 AA; 64019 MW; 8BCC78AD8CA5B816 CRC64;

Query Match 21.3%; Score 692.5; DB 1; Length 554;
Best Local Similarity 31.1%; Pred. No. 2.3e-39;
Matches 179; Conservative 113; Mismatches 241; Indels 43; Gaps 15;

QY 51 VASTDSVQRRVGNVYNSNLWDDDFIQSLISTPYGAPD-----YRERADRLIGEVDIMFN 104
DB 14 LSSNKDEMPPKADFQPSIWGDFPL-----NCPDKNIDAEFTQKRHQQLKEEVRKMI-- 63

QY 105 FKSLEDGNDLLQRLLLVDVERLGIDRHFKKEIKTALDYVNSYWNKEIGCGRESVVTDL 164
DB 64 ---VAPMANSTL-KLAFIDSVQGLGVSYHFTKEIJELE--NIYHN-----NND AEND 110

QY 165 INSTALGLRTLRLHGTVSSDVLNVFKDKNGQFSSTANIQIEGIRGVNLFRASLVAFP 224
```

111 LYTTSLRFRLLREHGFHVSCDVFNKFEQGNFKSS---VTSVFRGLLELYQASYLRVH 166
225 GEKWDDEAETSTKYLRALQKIPASSILSLRDLVLEYGWHITNLPRLRNMYDVFQGH 284
167 GEDILDEAISFTSNHLSLAVASL--DHPLESEVSHALKQISRRGLPRVEARHYSVY-QD 223
285 TKNKNAAEKLELAKLEFNIHFSLQERELKHVSRWMD-SGSPMTFCRHRHVEYYALAS 343
224 IESHN--KVLLEFAKIDFNWQVLHRLKELSEISRWWKDLDFQRKLPYARDRVVEGYFWS 281
344 CIAFEPQHSFRLGFTKMSHLITVLDWYDVEGTVDELELFTATIKRWDPSAMECLPEYM 403
282 GYTFEPQYSLGRKMLTKVIAMASIVDDTYDSYATYELIPYTNAIERWDIKCIDELPEYM 341
404 KGYVMVYHTVNMARVAEKAQCRDITLNYARQAWBACFDSYMQEAKIATGYLPTFEYVL 463
342 KPSYKALLDVEEEMEQLVAEHGRQYVEYAKNAMIRLAQSYLVEARWTLQNYKPSFEFVK 401
464 ENGKVSASHPALQIPILTL-DIPFPDHLKEVDFPSKLNLDLICIILRLRGDTRCYKADR 522
402 ANALEPCGYAMLAITSFVGMGDIPTBEPFKWAANDP-KIIQASTIICRFMDVTEHKFKH 460
523 ARGEASSISCYMKDNPGLTEEDALNHNFMIRDAIRELNWELLKPDNSVPTSKHAFD 582
461 RREDDOAIECYMEBY-GVTAQEAIVYFNKGVESAMKDVNQGFLKP-TEMPTEVLNRSLN 518
583 ISRVMHGGRYRDGYSFANVETKSLVMRTVIEPVL 618
519 LARVMDVLYREGDGYTVGKAKGITSLLIEPIAL 554

RESULT 12
CASS_RICCO STANDARD; PRT; 601 AA.

AC P59287;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Casbene synthase, chloroplast precursor (EC 4.2.3.8).
OS Ricinus communis (Castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Malpighiales; Euphorbiaceae; Acalyphoideae; Acalyphaceae;
OC Ricinus.
OX NCBI_TaxID=3988;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94359958; PubMed=8078910;
RA Mau C.J., West C.A.;
RT "Cloning of casbene synthase cDNA: evidence for conserved structural
RT features among terpenoid cyclases in plants.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:8497-8501(1994).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=97115639; PubMed=8954576;
RA Hill A.M., Cane D.E., Mau C.J., West C.A.;
RT "High level expression of Ricinus communis casbene synthase in
RT Escherichia coli and characterization of the recombinant enzyme.";
RL Arch. Biochem. Biophys. 336:283-289(1996).
CC -1- FUNCTION: Catalyzes the cyclization of geranylgeranyl diphosphate
CC to casbene, a diterpene phytoalexin with antibacterial and
CC antifungal activity.
CC -1- CATALYTIC ACTIVITY: Geranylgeranyl diphosphate = casbene +
CC diphosphate.
CC -1- SUBCELLULAR LOCATION: Chloroplast.
CC -1- INDUCTION: By oligosaccharonide fragments released by fungal
CC infection. Detected after 5 h of incubation with the pectic
CC fragments and reaches a maximum after 10-12 h.
CC -1- MISCELLANEOUS: The Km of this enzyme is 1.9 micromol.
CC -1- SIMILARITY: Belongs to the terpene synthase family.
CC -1- CAUTION: It is uncertain whether Met-1 or Met-8 is the initiator.
CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL; L32134; -, NOT_ANNOTATED_CDS.
DR InterPro; IPR008930; Terp_cyc_toroid.
DR InterPro; IPR001906; Terp_synth-like.
DR InterPro; IPR005630; Terpene_synth_C.
DR InterPro; IPR008949; Terpenoid_synth.
DR Pfam; PF01397; Terpene_synth_1.
DR Pfam; PF03936; Terpene_synth_C; 1.
KW plant defense; lyase; chloroplast; transit peptide.
FT TRANSIT 1 56 CHLOROPLAST (POTENTIAL).
FT CHAIN 57 601 CASBENE SYNTHASE.
FT ACT_SITE 500 500 BY SIMILARITY.
FT ACT_SITE 575 575 BY SIMILARITY.
FT ACT_SITE 579 579 BY SIMILARITY.
SQ SEQUENCE 601 AA; 68965 MW; F7B362D286747957 CRC64;

Query Match 20.5%; Score 667; DB 1; Length 601;
Best Local Similarity 29.8%; Pred. No. 1.3e-37;
Matches 174; Conservative 132; Mismatches 230; Indels 48; Gaps 19;

47 CLTSVASTDSVQRVGNVHNSLWDDDFIQSLISTPYGAPDYRRADRLIGEVKDIMFNFK 106
54 CLASS--TTHQEVRLAYFPPTWGNRF-ASLTNPSEFESYDERIVLKKVKDILISST 110
107 SLEDGNDLLQRLLLVDVERLGIDRHFKKEIKTALDYV-NS--YWNKEGIGGRESVV 162
111 S-----DSVETVILIDLCLRGVSHFENDIEBLLSKIFNSQDPLVDEK-----E 155
163 TDLNSTALGLRTLRLHGYTVSSDVLVNFKDNQGFSSSTANIQTGEIRGVNLFRASLVA 222
156 CDLYTAIVFRVFRQHGFKMSSDVFSKFKDSGKFES---LRGDAKGMLSLFEASHLS 211
223 FPGKWDDEAETSTKYLR-EALQKIPASSILSLRDLVLEYGWHITNLPRLRNMYDVF 281
212 VHGEDILBEAFAFTKDYLQSSAVELEPN--LKRHITNALBQPHSGVPRLEARKFIDLY 268
282 GQHTKNNAAEKLELAKLEFNIHFSLQERELKHVSRWMDSG-SPEMTFCRHRHVEYYA 340
269 EADIECRN--ETLLEFAKLDVNRVQLHQELCQFSKWKMDLNLASDIPYARDMAEIFF 326
341 LASCIAFEPQHSFRLGFTKMSHLITVLDWYDVEGTVDELELFTATIKRWDPSAMECLP 400
327 WAVAMYFEPDYAHTRMIIAKVLLISLDDTIDAYATMEETHILAEAVARWMSCLEKLP 386
401 EYMKGYVMVYHTVNMARVAEKAQCRD-TLNYARQAWBACFDSYMQEAKIATGYLPTF 459
387 DYMKVITYKLLNTFSEFEKEL-TAEKSYSVKYGREAFQELVGRGYLLEAVWRDEGKIPSF 445
460 EBYLENGKVSASHPALQIPILTLDIPPDHI--LKE--VDFPSKLNLDLICIILRLRGD 514
446 DDYLYNGSMTT---GLPLVSTASFWGVQETGLNEFQWLETPKLSYASGAFIRLVND 500
515 TRCYKADRARGEWASSISCYMKDNPGLTEEDALNHNFMIRDAIRELNWELLKPDNSVPI 574
501 LTSHTVEQQRGHVASCIDCYMNGH-GVSKDEAVKILQKMATQWKEINEECMR-QSQVSV 558
575 TSKKHAFDISRVMHGGRYRDGYSFANVETKSLVMRTVIEPVL 618
559 GHLMRIYVLARLVDSYKYGDGYTDSQ-QLKQFVKGLFVDPISL 601

RESULT 13
SEAS_TOBAC STANDARD; PRT; 548 AA.
ID SEAS_TOBAC
AC Q40577;
DT 15-JUL-1998 (Rel. 36, Created)

```

DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Aristolochene synthase (EC 4.2.3.9) (5-epi-aristolochene synthase)
DS (EAS).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 56-73.
RP STRAIN=cv. NK326;
RX MEDLINE=93066390; PubMed=1438319;
RA Faccini P.J., Chappell J.
RT "Gene family for an elicitor-induced sesquiterpene cyclase in
RT tobacco.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:11088-11092(1992).
RN [2]
RN X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS), AND REVISIONS.
RX MEDLINE=97442533; PubMed=9295271;
RA Starks C.M., Back K., Chappell J., Noel J.P.
RT "Structural basis for cyclic terpene biosynthesis by tobacco 5-epi-
RT aristolochene synthase."
RL Science 277:1815-1820(1997).
CC -1- FUNCTION: Catalyzes the cyclization of trans,trans-farnesyl
CC diphosphate (FPP) to the bicyclic intermediate 5-epi-
CC aristolochene, initial step in the conversion of FPP to the
CC sesquiterpenoid antifungal phytoalexin capsidiol.
CC -1- CATALYTIC ACTIVITY: Trans,trans-farnesyl diphosphate =
CC aristolochene + diphosphate.
CC -1- COFACTOR: Binds 3 magnesium ions per subunit.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- INDUCTION: By fungal elicitor.
CC -1- SIMILARITY: Belongs to the terpene synthase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L04680; AAA19216.1; -.
DR PIR: T03714; T03714.
DR PDB; SEAS; 15-OCT-97.
DR PDB; SEAT; 12-NOV-97.
DR PDB; SEAU; 08-APR-98.
DR InterPro; IPR008930; Terp_cyc_toroid.
DR InterPro; IPR001906; Terp_synth-like.
DR InterPro; IPR005630; Terpene_synth_C.
DR InterPro; IPR008949; Terpenoid_synth.
DR Pfam; PF01397; Terpene_synth; 1.
DR Pfam; PF03936; Terpene_synth_C; 1.
DR Lyase; Magnesium; 3D-structure.
KM ACT_SITE 273 273 PROTON ACCEPTOR.
FT ACT_SITE 444 444
FT ACT_SITE 520 520
FT ACT_SITE 525 525
FT CONFLICT 42 42 Y -> YTY (IN REF. 1).
FT CONFLICT 44 44 K -> Q (IN REF. 1).
FT CONFLICT 55 55 N -> S (IN REF. 1).
FT CONFLICT 62 62 M -> R (IN REF. 1).
FT CONFLICT 73 73 T -> I (IN REF. 1).
FT CONFLICT 89 89 D -> E (IN REF. 1).
FT CONFLICT 388 388 T -> M (IN REF. 1).
FT HELIX 26 29
FT HELIX 36 57
FT TURN 58 58
FT TURN 60 61
FT HELIX 64 76
FT TURN 77 78

```

[illegible]


```

OY 165 LNSTALGLRTLRLHGTVSSDVIANVFKDNQGFSSSTANIQIEGEIRGVNLNFRASLVAFP 224
    |::|||::|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 104 LCTSLAQFRLRLRQHGFINISPEIFSKQDENGKFKES---LASDVLGLINLYEASHVRTH 159

OY 225 GEKVMDAETFSTKYLREALOKIPASSILSLEIRDVLEYGWHITNLPRLRNMYMDVFGOH 284
    ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 160 ADDILEDALAFSTIHLESAPHU--KSPLRQVTHALEQCLHKGVPRVETRFPISSIIDK 217

OY 285 TKNKNAEKLLELAKLEFNIFHSQERELKHVSRWKCD-SGSPEMTEGRHRHVEYYALAS 343
    ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 218 EQSKN--NVLRFKALDENLQMLHKQELAQVSRWKKDLDFVTTLPYARDRVECYFWAL 275

OY 344 CIAFEPQHSGRIGFTKMSHLITVLDMYDVEGTVDLELFTATIKRWDPSAMECLPEYM 403
    :|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 276 GVFEPQYSQARVMLVKTISWISLVDTFDAYGTVKELAYTDAIQRDINEIDRLPDYM 335

OY 404 KGVYMMVYHTVNEMARVAEKAQGRDTLNYARQAMEACFDSYMQEAKVIATGYLLPTFEBYL 463
    |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 336 KISYKAILDLYKDYEKELSSAGRSHIVCHAIERMKEVVRNRYNVSESTWFTIEGYTPPVSEYL 395

OY 464 ENGVSSAHRPCALQPILTLDIPFPDHILKEVDFP----SKLNDLICILRLRGDTRCY 518
    |:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 396 SNALATTTYLLATTSYLCM-----KSATEQDFEWLSPKPILEASVITICRVIDDTATY 449

OY 519 KADRARGEASSISCYMKDNPGLTEDALNHINFMIRDAIRELNWELLKPDNSVPITSK- 577
    ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 450 EVEKSRGOIATGIECCMRDY-GISTKEAMAKFQNMMAETAMKDINEGLLRP--TPVSTEF 505

OY 578 -KHAFDIRVWMHGYR-R-DGYSFANVETKSLVMRTVIEPVPL 618
    ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 506 LTPILNLARIVEVTYIHNLDGYTHPEKVLKPHIINLVDISIKI 548

```

```

RESULT 14
UBR1_KLULA
ID _UBR1_KLULA          STANDARD;          PRT; 1941 AA.
AC O60014;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE N-end-recognizing protein (Ubiquitin-protein ligase E3 component) (N-
DE recognin).
GN UBR1.
OS Kluyveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28985;
RN [1]
RP SEQUENCE FROM N.A.
RA Waller P.R.H., Varshavsky A.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Recognition component of the N-end rule pathway. Binds
CC to proteins bearing amino-terminal residues that are destabilizing
CC according to the N-end rule, but does not bind to otherwise
CC identical proteins bearing stabilizing amino-terminal residues.
CC -1- SIMILARITY: Contains 1 UBR1-type zinc finger.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF061554; AAC15841.1; -.
DR PIR; T30554; T30554.
DR InterPro; IPR003126; Znf_Nrecognin.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF02207; zf-UBR1; I.
DR SMART; SM00184; RING; 1.
DR SMART; SM00396; Znf UBR1; 1.

```

| | |
|----------------------------|--|
| KW | Ligase; Ubl conjugation pathway. |
| SEQ | SEQUENCE 1941 AA; 223682 MW; 37C2E1BCA0803268 CRC64; |
| Query Match | 4.1%; Score 133; DB 1; Length 1941; |
| Best Local Similarity | 29.3%; Pred. No. 0.81; |
| Matches; 141; Conservative | 85; Mismatches 244; Indels 226; Gaps 34; |

| | | | |
|----|-----|--|-----|
| QY | 104 | NFKSLEDGG-----NDLLORLL--LVD---DVERLGID-----R | 132 |
| Db | 176 | NCKGAEDNGRLIEDHFDHDGKISKMLSVLIELFDHFIDVFENQNIETTTIQKPLIAKL R | 235 |
| QY | 133 | HFKKE-----IKTALDVNSYWNEKGIGCGRESVWTDLNSTALGURTL---RLHG Y | 180 |
| Db | 236 | YFNPEREIEQADMLRLRAYRNQYMDEESSNKRHLTSLDPLSTLKDYAILVYYDEFHN Y | 295 |
| QY | 181 | TWSSDVLVNFKDQIGQFS-STANIQIEGEIRGVNLFRASLVAFPG----- | 225 |
| Db | 296 | SQASAARIQGPDNKHIDLITAKIDSEG--RSLIRC-SADIASLMGRIFSVQSNGLSCTI | 352 |
| QY | 226 | ----EKVMDEAETESTKYLRALQIKIPASSILSL-----EI | 257 |
| Db | 353 | TOMYEYLHQEACKYSIMMINDCL-NIPNSTFQSFLRNAIGKVLCSKYPEFYOSIDMTSV V | 411 |
| QY | 258 | RDLVEYGWHTNLPRLBARNYMDVFGOHTKNKAAEKLE-----LAKLEFNIFHS | 307 |
| Db | 412 | RDYFSDSYLSDDPYLYADH--SVLGEGVKPIPLGRHKSLDPGDISAISPILNKVIAEDHE | 469 |
| QY | 308 | LQERELKHV---SRWKD-----SGS-- | 325 |
| Db | 470 | YTNSRLQYVLFLENRYMKUKRIQVDLIPTLASSAVQKPMFTDQLVEIPPHMTRSGTFM | 529 |
| QY | 326 | ---PENTFCRHHRHVEYYVALASCIAFEPOHSGFRLGFTKMSHLITVLDMYDVFGTVDEL E | 382 |
| Db | 530 | DREPQTLSTRSVQLFTCP-TAYSIFHSG-----HENYLIWSVIDVFVDFSTMDEGT | 582 |
| QY | 383 | LFTATIKRWDP-----AMECL-----PEYM--KGVYMWVY---HTVNEMAR | 419 |
| Db | 583 | LVMQRVQRSNPSPSKSYSISFKOGLAIVETLTSKITDPNLLKPGEFIMIVTLCLEFNCAWK | 642 |
| QY | 420 | VAEKAQGRDT-----LNTARQAW-EACFDSYMOEAK-----WIATGYLPTPEBY | 462 |
| Db | 643 | IKKKREGEHVLRDQHFIPLYEYTTVSYSIIQTFDKVLQOSKDHIDQRLIGA INLDSF | 702 |
| QY | 463 | LENGKVS-----SAHRPCALOPILTLDIPFPDHIKEVDER--SKLNDLIC | 506 |
| Db | 703 | LGHRLNLSYKLYCDFEIIKFQISKEQVSMFNPVHTLFCFLVQHVPLOVSIQVLSQSKDYLV | 762 |
| QY | 507 | II-LRLRGDTRCYKADRA-----RGEAASSISCYMKDNPG L--TEEDALNHINEMI--RD | 556 |
| Db | 763 | ISDFALRSVVLCSQIDIGFWVRNGMSVLHQSAYYYKNNPEMSSYSRDIQLNQLAFLIEKND | 822 |
| QY | 557 | AIREL-----NMWLK-PDNSVPITSKGAHAFDISRV | 586 |
| Db | 823 | FQRVITYNMLDRWILLDWFDGSVPESTETVYDKISSI | 858 |

| RESULT 15 | | | |
|------------|---|--|---------------|
| BXA2_CLOBO | | | |
| ID | BXA2_CLOBO | STANDARD; | PRT; 1295 AA. |
| AC | Q45894; P77780; | | |
| DT | 28-FEB-2003 (Rel. 41, | Created) | |
| DT | 28-FEB-2003 (Rel. 41, | last sequence update) | |
| DT | 28-FEB-2003 (Rel. 41, | last annotation update) | |
| DE | Botulinum neurotoxin type A precursor (EC 3.4.24.69) (BoNT/A) | | |
| DE | (Bontoxilysin A) (BoTX) [Contains: Botulinum neurotoxin A, light-chain; Botulinum neurotoxin A, heavy-chain]. | | |
| GN | BoTA OR BNA OR ATX. | | |
| OS | Clostridium botulinum. | | |
| OC | Bacteria; Firmicutes; | Clostridia; Clostridiales; Clostridiaceae; | |
| OC | Clostridium. | | |
| OX | NCBI_TaxID=1491; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |

RC STRAIN=Kyoto-F;
RX MEDLINE=94143603; PubMed=8310180;
RA Willems A., East A.K., Lawson P.A., Collins M.D.;
RT "Sequence of the gene coding for the neurotoxin of Clostridium
RT botulinum type A associated with infant botulism: comparison with
RT other clostridial neurotoxins.";
RL Res. Microbiol. 144:547-556(1993).
[2]
RN SEQUENCE OF 1-65 FROM N.A.
RP STRAIN=Kyoto-F;
RC MEDLINE=97016817; PubMed=8863443;
RX East A.K., Bhandari M., Stacey J.M., Campbell K.D., Collins M.D.;
RA "Organization and phylogenetic interrelationships of genes encoding
RT components of the botulinum toxin complex in proteolytic Clostridium
RT botulinum types A, B, and F: evidence of chimeric sequences in the
RT gene encoding the nontoxic nonhemagglutinin component.";
RL Int. J. Syst. Bacteriol. 46:1105-1112(1996).
CC -I- FUNCTION: Inhibits acetylcholine release. The botulinum toxin
CC binds with high affinity to peripheral neuronal presynaptic
CC membrane, is then internalized by receptor-mediated endocytosis.
CC The C-terminus of the heavy chain (H) is responsible for the
CC adherence of the toxin to the cell surface while the N-terminus
CC mediates transport of the light chain from the endocytic vesicle
CC to the cytosol. After translocation, the light chain (L)
CC hydrolyzes the 197-Gln-|-Arg-198 bond in SNAP-25, thereby blocking
CC neurotransmitter release. Inhibition of acetylcholine release
CC results in flaccid paralysis, with frequent heart or respiratory
CC failure (By similarity).
CC -I- CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the
CC neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No
CC detected action on small molecule substrates.
CC -I- SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a
CC heavy chain (H) (By similarity).
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- MISCELLANEOUS: There are seven antigenically distinct forms of
CC botulinum neurotoxin: Types A, B, C1, D, E, F, and G.
CC -I- SIMILARITY: Belongs to peptidase family M27.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC
DR EMBL; X73423; CAAS1824.1; -;
DR EMBL; X87974; CAA61234.1; -;
DR PIR; I40645; I40645.
DR HSSP; P10845; 3BTA.
DR MEROPS; M27.002; -;
DR InterPro; IPR008985; ConA_like_1ec_g1.
DR InterPro; IPR002160; Kunitz_legume.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR000395; Peptidase_M27.
DR Pfam; PF01742; Peptidase_M27; 1.
DR PRINTS; PR00760; BONTOXILYSIN.
DR ProDom; PD001963; Bontoxilysin; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; FALSE NEG.
KW Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; zinc.
FT INIT MET 0
FT CHAIN 1 447
FT CHAIN 448 1295 BOTULINUM NEUROTOXIN A, LIGHT-CHAIN.
FT METAL 222 222 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT SITE 223 223 BY SIMILARITY.
FT METAL 226 226 ZINC (CATALYTIC) (BY SIMILARITY).
FT DISULFID 429 453 INTERCHAIN (BY SIMILARITY).
FT DISULFID 1234 1279 BY SIMILARITY.
FT TRANSMEM 626 646 POTENTIAL.
FT TRANSMEM 655 675 POTENTIAL.
SQ SEQUENCE 1295 AA; 149279 MW; SDA04A13D98D6372 CRC64;

Query Match 3.8%; Score 125; DB 1; Length 1295;

Best Local Similarity 19.0%; Pred. No. 1.6;
Matches 138; Conservative 102; Mismatches 247; Indels 238; Gaps 32;
QY 3 LLSITP---LVSRSCLASSSHEIKALRR-----TIPTIGI 33
DB 150 LVIGPSADIIQFECKSFQHDVNLTRNGYSTQYIRFSPDFTGFEBESLEVDTNPLGA 209
QY 34 CR----PGKSAHSINMCLTSVASTDSVQRVGNHSLM-----D 70
DB 210 GKFAIDPAVTLAHELHAHEHLVGAIAINPNRVFKVNTNAVYEMSGLEVSFEELRTFGHD 269
QY 71 DDFIQSLISTPYGAPDYRERAD--RLIGEVDIMFNFKSLDEGNDLLQRLLVDD---- 124
DB 270 AKFIDSLQENEFRLYYNKFQDVASTLNKAKSIIQTASLQYMKVFKEXYLLSEDTSGK 329
QY 125 --VERLGIDRHFK--KEIKTALDVN-----SYWN-EKGIGGRESVTDLNSTALG 171
DB 330 FSVDKLKFDKLYKMLTEIYTEEDNFVNFVKVNRKTYLNFDAV--FRINIVDENYTIKD 387
QY 172 LRTFLRHGYTVSSDVLNVFKDKNGQFSSTANIQIEGEIRGVNLFRASLV--AFPGKVM 229
DB 388 --GKNLKGANLSTN---FNGQTEINSRNFTRLK-NFTGLFEFFYKLLCVRGIIP----- 435
QY 230 DEAFNESTKYLREALQKI-----PASSISLEIRDVLEYGWHNTLPLRE 273
DB 436 -----FKTKSLDEGYNKALNDLCIKVNNWDLFFSPSEDNFTNDLKVEITADTNIKAE 490
QY 274 ARNTMDVFGQH-----TKXNAAEKLE--LAKLE-----FNIF 305
DB 491 ENISLDLIQYYLTFDFDNEPENISIENTSSDIIGQLEPMNIERFPNGKVELDKYTMF 550
QY 306 HSLQREELKH-VSRWVKDSGSE-----MTFCRHRYVEYYALA-SCIAFEPQHSGR 355
DB 551 HYLRAQEFEGHDSRIILTNSAEALLPNAVYTFSSKYKINKAVEAFMLNWAEBELV 610
QY 356 LGFTKMSHLITVLDDMYDVF-----GTVDELELFTATIKRWDPSSAME 397
DB 611 YDFDETNEVTMDKIADITIIIVYIGPALNIGNMLSKGEVEAIIFTGVV----AMLE 665
QY 398 CLPEYMKGVYMMVYHTVNEMARVAEKAQGRDTLNYA---RQAWACFDSYMQEAKWIAT 453
DB 666 FIFEYA---LPVFGTFAIVSYLANKVLLTVQTINNALSKEKWEDEVY-----KYTVT 714
QY 454 GYLPTFEYLENGKVVSAHRPCALQPIITLDIPPDHILKEVDPPSKLNDLCIILRLRG 513
DB 715 NWL-----AKVNTQIDLIRES--- 729
QY 514 DTRCYKADRARGEASSISCYMKDNPGLTTEEDALNHINFMIRDAIRELNWELKPDNSVP 573
DB 730 --KMKKALENOAEATKAIINYQYNQ--YTEEEK-NNINFNIDDLSSKLNESI---NSAM 780
QY 574 ITSCK 578
DB 781 ININK 785

Search completed: July 23, 2004, 09:02:52
Job time : 16 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 23, 2004, 08:59:52 ; Search time 42 Seconds

(without alignments)
4642.625 Million cell updates/sec

Title: US-10-025-145A-65

Perfect score: 3251

Sequence: 1 MALSLITPLVSRSLSSSHE.....FANVETKSLVMTVIEPVPL 618

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-----------|--------------------|
| 1 | 3251 | 100.0 | 618 | 10 Q948Z0 | Q948Z0 abies grand |
| 2 | 2416 | 74.3 | 623 | 10 Q94FW0 | Q94FW0 abies grand |
| 3 | 2328.5 | 71.6 | 629 | 10 Q84KL6 | Q84KL6 pinus taeda |
| 4 | 2266.5 | 69.7 | 627 | 10 Q84KL4 | Q84KL4 pinus taeda |
| 5 | 2264 | 69.6 | 630 | 10 Q9M7D1 | Q9M7D1 abies grand |
| 6 | 2237 | 68.8 | 633 | 10 Q94KA5 | Q94KA5 picea abies |
| 7 | 2205.5 | 67.8 | 633 | 10 Q94KA4 | Q94KA4 picea abies |
| 8 | 2163.5 | 66.5 | 627 | 10 Q84SM8 | Q84SM8 picea abies |
| 9 | 2151 | 66.2 | 628 | 10 Q84KL3 | Q84KL3 pinus taeda |
| 10 | 2137 | 65.7 | 630 | 10 Q9M7D0 | Q9M7D0 abies grand |
| 11 | 2084.5 | 64.1 | 637 | 10 Q9M7C9 | Q9M7C9 abies grand |
| 12 | 2041.5 | 62.8 | 637 | 10 Q94FV9 | Q94FV9 abies grand |
| 13 | 1985.5 | 61.1 | 615 | 10 Q84KL2 | Q84KL2 pinus taeda |
| 14 | 1909 | 58.7 | 574 | 10 Q84KL5 | Q84KL5 pinus taeda |
| 15 | 1295.5 | 39.8 | 581 | 10 Q64A04 | Q64A04 abies grand |
| 16 | 1242.5 | 38.2 | 579 | 10 Q94FW3 | Q94FW3 abies grand |

| | | | | | |
|----|--------|------|-----|-----------|---------------------|
| 17 | 1240 | 38.1 | 577 | 10 Q94KA3 | Q94KA3 picea abies |
| 18 | 1231 | 37.9 | 593 | 10 Q64A05 | Q64A05 abies grand |
| 19 | 1187 | 36.5 | 783 | 10 Q9SAU6 | Q9SAU6 abies grand |
| 20 | 1187 | 36.5 | 817 | 10 Q81086 | Q81086 abies grand |
| 21 | 1178.5 | 36.3 | 816 | 10 Q94FW2 | Q94FW2 abies grand |
| 22 | 1131 | 34.8 | 873 | 10 Q947C4 | Q947C4 ginkgo bilbo |
| 23 | 1055.5 | 32.5 | 853 | 10 Q94FW1 | Q94FW1 abies grand |
| 24 | 1052.5 | 32.4 | 868 | 10 Q38710 | Q38710 abies grand |
| 25 | 836 | 25.7 | 603 | 10 Q8GUE4 | Q8GUE4 cinnamomum |
| 26 | 824 | 25.3 | 606 | 10 Q8L5K1 | Q8L5K1 citrus limo |
| 27 | 821 | 25.3 | 606 | 10 Q8L5K1 | Q8L5K1 citrus limo |
| 28 | 812 | 25.0 | 597 | 10 Q93X23 | Q93X23 quercus ile |
| 29 | 796.5 | 24.5 | 595 | 10 Q9AR86 | Q9AR86 populus x c |
| 30 | 794.5 | 24.4 | 595 | 10 Q7XAS7 | Q7XAS7 populus tre |
| 31 | 765.5 | 23.5 | 606 | 10 Q8H2B4 | Q8H2B4 mentha aqua |
| 32 | 757 | 23.3 | 576 | 10 Q84LB2 | Q84LB2 malus domes |
| 33 | 749.5 | 23.1 | 582 | 10 Q94G53 | Q94G53 artemisia a |
| 34 | 747.5 | 23.0 | 607 | 10 Q8M1J9 | Q8M1J9 perilla fru |
| 35 | 744 | 22.9 | 613 | 10 Q94OE7 | Q94OE7 agastache r |
| 36 | 742 | 22.8 | 583 | 10 Q7Y1V1 | Q7Y1V1 melaleuca a |
| 37 | 736.5 | 22.7 | 598 | 10 Q81192 | Q81192 salvia offi |
| 38 | 732 | 22.5 | 583 | 10 Q9SPN1 | Q9SPN1 artemisia a |
| 39 | 728.5 | 22.4 | 567 | 10 Q9SPN0 | Q9SPN0 artemisia a |
| 40 | 727 | 22.4 | 620 | 10 Q9FWU5 | Q9FWU5 schizonepet |
| 41 | 724.5 | 22.3 | 599 | 10 Q40322 | Q40322 mentha spic |
| 42 | 721 | 22.2 | 597 | 10 Q815J7 | Q815J7 salvia sten |
| 43 | 717.5 | 22.1 | 599 | 10 Q9SW76 | Q9SW76 mentha long |
| 44 | 710.5 | 21.9 | 551 | 10 Q91KN1 | Q91KN1 gossypium h |
| 45 | 710.5 | 21.9 | 603 | 10 Q04806 | Q04806 perilla fru |

ALIGNMENTS

RESULT 1
Q948Z0 ID Q948Z0 PRELIMINARY; PRT; 618 AA.
AC Q948Z0; MEDLINE=97413772; PubMed=9268308;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE (-)-camphene synthase;
GN AG6.5.
OS Abies grandis (Grand fir).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferales; Pinaceae; Abies.
OX NCBI_TaxID=46611;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97413772; PubMed=9268308;
RA Bohlmann J., Steele C.L., Croteau R.;
RT "Monoterpene synthases from grand fir (Abies grandis). cDNA isolation,
RT characterization, and functional expression of myrcene synthase, (-)-
RT (4S)-limonene synthase, and (-)-(1S,5S)-pinene synthase.";
RL J. Biol. Chem. 272:21784-21792(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99373092; PubMed=10441373;
RA Bohlmann J., Phillips M., Ramachandiran V., Katoh S., Croteau R.;
RT "cDNA cloning, characterization, and functional expression of four new
RT monoterpene synthase members of the Tpsd gene family from grand fir.
RT (Abies grandis).";
RL Arch. Biochem. Biophys. 368:232-243(1999).
DR EMBL; U87910; AAB70707.1; .
DR GO; GO:0016829; F-lyase activity; IEA.
DR GO; GO:0008152; P-metabolism; IEA.
DR InterPro; IPR005630; Terpene_synth_C.
DR InterPro; IPR008949; Terpeneoid_synth_C.
DR InterPro; IPR008930; Terp_cyc_fooid.
DR InterPro; IPR001906; Terp_synth-like.
DR Pfam; PF01397; Terpene_synth; 1.
DR Pfam; PF03936; Terpene_synth_C; 1.
SQ SEQUENCE 618 AA; 70749 MW; B07B5185CE5C4CE1 CRC64;

Query Match 100.0%; Score 3251; DB 10; Length 618;
Best Local Similarity 100.0%; Pred. No. 9e-232;
Matches 618; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALISITPLVSRSCSSSHEIKALRRTIPTLGICRPGKSVASHINMCLTSVASTDSVQR 60
Db 1 MALISITPLVSRSCSSSHEIKALRRTIPTLGICRPGKSVASHINMCLTSVASTDSVQR 60
QY 61 VGNVHSNLMWDDFIQSLISTPYGAPDYRERADRLIGEVDIMFNFKSLLEDGNDLQRL 120
Db 61 VGNVHSNLMWDDFIQSLISTPYGAPDYRERADRLIGEVDIMFNFKSLLEDGNDLQRL 120
QY 121 LVDDVERLGIDRHFKKEIKTALDVNSYWNKEGICGRESVVTDLNSTALGLRTLRLHG 180
Db 121 LVDDVERLGIDRHFKKEIKTALDVNSYWNKEGICGRESVVTDLNSTALGLRTLRLHG 180
QY 181 TVSSDVLNVFKDNGQFSSSTANIQIEGIRGVNLFRASLVAFPEKVMDEAETFTSKYL 240
Db 181 TVSSDVLNVFKDNGQFSSSTANIQIEGIRGVNLFRASLVAFPEKVMDEAETFTSKYL 240
QY 241 REALOKIPASSILSLRIRDVLEYGHTNLPRLRARNYMDVFGQHTKNKNAEKLLEAKL 300
Db 241 REALOKIPASSILSLRIRDVLEYGHTNLPRLRARNYMDVFGQHTKNKNAEKLLEAKL 300
QY 301 EFNIFHSLQERELKHVSRRWKDSSGSPMTFCRHRHVEYYALASCIAPFPQHSGFRLGFTK 360
Db 301 EFNIFHSLQERELKHVSRRWKDSSGSPMTFCRHRHVEYYALASCIAPFPQHSGFRLGFTK 360
QY 361 MSHLITVLDDMYDVFGTVDELELFTATIKRWDPSAMECLPEYMKGVYMMVYHTVNEMAR 420
Db 361 MSHLITVLDDMYDVFGTVDELELFTATIKRWDPSAMECLPEYMKGVYMMVYHTVNEMAR 420
QY 421 AEKAGRDTLNYARQAEACFDSYMOEAKMIATGYLPTPEEYLENGKVSSAHRPCALQPI 480
Db 421 AEKAGRDTLNYARQAEACFDSYMOEAKMIATGYLPTPEEYLENGKVSSAHRPCALQPI 480
QY 481 LTLDIPEPDHILKEVDFPSKLNLCIILRLRGDTRCYKADRARGEAASSISCYMKDNP 540
Db 481 LTLDIPEPDHILKEVDFPSKLNLCIILRLRGDTRCYKADRARGEAASSISCYMKDNP 540
QY 541 LTEDALNHINFMIRDAIRELNMWELKPDNSVPITSSKGAFPDISRVWHGGRYRDGYSPA 600
Db 541 LTEDALNHINFMIRDAIRELNMWELKPDNSVPITSSKGAFPDISRVWHGGRYRDGYSPA 600
QY 601 NVETKSLVMRTVIEPVPL 618
Db 601 NVETKSLVMRTVIEPVPL 618

RESULT 2

Q94FW0 PRELIMINARY; PRT; 623 AA.
ID Q94FW0; O94FW0;
AC Q94FW0;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Pinene synthase (Fragment).
OS Abies grandis (Grand fir).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.
OX NCBI_TaxID=46611;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21297238; PubMed=11404343;
RA Trapp S.C., Croteau R.B.;
RT "Genomic organization of plant terpene synthases and molecular
evolutionary implications.";
RL Genetics 158:811-832(2001).
DR EMBL; AF326517; AAK83564.1; -;
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005630; Terpene_synth_C.

DR InterPro; IPR008949; Terpenoid_synth.
DR InterPro; IPR008930; Terp_cyc_loroid.
DR InterPro; IPR001906; Terp_synth-like.
DR Pfam; PF01397; Terpene_synth; 1.
DR Pfam; PF03936; Terpene_synth_C; 1.
FT NON TER
SQ SEQUENCE 623 AA; 70948 MW; 823B82B38113467B CRC64;

Query Match 74.3%; Score 2416; DB 10; Length 623;
Best Local Similarity 74.8%; Pred. No. 5.2e-170;
Matches 467; Conservative 59; Mismatches 82; Indels 16; Gaps 6;

QY 8 PLVSRSCl-----SSSHEIKALRRTIPTLGICRPGKSVASHINMCLTSVASTDSVQRV 62
Db 3 PLASKSCLHKSLSISTHELKALSRITPALGMSRSGKSTPSISMSSTVTTDDGVRRMG 62
QY 63 NYHSNLMWDDFIQSLISTPYGAPDYRERADRLIGEVDIMFNFKSLLEDG-----NDLQ 117
Db 63 DFNHNLWDDDVITQSL-PTAYEEKSYLERAEKLIGEVEN-MFNMSMLEDELMSPINDLIQ 120
QY 118 RLILVDDVERLGIDRHFKKEIKTALDVNSYWNKEGICGRESVVTDLNSTALGLRTLRL 177
Db 121 RLWIVDSLGRLGIDRHFKKEIKSALDVYSYWGENGICGRESAVTDLNSTALGLRTLRL 180
QY 178 HGTVSSDVLNVFKDNGQFSSSTANIQIEGIRGVNLFRASLVAFPEKVMDEAETFTST 237
Db 181 HGYPVSSDVFKAFKQNGQSCSENIQTDEIRGVNLFRASLVAFPEKIMDEAETFTST 240
QY 238 KYLREALOKIPASSILSLRIRDVLEYGHTNLPRLRARNYMDVFGQHTKNKNA---AEKL 294
Db 241 KYLKEALOKIPVSS-LSREIGDVLEYGHTYLPRLRARNYIHVFGQDTEHTKSYVSKKL 299
QY 295 LELAKLEFNIFHSLQERELKHVSRRWKDSSGSPMTFCRHRHVEYYALASCIAPFPQHSGF 354
Db 300 LELAKLEFNIFQSLQRELESVRWKESGFPMTFCRHRHVEYYTLASCIAPFPQHSGF 359
QY 355 RLGFTHSHLITVLDDMYDVFGTVDELELFTATIKRWDPSAMECLPEYMKGVYMMVYHTV 414
Db 360 RLGFTHLITVLDDMYDTFGTVDELELFTATIMKRPDSSIDCLPEYMKGVYIAVYDITV 419
QY 415 NEMARVAEKAQGRDTLNYARQAEACFDSYMOEAKMIATGYLPTPEEYLENGKVSSAHRP 474
Db 420 NEMARAEAEQAQGRDTLTYARBAWEAYIDSYMOEARMIATGYLPSFDEYENGKVSCGHR 479
QY 475 CALQPIITLIDIPPDHILKEVDFPSKLNLCIILRLRGDTRCYKADRARGEAASSISCY 534
Db 480 SALQPIITMDIPPDHILKEVDFPSKLNLCALILRLRGDTRCYKADRARGEAASSISCY 539
QY 535 MKDNPGLTEDALNHINFMIRDAIRELNMWELKPDNSVPITSSKGAFPDISRVWHGGRYR 594
Db 540 MKDNPGVSEEDALDHINAMISDVYKGLNMWELKPDINVPISAKGAFPDIARAFHYGYKR 599
QY 595 DGYSFANVETKSLVMRTVIEPVPL 618
Db 600 DGYSVANVETKSLVTRITLESVPL 623

RESULT 3

Q84KL6 PRELIMINARY; PRT; 629 AA.
ID Q84KL6; Q84KL6;
AC Q84KL6;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE (-)-alpha-pinene synthase.
OS Pinus taeda (loblolly pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=3352;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22510022; PubMed=12623076;
RA Phillips M.A., Wildung M.R., Williams D.C., Hyatt D.C., Croteau R.;

RT "cDNA isolation, functional expression, and characterization of (+)-
RT alpha-pinene synthase and (-)-alpha-pinene synthase from loblolly pine
RT (Pinus taeda): Stereoccontrol in pinene biosynthesis.";
RL Arch. Biochem. Biophys. 411:267-276(2003).
DR EMBL; AF543527; AA061225.1; -
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005630; Terpene synth C.
DR InterPro; IPR008949; Terpenoid synth.
DR InterPro; IPR008930; Terp_cyc toroid.
DR InterPro; IPR001906; Terp_synth-like.
DR Pfam; PF01397; Terpene synth; 1.
DR Pfam; PF03936; Terpene synth C; 1.
SQ SEQUENCE 629 AA; 71807 MW; 39DDCD936BCB1791 CRC64;

Query Match 71.6%; Score 2328.5; DB 10; Length 629;
Best Local Similarity 72.0%; Pred. No. 1.6e-163;
Matches 456; Conservative 67; Mismatches 91; Indels 19; Gaps 8;

QY 1 MALISITPLVSRSCSS-----HEIKALRTIPTLGICRPGKSAH-SINMCLTSVAS 53
Db 1 MSPVSVISLPSDLCPLPTSFIDRSGRELIPLHITIPNVAMRQGLMTRASMSMLRTAVS 60
QY 54 TDSVQRRVGNVNSLWDDDFIQSLISTPYGAPDYRERADRLIGEVDIMFNKSLDGG- 112
Db 61 DDAVIRRRGDFHNSLMDDDLQSL-SSPYGEPYSRERAERLIGEYKN-SFNSMSNEDGES 118
QY 113 ----NDLLQRLLLVDDVERLGIDRHFKKEIKTALDVNSYWNKEGICGRESVTDLNST 168
Db 119 ITPLDLLIQLRMVDSVERLGIDRHFKKEIKSALDHVRYWSEKIGCGRESVTDLNST 178
QY 169 ALGLRTLRLHGYTVSSDVLVNFKDKNGQFSSTANIQIEGEIRGVNLPRASLVAFPEKV 228
Db 179 ALGLRTLRLHGYTVSSDVLVNFKDKNGQFSSTANIQIEGEIRGVNLPRASLVAFPEKV 237
QY 229 MDEAETSTKYLRALQKIPASSISLSLEIRDVLEYGWHNTLPRLEARNYMDVFGQHTKN 288
Db 238 MDEAESFSAKYLKEALQKIPASSISLSLEIRDVLEYGWHNTLPRLEARNYMDVFGQHTKN 296
QY 289 NA---AEKLELAKLEFNIHFSLOERELKHVSRWMDSGSPMTFCRHRHVEYYALASCI 345
Db 297 KSYMTEKLELAKLEFNIHFSLOERELKHVSRWMDSGSPMTFCRHRHVEYYALASCI 356
QY 346 AFEPOHSGFRLGFTKMSHLITVLDWYDVGTVDELFTATIKRWDPSAMECLPEYMKG 405
Db 357 AFEPOHSGFRLGFAKACHITVLDWYDVGTVDELFTATIKRWDPSATECLPEYMKG 416
QY 406 VYMWVYHTVNMARVAEKAQGRDTINYARQAWACFDSYMOEAKWIATGYLPTFEELYEN 465
Db 417 VYMWVYHTVNMESQEAADKAQGRDTINYCRQAWEEYIDAYMOEAKWIASGEVPTFEELYEN 476
QY 466 GKSSAHRPCALQPIITLDIPFPDHILKEVDFPSKLANDLICITILRLRGDTRCYKADRARG 525
Db 477 GKSSGHRVSALQPIITLDIPFPDHILKEVDIPSLNDLASAILRLRGDTRCYQADRARG 536
QY 526 EEASSISCYMKDNPGLTEEDALNHINFMIRDAIRELNMWELKPDNSVPITSKHAFDISR 585
Db 537 EEASSISCYMKDNPGLTEEDALNHINAMISDVIKGLNMWELKPDNSVPISAKHAFDISR 596
QY 586 VWHGYRYRDGYSFANVETKSLVMRTVIEPVPL 618
Db 597 AFHGYKYRDGYSVANIEETKSLVKRTVIDPVTL 629

RESULT 4
Q84KL4
ID Q84KL4 PRELIMINARY; PRT; 627 AA.
AC Q84KL4;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DB Alpha-terpineol synthase.
OS Pinus taeda (loblolly pine).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Conifercopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=3352;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22510022; PubMed=12623076;
RA Phillips M.A., Wildung M.R., Williams D.C., Hyatt D.C., Croteau R.;
RT "cDNA isolation, functional expression, and characterization of (+)-
RT alpha-pinene synthase and (-)-alpha-pinene synthase from loblolly pine
RT (Pinus taeda): Stereoccontrol in pinene biosynthesis.";
RL Arch. Biochem. Biophys. 411:267-276(2003).
DR EMBL; AF543529; AA061227.1; -
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005630; Terpene synth C.
DR InterPro; IPR008949; Terpenoid synth.
DR InterPro; IPR008930; Terp_cyc toroid.
DR InterPro; IPR001906; Terp_synth-like.
DR Pfam; PF01397; Terpene synth; 1.
DR Pfam; PF03936; Terpene synth C; 1.
SQ SEQUENCE 627 AA; 71883 MW; FACAA215FA7739B63 CRC64;

Query Match 69.7%; Score 2266.5; DB 10; Length 627;
Best Local Similarity 70.0%; Pred. No. 6e-159;
Matches 443; Conservative 78; Mismatches 91; Indels 21; Gaps 9;

QY 1 MALISITPLVSRSCS-----SSSHEIKALRTIPTLGICRPGKSAH-SINMCLTSVAS 53
Db 1 MDLISVLPASAKSCVCLHKLPLSSSTHKLKPFCKTIRILVMPRMEFARPS--MSLSTVAS 58
QY 54 TDSVQRRVGNVNSLWDDDFIQSLISTPYGAPDYRERADRLIGEVDIMFNKSLDGG- 112
Db 59 EDDIQRRGTGYLSNLWDDVIO-FLSTPYGELAYRERAERLIDEVRDI-FSSMSLEDGEF 116
QY 113 NDLLQRLLLVDDVERLGIDRHFKKEIKTALDVNSYWNKEGICGRESVTDLNSTALGL 172
Db 117 SDLIQRLMWVDMVERLGIDRHFKKEIKSALDVVSYWSEKIGCGTKSIITNLNSTALGF 176
QY 173 RTLRLHGYTVSSDVLVNFKDKNGQFSSTANIQIEGEIRGVNLPRASLVAFPEKV 228
Db 177 RTLRLHGYTVSSDVLVNFKDKNGQFSSTANIQIEGEIRGVNLPRASLVAFPEKV 235
QY 229 MDEAETSTKYLRALQKIPASSISLSLEIRDVLEYGWHNTLPRLEARNYMDVFGQHTKN- 287
Db 236 MDEAESSEKYLKETLQKIPDCS-LSREIGDVLEHGMHTNLPRLERARNYIDVFGQHTKN 294
QY 288 --KNAEKLLELAKLEFNIHFSLOERELKHVSRWMDSGSPMTFCRHRHVEYYALASCI 345
Db 295 EPNRTEKLELAKLEFNIHFSLOERELKHVSRWMDSGSPMTFCRHRHVEYYALASCI 354
QY 346 AFEPOHSGFRLGFTKMSHLITVLDWYDVGTVDELFTATIKRWDPSAMECLPEYMKG 405
Db 355 AFEPOHSGFRLGFAKACHITVLDWYDVGTVDELFTATIKRWDPSATDCLPQYMKG 414
QY 406 VYMWVYHTVNMARVAEKAQGRDTINYARQAWACFDSYMOEAKWIATGYLPTFEELYEN 465
Db 415 IYMWVYHTVNMESABEAQKQGRDTINYARQAWMEDCLDSHMOEAKWIATGFLPTFEELYEN 474
QY 466 GKSSAHRPCALQPIITLDIPFPDHILKEVDFPSKLANDLICITILRLRGDTRCYKADRARG 525
Db 475 GKSSAHRVSALQPMITMDIPFPDHILKEVDFPSNLNDLACAMLRRLRGDTRCYQADRARG 534
QY 526 EEASSISCYMKDNPGLTEEDALNHINFMIRDAIRELNMWELKPDNSVPITSKHAFDISR 585
Db 535 EETSCISCYMKDNPGLTEEDALNHINMISGVIKELNMWELKPDNSVPISSKINFIDTR 594
QY 586 VWHGYRYRDGYSFANVETKSLVMRTVIEPVPL 618
Db 595 AFHGYKYRDGYSVSVETKSLVMRTVIEPVPL 627

RESULT 5
Q9M7D1

ID Q9M7D1 PRELIMINARY; PRT; 630 AA.
AC Q9M7D1;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Beta-phellandrene synthase.
GN AGC8.
OS Abies grandis (Grand fir).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.
OX NCBI_TaxID=46611;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stem;
RX MEDLINE=99373092; PubMed=10441373;
RA Bohlmann J., Phillips M., Ramachandiran V., Katoh S., Croteau R.;
RT "cDNA cloning, characterization, and functional expression of four new
RT monoterpene synthase members of the Trsd gene family from grand fir
RT (Abies grandis).";
RL Arch. Biochem. Biophys. 368:232-243(1999).
DR EMBL; AF139205; AAF61453.1; -.
DR HSSP; Q40577; SEAU.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005630; Terpene synth_C.
DR InterPro; IPR008949; Terpenoid synth.
DR InterPro; IPR008930; Terp_cyc toroid.
DR InterPro; IPR001906; Terp_synth-like.
DR Pfam; PF01397; Terpene synth; 1.
DR Pfam; PF03936; Terpene synth_C; 1.
SQ SEQUENCE 630 AA; 72784 MW; B8E4374B262FF2D1 CRC64;

Query Match 69.6%; Score 2264; DB 10; Length 630;
Best Local Similarity 68.3%; Pred. No. 9.2e-159;
Matches 435; Conservative 78; Mismatches 98; Indels 26; Gaps 9;

QY 1 MALLSITPLVSRCL-----SSSHEIKALRRTIPTLGICRPGKSAHSIMCLTSVAST 54
DB 1 MALVSSAP--KSCLHKSLIRSTHBLKPLRRTIPTLGMCRCRGSFTPSVSMSTTAVSD 57
QY 55 DSVQRVRVGNYSNLWDDDFIQSLISTPYGAPDYRERADRLIGEVDIMENFKSLDEG-- 112
DB 58 DGLQRRIGDYHSNLWDDDFIQSL-STPYGEPsYRERAEKLIGVKE-MFNSMPSEDESM 115
QY 113 ---NDLLQRLLLVDVERLGIDRHFKKEIKTALDYVNSYWNKEGIGCGRESVVTDLNSTA 169
DB 116 SPLNDLIERLWMDVSVERLGIDRHFKKEIKSALDYVNSYWNKEGIGCGRDSVPDVNSTA 175
QY 170 LGLRTLRLHGYTVSSDVLNVFKDNGQFSSSTANIQIEGEIRGVNLFRASLVAFPGEKVM 229
DB 176 SGFRTRLRHGYSVSSSEVLKVFQDNGQFAFSPSTK-ERDIRTVNLVRSFIAFPGEKVM 234
QY 230 DEAEFTSTKYLRREALOKIPASSISLSLEIRDVLEYGWHNTNLRLEARNYMDVFGQHT---- 285
DB 235 EEAEIFFSSRYLKEAVOKIPVSS-LSQEI DYTLEYGWHNTNMPRLLETRNYLDVFGHTSPWL 293
QY 286 KKNKA----AEKLLELAKLEFNI FHSLOERELKHVSRWKDSGSPEMTFCRHRHVEYYAL 341
DB 294 KKKRQYLDSEKLELAKLEFNI FHSLOERELQYLSRWMIHSGLPBELTGRHRHVEYYTL 353
QY 342 ASCIAFEPQHSFRLGFTKMSHLITVLDMDYDVFGTVDELELFTATIKRWDPSAMECLPE 401
DB 354 SSCIATEPKHSAFRLGFAKTHLITVLDIDYDTFGTMEIELEFNEAVRRWNPSEKERLPE 413
QY 402 YMKGYMMVYHTVNEMARVAEKAQGRDTLNYARQAEACFDSYMQEAKWIATGYLPTFEE 461
DB 414 YMKETYMALYEALTDMAREAEKTOGRDTLNYARKAMEVYLDSTYQEAKWIASGYLPTFEE 473
QY 462 YLENGKVSAAHRPCALQPIITLDIPFPDHILKEVDFPSKLANDLICILRLRGDTRCYKAD 521
DB 474 YLENKAVSSGHRRAALTPLTLTDVPLPDDVYLGIDFSPSRFNDLASSFLRLRGDTRCYKAD 533
QY 522 RARGEASSISCYMKDNPGLTEEDALNHINFMIRDAIRELWELLKPDNSVPITSKHAF 581

DB 534 RARGEASSISCYMKDNPGLTEEDALNHINAMINDI IKELNWECLKPDNSNIPMTARGAY 593
QY 582 DISRWVHHGYRRDGYSPFANVETKSLVMRTVIEPVP 618
DB 594 EITRAFHLKYKRDGFSVATQETKSLVVRTVLEPVP 630

RESULT 6
Q94KA5 PRELIMINARY; PRT; 634 AA.
ID Q94KA5
AC Q94KA5;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Beta-phellandrene synthase-like protein.
OS Picea abies (Norway spruce) (Picea excelsa).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
OX NCBI_TaxID=3329;
RN [1]
RP SEQUENCE FROM N.A.
RA Morency M.J., Nicole M.C., Seguin A.;
RT "Terpene synthase from Norway spruce, cDNA isolation and
RT characterization of beta-phellandrene synthase-like gene.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF369918; AAK39127.2; -.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005630; Terpene synth_C.
DR InterPro; IPR008949; Terpenoid synth.
DR InterPro; IPR008930; Terp_cyc toroid.
DR InterPro; IPR001906; Terp_synth-like.
DR Pfam; PF01397; Terpene synth; 1.
DR Pfam; PF03936; Terpene synth_C; 1.
SQ SEQUENCE 634 AA; 72768 MW; EE140A49C46B4404 CRC64;

Query Match 68.8%; Score 2237; DB 10; Length 634;
Best Local Similarity 68.0%; Pred. No. 9.2e-157;
Matches 434; Conservative 75; Mismatches 105; Indels 24; Gaps 10;

QY 1 MALLSITPLVSRCL-----SSSHEIKALRRTIPTLGICRPGKSA-HSINMCLT-SVAS 53
DB 1 MSPSVIPLAYKLCPLRSLMSSREVKPLHITIPNLGMCRCRGSMAFSTSMILTAVSD 60
QY 54 TDSVQRVRVGNYSNLWDDDFIQSLISTPYGAPDYRERADRLIGEVDIMENFKSLDEG-- 112
DB 61 DDRVQRVRGNYSNLWDDDFIQSL-STPYGEPsYRERAEITLKEIKK-MFRSISKDDEL 118
QY 113 ---NDLLQRLLLVDVERLGIDRHFKKEIKTALDYVNSYWNKEGIGCGRESVVTDLNST 168
DB 119 ITPNLNDLIQRLWMDVSVERLGIDRHFKKEIKSALDYVNSYWNKEGIGCGRDSVVADLNST 178
QY 169 ALGRTLRLHGYTVSSDVLNVFKDNGQFSSSTANIQIEGEIRGVNLFRASLVAFPGEKV 228
DB 179 ALGFRTRLRLHGYTVSSSEVLKVFEDQNGQFACSPS-KTEGEIRSALNLVRSALIAFPGEKV 237
QY 229 MDEAFTSTKYLRREALOKIPASSISLSLEIRDVLEYGWHNTNLRLEARNYMDVFGQHT--- 285
DB 238 MDAEIFFSSRYLKEAVOKIPDCS-LSQEIAYAL EYGWHNTNMPRLLEARNYMDVFGHPSSPW 296
QY 286 --KKNKA----AEKLLELAKLEFNI FHSLOERELKHVSRWKDSGSPEMTFCRHRHVEYYA 340
DB 297 LKKNKTQYMDGEKLELAKLEFNI FHSLOERELQYISRWKDSGLPKLAFSRHRHVEYTT 356
QY 341 LASCIAFEPQHSFRLGFTKMSHLITVLDMDYDVFGTVDELELFTATIKRWDPSAMECLP 400
DB 357 LGSCTIATDPKHRAFRLGFAKTHLINTVLDIDYDTFGTMEIELEFTEAVRRWDPSETESLP 416
QY 401 EYMKGYMMVYHTVNEMARVAEKAQGRDTLNYARQAEACFDSYMQEAKWIATGYLPTFE 460
DB 417 DYMKGYYMVLYEALTMAQEAQKTQGRDTLNYARKAMEIYLDSTYQEAKWIAATGYLPTFQ 476

| | | |
|----|--|-----|
| Qy | 461 EYLENGKVSSAHRPCALQPILTLDIPEDHILKEVDFPSKNDLCIILRLRGDTRCYKA | 520 |
| Dd | 477 EYFENGKISSAYRAALTPILTLDVPEYLKGIDFPSRFNDLASSFLRLRGDTRCYKA | 536 |
| Qy | 521 DRARGEASSISCYMKONPGLTEEDALNHINFMIRDAIRELNWELLKPONSVPITSKGA | 580 |
| Dd | 537 DRARGEASASCICYMKONPGSTGEDALNHINSMINEIKELNWMELLRPSDNIEPWARKGA | 596 |
| Qy | 581 FDISRVWHHGYYRDRGYSFANVETKSLVMRTVIEPVPL | 618 |
| Dd | 597 FDITRALHLKYIRDGFVSATKETKSLVRMVLEPVPL | 634 |

RESULT 7

| ID | Q94KA4 | PRELIMINARY; | PRT; | 633 AA. |
|----|--|--------------|------|---------|
| AC | Q94KA4; | | | |
| DT | 01-DEC-2001 (TREMBLrel. 19, Created) | | | |
| DT | 01-OCT-2002 (TREMBLrel. 22, Last sequence update) | | | |
| DT | 01-OCT-2003 (TREMBLrel. 25, Last annotation update) | | | |
| DE | Myrcene synthase-like protein. | | | |
| OS | Picea abies (Norway spruce) (Picea excelsa). | | | |
| OC | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; | | | |
| OC | Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea. | | | |
| OX | NCBI_TaxID=33329; | | | |
| RN | (1) | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RA | Morency M.J., Nicole M.C., Seguin A.; | | | |
| RT | "Terpene synthase form Norway spruce, cDNA isolation and | | | |
| RT | characterization or myrcene synthase-like gene by 5'-and 3'-RACE | | | |
| RT | amplification."; | | | |
| RL | Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases. | | | |
| DR | EMBL; AF369919; AAK39128.2; - | | | |
| DR | GO; GO:0016829; F:lyase activity; IEA. | | | |
| DR | GO; GO:0008152; P:metabolism; IEA. | | | |
| DR | InterPro; IPR005630; Terpene_synth_C. | | | |
| DR | InterPro; IPR008949; Terpenoid_synth. | | | |
| DR | InterPro; IPR008930; Terp_cyc_Toroid. | | | |
| DR | InterPro; IPR001906; Terp_synth-like. | | | |
| DR | Pfam; PF01397; Terpene_synth_1. | | | |
| DR | Pfam; PF03936; Terpene_synth_C; 1. | | | |
| DR | SEQUENCE 633 AA; 72576 MW; B6C7C7CA895A7DB1 CRC64; | | | |

| | | | | |
|-----------------------|--------------|-------------------|-----------------|-------------|
| Query Match | 67.8%; | Score 2205.5; | DB 10; | Length 633; |
| Best Local Similarity | 67.7%; | Pred. No. 2e-154; | | |
| Matches 430; | Conservative | 79; | Mismatches 103; | Indels 23; |
| | | | | Gaps 9; |

```

0Y 1 MALLSITPLVSRSC-----SSSHEIKALRRTIPTLGICRPGKSAVHSINCLTSVAS-T 54
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 1 MSPSVSVPLACKLCLCRSMTSSTDELKPLPTTIPTRGMCGRRMSVTPSM$SLNTVVSDN 60

0Y 55 DSVQRRVGNVH$NLWDDDFIO$LISTPYGAPDYERADRLLIGEVDKIMFN$KSL$EDG-- 112
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 61 DAVQRRIGDYH$NLWDDDFIO$L-TTPYGAPSYIERADGLISEVKE-MFNRMCM$EDGELM 118

0Y 113 ---NDLLQRLLLVDVVERLGIDRH$FKEIKTALDYVNSYWN$KGIGCGRESVVTDLNSTA 169
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 119 SPLNDLIQRLMTVDSVERLGIDRH$FKEIKASLDYVSYWN$KGIGCGRTSVVTDLNSTA 178

0Y 170 LGLRTLRLHGYTVSSDVLN$FKDNGQFSS$TANIQIEGEIRGVNL$FRASLVA$PGEKVM 229
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 179 LGAXILRLHGYTVSSEVLKVFEEENQFAC$PS-QTEGEIRSFLNLYRASLIFA$PGEKVM 237

0Y 230 DEAEFT$TKYLREALOKIPASSIISLEIRDVLEYGWH$TNL$PRL$EARNYMDVEGQHTK--- 286
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 238 EEAQIFSSRYLKEAVQKIPVSS-LSREIGDVLEYGWH$TNL$P$RWEARNYMDVEGQD$TNTPF 296

0Y 287 NKNA-----AEKLL$ELAKLEFNI$FHSLOEREL$KHSVRMWKDSG$P$M$TFCRRHVEYAL 341
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 297 NKNM$QYMNTEKILQ$LAKLEFNI$FHSLOERELQCLLRMWKESGLPQ$LT$FARHRYVEFYTL 356

0Y 342 ASCIAFEPQHS$GFRLGFTKM$HLITVLD$MYDVFGTVDEL$ELFTATIKRWDSAMECL$PE 401
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

| | | | |
|----|-----|--|-----|
| Db | 357 | ASCIATEPKHSAFRLGFAKCHLVTVLDDVYDTFGKMDLELELFTAAYKXNDLSETERLPE | 416 |
| Qy | 402 | YMKGVYMMVYHTVNEMARVAEKAQGRDTLNYARQAMEACFDSYMOEAKWATGYLPTFEE | 461 |
| Db | 417 | YMKGLYVVLFEVTNELAQEAEKTOGRNTLNYVRKAMEAYFDSYMKAEWNTSTGYLPTFEE | 476 |
| Qy | 462 | YLENGKVSSAHRPCALOPIITLIDIPFPDHILKEVDFPSKLANDLICITLRLRGDTRCYKAD | 521 |
| Db | 477 | YXENGKVSSAYRVAALQPIITLIDVQLPDDILKGIDFPSPRFNDLASSFLRLRGDTRCYXAD | 536 |
| Qy | 522 | RARGEASSISCYMKDNPGLTEBDALNHINFMRDAIRELNWELLPDNSVPITSKGAF | 581 |
| Db | 537 | RARGEASCSICYMKDHPGSTBEDAVNHNINAMINDIRELNWELFKPDNSNIPMPARKHAF | 596 |
| Qy | 582 | DISRVMHGYYRDRDYSFANVETKSLVMRTVIEPV | 616 |
| Db | 597 | DITRALHLLYIYRDGFVSASKETKNLVEKALLEAV | 631 |

RESULT 8

| ID | Q84SM8 | PRELIMINARY; | PRT; | 627 AA. |
|----|------------------------|--------------|------|-------------------------|
| AC | Q84SM8; | | | |
| DT | 01-JUN-2003 | (TREMBLrel. | 24, | Created) |
| DT | 01-JUN-2003 | (TREMBLrel. | 24, | last sequence update) |
| DT | 01-OCT-2003 | (TREMBLrel. | 25, | last annotation update) |
| DE | (+)-3-carene synthase. | | | |

OS Picea abies (Norway spruce) (Picea excelsa) .
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
OX NCBI_TaxID=33329;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22490501; PubMed=12602896;
RA Faeldt J., Martin D., Miller B., Rawat S., Bohlmann J.;
RT "Traumatic resin defense in Norway spruce (Picea abies): methyl
RT jasmonate-induced terpene synthase gene expression, and cDNA cloning
RT and functional characterization of (+)-3-carene synthase.";
RL Plant Mol. Biol. 51:119-133(2003).
DR EMBL: AF461460; FAO73863.1; -.
DR GO; GO:0016829; P-lyase activity; IEA.
DR GO; GO:0008152; P-metabolism; IEA.
DR InterPro; IPR005630; Terpene synth. C.
DR InterPro; IPR008949; Terpenoid_synth.
DR InterPro; IPR008930; Terp_cyc toroid.
DR InterPro; IPR001906; Terp_synth-like.
DR Pfam; PF01397; Terpene_synth; 1.
DR Pfam; PF03936; Terpene_synth_C; 1.
SO SEQUENCE 627 AA; 71512 MW; B1B1AD15FC50F47 CRC64;

| | | | | |
|-----------------------|------------------|---------------------|------------|-------------|
| Query Match | 66.5%; | Score 2163.5; | DB 10; | Length 627; |
| Best Local Similarity | 66.4%; | Pred. No. 2.5e-151; | | |
| Matches 419; | Conservative 81; | Mismatches 114; | Indels 17; | Gaps 7; |

```

QY      1 MALLSTITPLVRSCT,-----SSSHEIKALRRTIPTLGICRPGKSAHNSIMCLTSTVASTD 55
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      1 MSVISITPLASKSCITYKSLMSTTHELKALCRPIATLGMCRGKGSVMASKSTSLTTAVSD 60
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      56 SVQRRVGNVYHNSLWEDDFIQSLISTPYGAPDYRERADRLIGEVDKIMFNFKSLBEGG--- 112
      ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      61 GVQRRIGDHSNLWEDDFIQSL-SSPYGASSYGERAERLIGEYKEI-FNSLSRTDGE LVS 118
      ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      113 --NDLLQRLLLVDVYERLIGIDRHFEKKEIKTALDYVNSYWNKEGIGCGRESVTDLNTAL 170
      :||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      119 HVDDLQHLMSWMDNVERLIGIDRHFIQTEIKVSLDYVSYWSEKIGISGRDIVCTDLNTAL 178
      :||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      171 GLRTRLRLHGTYVSSDLVNVFKDKNGQFSSTANIQIEGEIRGVNLFRASLVAFPGEKVM 230
      ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      179 GFRILRLHGTYVFPDVFHFHQDMGRICASDN-HTERQISSILNLFRAFLIAFPGEKVM 237
      ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      231 EAETESTKYLREALQKIPASSILSLERDVLLEYGMHTNLPRLEARNYMDVFGHTKNKNA 290
      ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

Db 238 EAEIFSATYLKEALQTIPIVSS-LSQEIQYVLQYRWHSNLPRLEARTYIDILQENTKQML 296
QY 291 ---AEKLELELAKLEFNIFHSIQERELKHVSRRWKDSCSPENTFCRHRHVEYYALASCTAF 347
Db 297 DVNTKKVLELAKLEFNIFHSIQONELSKVSRRWKESGFPDLNFIHRHVEFYTLVSGIDM 356
QY 348 EPOHSGFRLGFTKMSHLITVLDMYDVFGTVDELLEFTATIKRWDPDSAMECLPEYMKGV 407
Db 357 EPKHCFTFRLSFVKMCHLITVLDMYDTFGTIDELRLFTAIVKRWDPSTTECLPEYMKGV 416
QY 408 MMVYHTVNEMARVAEKAQGRDNLNYARQAMEACFDSYMOEAKWIATGYLPTFEEYLENGK 467
Db 417 TVLYETVNEMAOEAQKSGRDTLSYVRQALBAYIGAYHKEAEMISSGYLPTFDEYFENGK 476
QY 468 VSSAHRPCALQPIRLTDPFPDHILKEVDFPSKLANDLICILRLRGDTRCYQADRARGE 527
Db 477 VSSGHRITATLOPTFMDIPFPHVLOEIDFPSKFNDPACSLRLRGDTRCYQADRARGE 536
QY 528 ASSISCYMKDNPGLTEEDALNHINFMIRDAIRELNWELKPDNSVPITSKHAFDISRYW 587
Db 537 ASSISCYMKDNPGSTQEDALNHINMIEETIKLNLWELKPDNNVPISSKHAFDINRGL 596
QY 588 HHGYRRDGYSPANVETKSLVMRTVIEPVPL 618
Db 597 HHFYNYRDGYTVASNETKNLVKTVLEPVPM 627

RESULT 9

Q84KL3 PRELIMINARY; PRT; 628 AA.
ID Q84KL3
AC Q84KL3;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE (+)-alpha-pinene synthase.
OS Pinus taeda (loblolly pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxId=3352;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22510022; PubMed=12623076;
RA Phillips M.A., Wildung M.R., Williams D.C., Hyatt D.C., Croteau R.;
RT "cDNA isolation, functional expression, and characterization of (+)-
RT alpha-pinene synthase and (-)-alpha-pinene synthase from loblolly pine
RT (Pinus taeda): Stereocontrol in pinene biosynthesis.";
RL Arch. Biochem. Biophys. 411:267-276(2003).
DR EMBL; AF543530; AA061228.1; -.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005630; Terpene synth_C.
DR InterPro; IPR008949; Terpenoid synth.
DR InterPro; IPR008930; Terp_cyc_foroid.
DR InterPro; IPR001906; Terp_synth-like.
DR Pfam; PF01397; Terpene_synth; 1.
DR Pfam; PF03936; Terpene synth_C; 1.
SQ SEQUENCE 628 AA; 71495 MW; 4208222612256837 CRC64;

Query Match 66.2%; Score 2151; DB 10; Length 628;
Best Local Similarity 65.8%; Pred. No. 2.1e-150;
Matches 416; Conservative 92; Mismatches 106; Indels 18; Gaps 8;

QY 1 MALLSTPLVSRSCS-----SSHEIKALRRTIPTLGICRPGKSAHSINM-CLTSVAST 54
Db 1 MALVSAPVPLNSKLCRLRTLFGFSHELKAIHSTVPLNGMCRGKSIAPSMSSSTTSVSN 60
QY 55 DSVQRRVGNYSNLMWDDFIQSLSTPYGAPDYRERADRLIGEVKDIMENFKSLDGG-- 112
Db 61 DGVRRRIAGHSNLMWDDSIASL-STSYEARPSYKRADKLIGEVKNI-FDLMSVEDGVFT 118
QY 113 ---NDLLQRLLLVDDVERLGIDRHFKKEIKTALDYVNSYANEKIGCGRESVTDLNSTA 169
Db 119 SPLSDLHRLMWDSVERLGIDRHFKDEINSALDHVYSYWTKEGIGRGRESGVTDLNSTA 178

QY 170 LGLRTLRLHGTVSSDVNLNVFKDKNGQFSSTANIOIEGIRGVNLFRASLVAFPGKYM 229
Db 179 LGLRTLRLHGTVSSSHVDHFKNEKGQFTCSA-IQTEGEIRDVLNLFASLIAFPGEXIM 237
QY 230 DEAEFTSTKYLRREALQKIPASSILSLERDVLLEYGMHTNULPRLEARNYMDVFGQFTKXN 289
Db 238 EAEIFSTMYLKDALQKIPRSG-LSQEIYLLFEGWHTNULPRMETRMVIDVFGEDTTEET 296
QY 290 ---AEKLELELAKLEFNIFHSIQERELKHVSRRWKDSCSPENTFCRHRHVEYYALASCTA 346
Db 297 PYLIREKLELELAKLEFNIFHSILVKRELQSLSRWKDYGFPEITFSRHRHVEYYTLACTA 356
QY 347 FEPQHSGFRLGFTKMSHLITVLDMYDVFGTVDELLEFTATIKRWDPDSAMECLPEYMKGV 406
Db 357 NDKHSAFRLGFGKISHMITLDDIYDTFGTMEELKLTAAFKRWDPSSIECLPDYMKGV 416
QY 407 YMMVYHTVNEMARVAEKAQGRDNLNYARQAMEACFDSYMOEAKWIATGYLPTFEEYLENG 466
Db 417 YMAVYDNINEMAREAQKIQGWDTVSARKSWEAFIGAYIQEAKWISSGYLPTFDEYLENG 476
QY 467 KVSASHRPCALQPIRLTDPFPDHILKEVDFPSKLANDLICILRLRGDTRCYQADRARGE 526
Db 477 KVSFGSRITTLPEMLTLGFPLPRILQEIDFPSKFNDLICAILRLKGDTCYKADRARGE 536
QY 527 EASSISCYMKDNPGLTEEDALNHINFMIRDAIRELNWELKPDNSVPITSKHAFDISRY 586
Db 537 EASAVSCYMKDHPGITEEDAVNQVAMVDNLTKELNLWELLRPDSGVPISYKKVAFDICRY 596
QY 587 HHGYRRDGYSPANVETKSLVMRTVIEPVPL 618
Db 597 HHGYRRDGYSPASIEIKNLVTRTVETVPL 628

RESULT 10

Q9M7D0 PRELIMINARY; PRT; 630 AA.
ID Q9M7D0
AC Q9M7D0;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Terpinolene synthase.
GN AGC9.
OS Abies grandis (Grand fir).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.
OX NCBI_TaxId=46611;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stem;
RX MEDLINE=99373092; PubMed=10441373;
RA Bohlmann J., Phillips M., Ramachandiran V., Katoh S., Croteau R.;
RT "cDNA cloning, characterization, and functional expression of four new
RT monoterpen synthase members of the Tpsd gene family from grand fir
RT (Abies grandis).";
RL Arch. Biochem. Biophys. 368:232-243(1999).
DR EMBL; AF139206; AAF61454.1; -.
DR HSSP; Q40577; SEAU.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005630; Terpene synth_C.
DR InterPro; IPR008949; Terpenoid synth.
DR InterPro; IPR008930; Terp_cyc_foroid.
DR InterPro; IPR001906; Terp_synth-like.
DR Pfam; PF01397; Terpene_synth; 1.
DR Pfam; PF03936; Terpene synth_C; 1.
SQ SEQUENCE 630 AA; 72508 MW; 452437B87F203DBA CRC64;

Query Match 65.7%; Score 2137; DB 10; Length 630;
Best Local Similarity 67.4%; Pred. No. 2.3e-149;
Matches 427; Conservative 73; Mismatches 114; Indels 20; Gaps 9;

QY 1 MALLSTPLVSRSCS-----SSHEIKALRRTIPTLGICRPGKSAHSINMCLTSVASTD 55

Db 1 MALVSLIPLSKSVLHAKSWIVSTYEHKAISRTIPNLGLRGKGYTHSLRMSLSTAVSD 60
QY 56 -SVGRVGNVHNSLWDDDFIQSLISTPYGAPDYRERADRLIGEVKDIMENFKSLEDG-- 112
Db 61 HGVORRIVEFHSNLWDDDFIQSL-STPYGAPSYRERADRLIVEVKG-FTSISAEDGELI 118
QY 113 ---NDLLQRLLLVDDVERLGIDRHFKKEIKTALDYVNSYWNKEGICGREGSVTDLNSTA 169
Db 119 TPLNDLIQRLMVDNVERLGIDRHFKKEIKTALDYVNSYWNKEGICGREGSVTDLNSTA 178
QY 170 LGRLTLRLHGYTVSSDVLNVFKD--KNGQFSSTANIQIEGEIRGVNLFRASLVAFPGEK 227
Db 179 LGFRILRLHGYSSVDVLEHFKKEKEGQFVCSA-IQTEBEIKSVNLFRASLVAFPGEK 237
QY 228 VMDEAETSTKYLRALQKIPASSILSLRDLVLEYGHTNLPRLRANVMDVFGQHTKN 287
Db 238 VMEAEIFSKYILKEALQNIAVSS-ISREIEVLEDGMQTMPRLETRNYIDVLGENDRD 296
QY 288 KNA---AEKLELAKLEFNIHSLQERELKHSRWKDSGSPMTFCRHRHVEYALASC 344
Db 297 ETLVNMMEKLEIAKLEFNIFHSLQRELKDLSRWKDSGFSHLTFPSRHRHVEYALASC 356
QY 345 IAFEPQHSGRFGFTKMSHLITVLDNMYDVFQTVDELELFTATIKRWDPSAMECLPEYMK 404
Db 357 IETDRKHSGRFGFTKMSHLITVLDNMYDVFQTVDELELFTAFKRWDPASATDLPPEYMK 416
QY 405 GYVMVYHTVNMARVAEKAQGRDTLNYARQAWACFDSYMOEAKWIATGYLPTFEBYLE 464
Db 417 GLVYVYETVNEIAREADKSQGRETLNDARAWAYLDSYMEKEWISSGYLPTFEYME 476
QY 465 NGKYSSAHRPCALQPIITLDIPPDHILKEVDFPSKNDLICIILRLRGDTRCYKADRAR 524
Db 477 TSKVSYFGYRIFALQPIITLDVPLTHILQEIIDFPLRFNDLICSILRLKNDTRCYKADRAR 536
QY 525 GEEASSISCYMKDNPGLTEEDALNHINFMIRDAIRELNMELKPDNSVPTSKEAFDIS 584
Db 537 GEEASSISCYMKENPGSTEEDALNHINAMVNNLIKEVNMELLRODGTAHIAKKAHFDIL 596
QY 585 RVMHGGRYRDGYSFANVETKSLVMRTVIEPVPL 618
Db 597 KGSLLHGYKYRDGFSVANKEVKWVRTVLESVPL 630

RESULT 11
Q9M7C9 PRELIMINARY; PRT; 637 AA.
AC Q9M7C9; 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE (-)-limonene/(-)-alpha-pinene synthase.
GN AGC11.
OS Abies grandis (Grand fir).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.
OX NCBI_TaxID=46611;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stem;
RX MEDLINE=99373092; PubMed=10441373;
RA Bohlmann J., Phillips M., Ramachandiran V., Katoh S., Croteau R.;
RT "cDNA cloning, characterization, and functional expression of four new
monoterpene synthase members of the Tpsd gene family from grand fir
(Abies grandis).";
RT Arch. Biochem. Biophys. 368:232-243 (1999).
RL EMBL; AF139207; AAF61455.1; -.
DR HSSP; Q40577; SEAS.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005630; Terpene synth C.
DR InterPro; IPR008949; Terpenoid_synth.
DR InterPro; IPR008930; Terp_cyc_toroid.

DR InterPro; IPR001906; Terp_synth-like.
DR Pfam; PF01397; Terpene_synth; 1.
DR Pfam; PF03936; Terpene synth C; 1.
SQ SEQUENCE 637 AA; 73273 MW; B3574986FEC96CFB CRC64;
Query Match 64.1%; Score 2084.5; DB 10; Length 637;
Best Local Similarity 64.9%; Pred. No. 1.8e-145;
Matches 417; Conservative 80; Mismatches 115; Indels 31; Gaps 13;
QY 1 MALSTPBL-VSRSC-----LSSSHEIKAL--RRTIPTLGICRPGKSAHSINMCLTSVA 52
Db 1 MALSTIVLQVPKSCGLKSLISSNVQKALCISTAVPTLRMRROKALV--INMKLTIVS 58
QY 53 STDS-----VQRRVGNVHNSLWDDDFIQSLISTPYGAPDYRERADRLIGEVKDIMENF-- 105
Db 59 HRDDNGGGVLQRRADHHPNLMEDDFIQSL-SSPYGSSYSERAVTVVEEVEKE-MFNSIP 116
QY 106 --KSLEDGNDLQRLLLVDDVERLGIDRHFKKEIKTALDYVNSYWNKE-GICGREGSV 162
Db 117 NNRELFGSONDLLTRLMMVDSIERLGIDRHFOEIRVALDYVSYWKEKEGICGRDSTF 176
QY 163 TDLNSTALGLRTLRLHGYTVSSDVLNVFKDKNGQFSSTANIQIEGEI-RGVNLFRASLV 221
Db 177 PDLNSTALALRTLRLHGYTVSSDVLVEYFKDQKGHFACPA-ILTEGQITRSVLNLYRASLV 235
QY 222 AFPGEKVMDEAETSTKYLRALQKIPASSILSLRDLVLEYGHTNLPRLRANVMDVF 281
Db 236 AFPGEKVMDEAEIFSASYLKEVLOKIPVSS-FSREIEVLEYGHTNLPRLRANVMDVF 294
QY 282 GQHTKNKN-----AAEKLELAKLEFNIHSLQERELKHSRWKDSGSPMTFCRHRH 335
Db 295 GQDSYESSNEMPYVNTQKLKALALEFNIHSLQOKELQYISRWKDSGSSHLTFTRRHRH 354
QY 336 VEYVALASCIAPFEPQHSGRFGFTKMSHLITVLDNMYDVFQTVDELELFTATIKRWDPSA 395
Db 355 VEYITMASCISMEPKHSAFRLGFKTCHLLITVLDNMYDFTGTLDELQFTTAFKRWDLSE 414
QY 396 MECLPEYMKGVYVMVYHTVNMARVAEKAQGRDTLNYARQAWACFDSYMOEAKWIATGY 455
Db 415 TKCLPEYMAVYMDLYQCLNELAQEAKTQGRDTLNYIRNAYESHFDSFMHEAKWISSGY 474
QY 456 LPTFEELYENGKVSARPCALQPIITLDIPPDHILKEVDFPSKNDLICIILRLRGDT 515
Db 475 LPTFEELYKNGKVSSSGSRATATLQPIITLDVPLPNYILQEIIDYPSRFNDLASSLRLRGDT 534
QY 516 RCYKADBARGEASSISCYMKDNPGLTEEDALNHINFMIRDAIRELNMELKPDNSVPT 575
Db 535 RCYKADBARGEASASISCYMKDHPGSTEEDALNHINMISDAIRELNMELLRPDSKSPIS 594
QY 576 SKGAHFDISRVMHGRYRDGYSFANVETKSLVMRTVIEPVPL 618
Db 595 SKGAHFDITRAFHLHYKYRDGYTVASSETKNLVMTKTVLEPVPL 637

RESULT 12
Q94FV9 PRELIMINARY; PRT; 637 AA.
AC Q94FV9; 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE (-)-4S-limonene synthase.
OS Abies grandis (Grand fir).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.
OX NCBI_TaxID=46611;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21297238; PubMed=11404343;
RA Trapp S.C., Croteau R.B.;
RT "Genomic organization of plant terpene synthases and molecular
evolutionary implications";
RT Genetics 158:811-832 (2001).

DR EMBL; AF326518; AAK83565.1; -
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005630; Terpene synth C.
DR InterPro; IPR008949; Terpenoid synth.
DR InterPro; IPR008930; Terp_cyc toroid.
DR InterPro; IPR001906; Terp_synth-like.
DR Pfam; PF01397; Terpene_synth; 1.
DR Pfam; PF03936; Terpene_synth C; 1.
SQ SEQUENCE 637 AA; 73535 MW; 2D86B2E14866F378 CRC64;

Query Match 62.8%; Score 2041.5; DB 10; Length 637;
Best Local Similarity 63.8%; Pred. No. 2.7e-142;
Matches 410; Conservative 84; Mismatches 118; Indels 31; Gaps 14;

QY 1 MALISTPL-VSRSC-----LSSHEIKAL--RRTIPTLGICRPGKSAHSINMCLTSTA 52
1 MALISTVSLQVPKSCGQKSLISSNVQKALCISTAVPTLRMRROKALV--INMCLTSTA 58
Db 53 STDS-----VQRRVGNHNSLWDDDFIQSLISTPYGAPDYRERADRLIGEVDIMNF-- 105
59 HRDNDGCVLQRIADHHPNLWEDDFIQSL-SSPYGSSYSERAETLVEBKE-MFNSIP 116
QY 106 --KSLEDGNDLLQRLLVVDVERLGIDRHFKKEIKTALDYVNSYWNK-GIGCGRESV 162
117 NNRELFGSQNDLITRLMMVDSIERLGIDRHQNEIRVALDYVSYWKEKEGIGCGRSTF 176
QY 163 TDINSTALGLRTLRLHGVTSSDVLVNFKDKNGQFSSSTANIQIEGEI-RGVNLFASLV 221
177 PDINSTALALRTLRLHGYNSSDVLEYFKDQKHAFACPA-ILTEGQITRSVLNLYRASLV 235
QY 222 APFGKVMDEAETSTKYLRALQKIPASSILSLEIRDVLEYGWHNTNLPRLAARNYMDVF 281
Db 236 APFGKVMEEAEIFSAASYLKEVLOKIPVSN-LSGEIEYVLEYGWHNTNLPRLAARNYIEVY 294
QY 282 ---GQHTKNKNA--AEKLELALAEFNIHFSLOERELKHVSRWVKDSSPEMTFCRHRH 335
295 EQSGYESLINEMPYNNMKLLQALKLEFNIHFSLORELQISRWKESGSSQLTFRHRH 354
QY 336 VEYVALASCIAPFQHSFRLGFTKMSHLITVLDMDYDVFQTVDELELFTATIKRWDPSA 395
Db 355 VEYTMASCISEMPKHSAFRMEFVYCHLVTVLDDIYDTFGTMMELQLFTDAIKRWDLST 414
QY 396 MECLPEYMKGVMMVYHTVNEMARVAEKAQGRDTLNYARQWEACFDSYMOEAKWIATGY 455
Db 415 TRMLPEYMKGVYMDLYQCINEMVEEAQKTQGRDMLNYIQNGWEALFDTFIOEAKWISSSY 474
QY 456 LPTFEYLVNGKVSSAHRPCALQPLITLDIPPDHILKEVDFPSKLANDLICITLRIGDT 515
Db 475 LPTFEYLVKNAKVSSGSRATLQPLITLDVPLPDYILQEIIDYPSRFNELASSILRLRGDT 534
QY 516 RCYKADRARGEASISCYMKDNPGLTEEDALNHINFMIRDAIRELNWELLKPDNSVPIT 575
Db 535 RCYKADRARGEASAISCYMKDHGSTEDALNHINAMISDAIRELNWELLRPPDSKSPIS 594
QY 576 SKGAFDISRVMHGYRYRDGYSPANVETKSLVMRTVIEPVPL 618
Db 595 SKGAFDITRAFHHVYKYRDGYTVSNNETKNLVMTVLEPLAL 637

RESULT 13

Q84KL2 PRELIMINARY; PRT; 615 AA.
ID Q84KL2;
AC Q84KL2;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Monoterpene synthase-like protein.
OS Pinus taeda (loblolly pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_Taxid=3352;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=22510022; PubMed=12623076;
RA Phillips M.A., Wildung M.R., Williams D.C., Hyatt D.C., Croteau R.;
RT "cDNA isolation, functional expression, and characterization of (+)-
RT alpha-pinene synthase and (-)-alpha-pinene synthase from loblolly pine
RT (Pinus taeda): Stereocontrol in pinene biosynthesis.";
RL Arch. Biochem. Biophys. 411:267-276(2003).
DR EMBL; AF543531; AA061229.1; -
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005630; Terpene synth C.
DR InterPro; IPR008949; Terpenoid synth.
DR InterPro; IPR008930; Terp_cyc toroid.
DR InterPro; IPR001906; Terp_synth-like.
DR Pfam; PF01397; Terpene_synth; 1.
DR Pfam; PF03936; Terpene_synth C; 1.
SQ SEQUENCE 615 AA; 70574 MW; B6F5F453A052AEC6 CRC64;

Query Match 61.1%; Score 1985.5; DB 10; Length 615;
Best Local Similarity 63.1%; Pred. No. 3.5e-138;
Matches 397; Conservative 82; Mismatches 123; Indels 27; Gaps 10;

QY 1 MALISTPLVS--RSCLSHHEIKALRRTIPTLGICRPGKSAHSINMCLT-SVASTDSV 57
3 LALVSAVLVSMRSLFSSPYELKSIDKTIPLNLMCKRMSGRPSIRVSTASVSNDDGV 62
QY 58 QRRVGNHNSLWDDDFIQSLISTPYGAPDYRERADRLIGEVDIMNFKSLDEG----- 112
63 RRRVGDYRYNMWDEDLIDSL-ATSYEAPSYLKRADTLVEATKD-RFNSMGVDDGQRMSP 120
QY 113 NDILQRLLVDDVERLGIDRHFKKEIKTALDYVNSYWNKIGCGRESVTDINSTALGL 172
Db 121 TDLYQRLMMVDSVERLGIDRHQNEIKSALDYVFSYWKEKIGRGROSATVDINSTALGL 180
QY 173 RTLRLHGVTSSDVLVNFKDKNGQFSSSTANIQIEGEIRGVNLPFASLVAFPGKVMDEA 232
Db 181 RTLRLHGYPVSSDVLENFKDHNGQF-TCSGIQTEGEIRGVNLPFASLVAFPGKVMQEA 239
QY 233 EFTSTKYLRALQKIPASSILSLEIRDVLEYGWHNTNLPRLAARNYMDVFQHTKNKNAE 292
Db 240 EIRSTMYLKHALQKIAVSS-LSQEIYVLEYGWHNTNPPRLAARNYMEVFQPDITYE---Q 295
QY 293 KLELAKLEFNIHFSLOERELKHVSRWVKDSSPEMTFCRHRHVEYVALASCIAPFQHS 352
Db 296 KLVELAKVEFNIHFSLOKRELQSLCRWKKHYGFPQLSFTRHIHVEYTFASCIATDPKOS 355
QY 353 GFRIGFTKMSHLITVLDMDYDVFQTVDELELFTATIKRWDPSAMECLPEYMKGVMMYTH 412
Db 356 AFRLGFAKMSYFVTVLDDIYDTYGTMELELFTPAIKRWDPSVVDCLPEYMKGVMAVYD 415
QY 413 TVNEMARVAEKAQGRDTLNYARQWEACFDSYMOEAKWIATGYLPTFEYLVNGKVSSAH 472
Db 416 TVNEMAKEAEKVQGRDTLNYARQWELYIDAYMPEAKWISSGYLPTFOEYLDSSKISFGT 475
QY 473 RPCALQPLITLDIPPDHILKEVDFPSKLANDLICITLRIGDTRCYKADRARG---EAS 529
Db 476 RTTIQPLITLGEPLSHIELQEIDFSAKFNLDISVILRLKG-----GQGSVQEAS 526
QY 530 SISCYMKDNPGLTEEDALNHINFMIRDAIRELNWELLKPDNSVPITSKGAFDISRVMH 589
Db 527 SVSCYMKDNAGLTEEDALHICINDMVNNLLKELNWEELLKPDNSNPISCRKAFAFDICRIFFH 586
QY 590 GYRYRDGYSPANVETKSLVMRTVIEPVPL 618
Db 587 GYKYRDGYGDATIEVKNLVKTVLEPVPL 615

RESULT 14

Q84KL5 PRELIMINARY; PRT; 574 AA.
ID Q84KL5;
AC Q84KL5;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)

```

DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)
DE Alpha-farnesene synthase.
OS Pinus taeda (loblolly pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=3352;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=22510022; PubMed=12623076;
RA Phillips M.A., Wildung M.R., Williams D.C., Hyatt D.C., Croteau R.;
RT "cDNA isolation, functional expression, and characterization of (+)-
RT alpha-pi-ene synthase and (-)-alpha-pi-ene synthase from loblolly pine
RT (Pinus taeda): Stereocontrol in pi-ene biosynthesis.";
RL Arch. Biochem. Biophys. 411:267-276 (2003).
DR EMBL; AF543528; AAO61226.1; -
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005630; Terpene synth_C.
DR InterPro; IPR008949; Terpenoid synth.
DR InterPro; IPR008930; Terp_cyc_loroid.
DR InterPro; IPR001906; Terp_synth-like.
DR Pfam; PF01397; Terpene_synth_1.
DR Pfam; PF03936; Terpene synth_C; 1.
SQ SEQUENCE 574 AA; 65941 MW; 26746BAE32ACF19A CRC64;

```

| | | | | |
|-----------------------|------------------|---------------------|------------|-------------|
| Query Match | 58.7%; | Score 1909; | DB 10; | Length 574; |
| Best Local Similarity | 63.3%; | Pred. No. 1.5e-132; | | |
| Matches 366; | Conservative 88; | Mismatches 110; | Indels 14; | Gaps 8; |

| | | | |
|----|-----|---|-----|
| Qy | 50 | SVASTDSVQRRVGNVHNSLWDDFIQSLISTPYGADPYRERADRLLGEVKDIMFNFKSL | 109 |
| Db | 2 | SSLAVDDAERRVGDYHFNLMWDALIQSL-STPYGASPYRDAEKLIGEIKE-MFASISIE | 59 |
| Qy | 110 | DGNDL---LQRLLLVDDVERLGDIDRHFKKEIKTALDYVNS-YWNEKIGCGRESVTTDL | 165 |
| Db | 60 | DGDEICYFLQRLWMIDNVERLGISRHFEENEIKAMEDVYSRHMDSKGIACGRHSVADL | 119 |
| Qy | 166 | NSTALGLRTLRLHGYTVSSDVLVNFCKDKNGQFSSSTANIQIEGETRGVLNLFASLVAFPG | 225 |
| Db | 120 | NSTALAFRTLRLHGYSVCSDVFKIFQDQKGEFACSD-QTEGEIKGILNLLRASLIAFPG | 178 |
| Qy | 226 | EKVMDAETPSTKYLRALQKIPASSILSLERDVLVEYGMHTNLPRLARNYMDVFGQH- | 284 |
| Db | 179 | ERLQEAEIFATTYLLKEALPKIQGSR-LSQIEYVLEYGWLTLPRLETRNYIEVLAEEI | 237 |
| Qy | 285 | ----TKNKNAAEKLLELAKLEFNIHSLQERELKHSRWKSDSGSPMTFCRHRHVEYYA | 340 |
| Db | 238 | TPYFKPCMAVEKLLKLAKIEFNLFHSLQOTELKHSRWKSDSGAQLFTTRHRHVEFYT | 297 |
| Qy | 341 | LASCIAPFQHSGFRLGFTKMSHLITVLDMDYDFEGTVDELELFTATIKRWDPNAMECLP | 400 |
| Db | 298 | LASCIAMEPKHSAFRLGFAKLCYLGIVLDDIYDTYGKMELELFTAIKRWDTSTTECLP | 357 |
| Qy | 401 | EYMGVYMMVYHTVNEMARVAEKAQGRDTLNYARQAMEACPDYSYQEAkwIATGYLPTFE | 460 |
| Db | 358 | EYMGVYMAFYDCVNEMARQAEKTQGWDTLDYARKTWEALIDAFMEBAKWISSGYVPTFQ | 417 |
| Qy | 461 | EYLENGKVSSAHRPCALOPILTLDIPFPDHLKEVDFPSKLNLCIITLRLRGDTRCYKA | 520 |
| Db | 418 | KYLDNGKVSFGYRAATLQPIILTLDIPPLHLIQEIDFPSSFNDLASSILRLRGDICYQA | 477 |
| Qy | 521 | DRARGEASSISCYMKDNPGLTEEDALNHINFMIRDAIRELNMWELLKPDNSVPITSKKHA | 580 |
| Db | 478 | ERSRGEQASSISCYMKDNPSTBEDALSHVNAMIGDKIPFNWEMKP-SKAPISSKRYA | 536 |
| Qy | 581 | FDISRVMHGGYRYRDGYSFANVETKSLVMRTVIEPVPL | 618 |
| Db | 537 | FDILRAFYHLYKYRDGFSIAKIETKCLVMRTVLDPPVM | 574 |

| | | | |
|----|--|-----------------------------|--|
| AC | 064404; | | |
| DT | 01-AUG-1998 (TREMBLrel. | 07, Created | |
| DT | 01-AUG-1998 (TREMBLrel. | 07, last sequence update) | |
| DT | 01-OCT-2003 (TREMBLrel. | 25, last annotation update) | |
| DE | D-selinene synthase. | | |
| OS | Abies grandis (Grand fir). | | |
| OC | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; | | |
| OC | Spermatophyta; Coniferales; Pinaceae; Abies. | | |
| OX | NCBI_TaxID=46611; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RX | MEDLINE=96113169; Pubmed=9442047; | | |
| RA | Steele C.L., Crock J., Bohlmann J., Croteau R.; | | |
| RT | "Sesquiterpene synthases from grand fir (Abies grandis). Comparison of | | |
| RT | constitutive and wound-induced activities, and cDNA isolation, | | |
| RT | characterization, and bacterial expression of delta-selinene synthase | | |
| RT | and gamma-humulene synthase." | | |
| RL | J. Biol. Chem. 273:2078-2089 (1998). | | |
| DR | EMBL; U92266; AAC05727.1; -. | | |
| DR | HSSP; Q40577; SEAU. | | |
| DR | GO; GO:0016829; F:lyase activity; IEA. | | |
| DR | GO; GO:0008152; P:metabolism; IEA. | | |
| DR | InterPro; IPR005630; Terpene_synth_C. | | |
| DR | InterPro; IPR008949; Terpenoid_synth. | | |
| DR | InterPro; IPR008930; Terp_cyc_toroid. | | |
| DR | InterPro; IPR001906; Terp_synth-like. | | |
| DR | Pfam; PF01397; Terpene_synth_C; 1. | | |
| DR | Pfam; PF03936; Terpene_synth_C; 1. | | |
| DR | SEQUENCE 581 AA; 67967 MW; 864622AEB8CC32C8 CRC64; | | |

| | | | | |
|-----------------------|-------------------|--------------------|------------|-------------|
| Query Match | 39.8% | Score 1295.5; | DB 10; | Length 581; |
| Best Local Similarity | 44.1%; | Pred. No. 3.5e-87; | | |
| Matches 255; | Conservative 118; | Mismatches 190; | Indels 15; | Gaps 8; |

| | | | |
|----|-----|--|-----|
| QY | 53 | STDSQRRVGNVYHSNLMDDDFIOSLISTPYGAPDYRERADRLLIGEVDIMFNFKSLEDGG | 112 |
| Db | 5 | SESSIPRTGNHGHNVMDDDLHSL-NSPYGAPAYELLQKLIQELIKULLTEMEMDDGD | 63 |
| QY | 113 | NDLLQRLLLVDDVERLGIDRHFKEIKT-ALDYVNSYWNKEGIGCG-RESVTDLNSTAL | 170 |
| Db | 64 | HDLIKRLQIVDTLECLGIDRHEHEIQTAALDYVRRWNEKEGIGESGRDSFSKDLNATAL | 123 |
| QY | 171 | GLRTLRHGYTVSSDVLTNFKDKNGQFSSTANIOIEG---EIRGVNLPRASLVAFPGE | 226 |
| Db | 124 | GFRALRLHRYNVSSGVLKNFXDKENGKFCFNFTGE-EGRGDKQVRSMLSLLRASEISFPGE | 182 |
| QY | 227 | KVMEAEFTSTKYLREAL---QKIPASSILSLEIRDVLEYGWMTNLPRLEARNYMDVFG | 282 |
| Db | 183 | KVMEAKAFTREYLNQVLGHGDVTDVDQSLREVKYALEFPMQSVPRWEARSFLEIYG | 242 |
| QY | 283 | QHTK--NKNAEKLLELALUEFNIFHSLOERELKHSRWKDKSGSPDMTCRHRHVEYYA | 340 |
| Db | 243 | HNHSLKSNINQKMLKALDENILOCKHKEIQFITRWRDRSGISQINFYRKRHVEYYS | 302 |
| QY | 341 | LASCIAFEPQHSGFRLGFKYKSHLITVLDMDYDVGTVDELEFATIKRWDPSAMECLP | 400 |
| Db | 303 | WVVMCIFEPESERIAFAKTAIILCTVLDLDTHTATLHEIKITIEGVRWDLSTDDL | 362 |
| QY | 401 | EYMGVYMMVYHTVENEMARVAEKAQGRDTLNTYARQAWEAFCFDSYNOEAKWIATGYLPTFE | 460 |
| Db | 363 | DYIKIAFOFFENTVNELVETVRKQGRDMTTIVKDCWKRYIESYQAEAWIATGHIPTFN | 422 |
| QY | 461 | EYLENGKVSSAHRPCALQPIITLDIPFPDHILKEVDFPSKLDNLICIIRLRGDTRCYKA | 520 |
| Db | 423 | EYIKNGMASSGMCILNLNPIILLDLKLPDNLIEQIHSPSKILDLLELTGRADDLKDFED | 482 |
| QY | 521 | DRARGEASSISCYMKONPGLTEBDALNHINFMIRDAIRELWELKPDNSVPITSKHA | 580 |
| Db | 483 | EKERGEMASSLOCYMKENEBSTEVENALNHIKILNRSLEEFNWEFMKOD-SVPMCKCKFT | 541 |
| QY | 581 | FDISRVMHGHYRYRDGYSFAVNETKSLVMRTVIEPVPL | 618 |
| Db | 542 | FNIGRGLOFIYKYRDGLYISDKVEVKDQIFKILVHQVPM | 579 |

RESULT 15
064404
ID 064404 PRELIMINARY;
PRT; 581 AA.

```
QY      581 FDISRVMHGGRYPDGSFANVETKSLVMRTVIEPVL 618  
       ||| |::||| ::||| : : : :  
Db      542 FNIGRGLFIYKYRDGLYSIDKEVKDQIFKILVHQVPM 579
```

Tue Jul 27 08:32:48 2004

us-10-025-145a-65.0723.rpt

Page 10

Search completed: July 23, 2004, 09:03:45
Job time : 45 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 26, 2004, 17:02:17 ; Search time 128 Seconds
(without alignments)
2679.372 Million cell updates/sec

Title: US-10-025-145A-65

Perfect score: 3251
Sequence: 1 MALSLITPLVSRSLSSHE.....FANVETKSLVMRTVIEFVPL 618

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10025145/runat_23072004_092623_22918/app_query.fasta_1.775
-DB=Issued_Patents_NA -OFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10025145 @CGN 1_1_105 @runat_23072004_092623_22918 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents_NA: *
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq: *
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq: *
6: /cgn2_6/ptodata/2/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------------------------------|
| 1 | 3251 | 100.0 | 2013 | 4 | US-09-360-545-64 Sequence 64, Appl |
| 2 | 2453 | 75.5 | 2018 | 4 | US-09-360-545-3 Sequence 3, Appl1 |
| 3 | 2453 | 75.5 | 2018 | 4 | US-09-398-395A-19 Sequence 19, Appl |
| 4 | 2453 | 75.5 | 2018 | 4 | US-09-887-586A-19 Sequence 19, Appl |
| 5 | 2453 | 75.5 | 2018 | 4 | US-09-895-752-19 Sequence 19, Appl |
| 6 | 2453 | 75.5 | 2018 | 4 | US-09-903-012B-19 Sequence 19, Appl |
| 7 | 2453 | 75.5 | 2018 | 4 | US-09-900-797-19 Sequence 19, Appl |
| 8 | 2264 | 69.6 | 2186 | 4 | US-09-360-545-66 Sequence 66, Appl |
| 9 | 2200.5 | 67.7 | 2196 | 4 | US-09-360-545-1 Sequence 1, Appl1 |
| 10 | 2200.5 | 67.7 | 2196 | 4 | US-09-398-395A-29 Sequence 29, Appl |
| 11 | 2200.5 | 67.7 | 2196 | 4 | US-09-887-586A-29 Sequence 29, Appl |
| 12 | 2200.5 | 67.7 | 2196 | 4 | US-09-895-752-29 Sequence 29, Appl |

| | | | | | | |
|----|--------|------|------|---|-------------------|-------------------|
| 13 | 2200.5 | 67.7 | 2196 | 4 | US-09-903-012B-29 | Sequence 29, Appl |
| 14 | 2200.5 | 67.7 | 2196 | 4 | US-09-900-797-29 | Sequence 29, Appl |
| 15 | 2197.5 | 67.6 | 2205 | 4 | US-09-360-545-31 | Sequence 31, Appl |
| 16 | 2137 | 65.7 | 1890 | 4 | US-09-360-545-77 | Sequence 77, Appl |
| 17 | 2084.5 | 64.1 | 2425 | 4 | US-09-360-545-68 | Sequence 68, Appl |
| 18 | 2031.5 | 62.5 | 2085 | 4 | US-09-360-545-5 | Sequence 5, Appl1 |
| 19 | 2031.5 | 62.5 | 2085 | 4 | US-09-398-395A-57 | Sequence 57, Appl |
| 20 | 2031.5 | 62.5 | 2085 | 4 | US-09-887-586A-57 | Sequence 57, Appl |
| 21 | 2031.5 | 62.5 | 2085 | 4 | US-09-895-752-57 | Sequence 57, Appl |
| 22 | 2031.5 | 62.5 | 2085 | 4 | US-09-903-012B-57 | Sequence 57, Appl |
| 23 | 2031.5 | 62.5 | 2085 | 4 | US-09-900-797-57 | Sequence 57, Appl |
| 24 | 1295.5 | 39.8 | 1865 | 4 | US-09-398-395A-47 | Sequence 47, Appl |
| 25 | 1295.5 | 39.8 | 1865 | 4 | US-09-887-586A-47 | Sequence 47, Appl |
| 26 | 1295.5 | 39.8 | 1865 | 4 | US-09-895-752-47 | Sequence 47, Appl |
| 27 | 1295.5 | 39.8 | 1865 | 4 | US-09-903-012B-47 | Sequence 47, Appl |
| 28 | 1295.5 | 39.8 | 1865 | 4 | US-09-900-797-47 | Sequence 47, Appl |
| 29 | 1295.5 | 39.8 | 1885 | 3 | US-09-234-393-45 | Sequence 45, Appl |
| 30 | 1295.5 | 39.8 | 1885 | 3 | US-09-234-393-47 | Sequence 47, Appl |
| 31 | 1295.5 | 39.8 | 1885 | 4 | US-09-865-171-45 | Sequence 45, Appl |
| 32 | 1295.5 | 39.8 | 1885 | 4 | US-09-865-171-47 | Sequence 47, Appl |
| 33 | 1295.5 | 39.8 | 1888 | 3 | US-09-234-393-19 | Sequence 19, Appl |
| 34 | 1295.5 | 39.8 | 1888 | 4 | US-09-865-171-19 | Sequence 19, Appl |
| 35 | 1291.5 | 39.7 | 1885 | 3 | US-09-234-393-43 | Sequence 43, Appl |
| 36 | 1291.5 | 39.7 | 1885 | 4 | US-09-865-171-43 | Sequence 43, Appl |
| 37 | 1250.5 | 38.5 | 1967 | 3 | US-09-234-393-14 | Sequence 14, Appl |
| 38 | 1250.5 | 38.5 | 1967 | 4 | US-09-360-545-17 | Sequence 17, Appl |
| 39 | 1250.5 | 38.5 | 1967 | 4 | US-09-865-171-14 | Sequence 14, Appl |
| 40 | 1240.5 | 38.2 | 2700 | 3 | US-09-315-861-1 | Sequence 1, Appl1 |
| 41 | 1240.5 | 38.2 | 2700 | 4 | US-09-398-395A-43 | Sequence 43, Appl |
| 42 | 1240.5 | 38.2 | 2700 | 4 | US-09-887-586A-43 | Sequence 43, Appl |
| 43 | 1240.5 | 38.2 | 2700 | 4 | US-09-895-752-43 | Sequence 43, Appl |
| 44 | 1240.5 | 38.2 | 2700 | 4 | US-09-903-012B-43 | Sequence 43, Appl |
| 45 | 1240.5 | 38.2 | 2700 | 4 | US-09-593-253-1 | Sequence 1, Appl1 |

ALIGNMENTS

RESULT 1
US-09-360-545-64
; Sequence 64, Application US/09360545
; Patent No. 6429014
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B
; APPLICANT: Bohlmann, Joerg
; APPLICANT: Steele, Christopher L
; APPLICANT: Phillips, Michael A
; TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
; FILE REFERENCE: wau13885
; CURRENT APPLICATION NUMBER: US/09/360, 545
; EARLIER FILING DATE: 1999-07-26
; EARLIER APPLICATION NUMBER: 60/052, 249
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: PCT/US98/14528
; EARLIER FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 64
; LENGTH: 2013
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)..(1889)
US-09-360-545-64

Alignment Scores:
Pred. No.: 0
Score: 3251.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4
Length: 2013
Matches: 618
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-025-145A-65 (1-618) x US-09-360-545-64 (1-2013)

QY 1 MecAlaLeuSerIleThrProLeuValSerArgSerCysLeuSerSerSerHisGlu 20
Db 36 ATGGCTCTTCTTCTATTACTCCGCGTGGTTCCAGTCTGCTCCTCAGTCTTCTCATGAG 95
QY 21 IleYsAlaLeuArgArgThrIleProThrLeuGlyIleCysArgProGlyLysSerVal 40
Db 96 ATTAAGGCTCTCCGTAGAACAACTCCAATCTTGAATCTGCAGGCCGGGGAATCCGTC 155
QY 41 AlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAspSerValGlnArgArg 60
Db 156 GCGCATTCATTAACATGTGTTGCAAGCGTCGCATCTACTGATCTGTACAGAGACGC 215
QY 61 ValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGlnSerLeuIleSerThr 80
Db 216 GGGGCACTATCATCTCAACCTGTGGGACGATGATTCTATACAGTCTCTGATCTCAACG 275
QY 81 ProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIleGlyGluValLysAsp 100
Db 276 CCTTAGAGACACCTGATTACCGGGAACGTGCTGACAGACTTATTGGGGAAGTAAAGAT 335
QY 101 IleMetPheAsnPhelysSerLeuGluAspGlyLysAsnAspLeuGlnArgLeuLeu 120
Db 336 ATAATGTTCAATTTCAAGTCGCTGGAAGATGAGGCAATGATCTCTCAACGACTTTTG 395
QY 121 LeuValAspAspValGluArgLeuGlyIleAspArgHisPheLysGluIleLysThr 140
Db 396 CTGGTCGATGACGTTGACGTTGGGAATCGACAGGCATTTCAAAAAGAGATAAAACG 455
QY 141 AlaLeuAspTyrValAsnSerTyrTrpAsnGluLysGlyIleGlyCysGlyArgGlySer 160
Db 456 GCACCTCGATTATGTTAACAGTTATTGGAAAGGCAAAAAGGCAATTGGATGTGGAGGAGAGT 515
QY 161 ValValThrAspLeuAsnSerThrAlaLeuGlyLeuArgThrLeuArgLeuHisGlyTyr 180
Db 516 GTTGATGACTGACCTCAACTCAACCGCTTGGGGCTTCGAACCTCTCCGACTACACGGATAC 575
QY 181 ThrValSerSerAspValLeuAsnValPheLysAspLysAsnGlyGlnPheSerSerThr 200
Db 576 ACTGTGTTCTCAGATGTTTGAACGTTTAAAGACAAAATGGGCAATTTCTCCACT 635
QY 201 AlaAsnIleGlnIleGluGlyLysIleArgGlyValLeuAsnLeuPheArgAlaSerLeu 220
Db 636 GCCAATATTCAAGTAGAGGAGAGATTAGAGCGCTTCTCAATTTATTCAAGGCGCTCCCTC 695
QY 221 ValAlaPheProGlyGlyLysValMetAspGluAlaGluThrPheSerThrLysTyrLeu 240
Db 696 GTGCGCTTCCCGCGGAGAAAGTTATGGATGAAGCTGAACAATCTCTACAATAATATTTA 755
QY 241 ArgGluAlaLeuGlnLysIleProAlaSerSerIleLeuSerLeuGlnIleArgAspVal 260
Db 756 AGAGAACCCCTGCATAAAGATTCCGGCATTCAGTATCTTCACTAGAGATACGGGACGTT 815
QY 261 LeuGluTyrGlyTyrPheIleThrAsnLeuProArgLeuGluAlaArgAsnTyrMetAspVal 280
Db 816 CTGAATATAGTTGGCACACCAATTTGCCACGCTTGAAGCAAGGAATTACATGAGACGTC 875
QY 281 PheGlyGlnHisThrLysAsnLysAsnAlaGluLysLeuLeuGluLeuAlaLysLeu 300
Db 876 TTTGGACAGCACATAAAATAAGAACGCCGCCGAGAAACTTTTGAACCTTGCAAAATTG 935
QY 301 GluPheAsnIlePheHisSerLeuGlnGluArgGluLeuLysHisValSerArgTyrTrp 320
Db 936 GAATTCATATATATTTCACCTCTTACAGAGAGAGAGTTAAACAATGTTCCCGATGCTGG 995
QY 321 LysAspSerGlySerProGluMetThrPheCysArgHisArgHisValGluTyrTyrAla 340
Db 996 AAAGACTCGGGTCTCTCTGAGATGACCTTCTGTGACATCGTCACTGGAATACTACGCT 1055
QY 341 LeuAlaSerCysIleAlaPheGluProGlnHisSerGlyPheArgLeuGlyPheThrLys 360
Db 1056 TTGGCTTCTGCAATTGCGTTGAGCGCTCAACATTTCTGATTCAAGATCGGCTTTACCAAG 1115

QY 361 MetSerHisLeuIleThrValLeuAspAspMetTyrAspValPheGlyThrValAspGlu 380
Db 1116 ATGTCATCTTATACGCGTTCTTGACGACATGTACGACGTCTTCGGCACAGTAGACGAG 1175
QY 381 LeuGluLeuPheThrAlaThrIleLysArgTyrAspProSerAlaMetGluCysLeuPro 400
Db 1176 CTGGAACCTTTCACAGCGCAATTAAAGATGGATCCGTCGGCATGGAATGCCCTTCCA 1235
QY 401 GluTyrMetLysGlyValTyrMetMetValTyrHisThrValAsnGluMetAlaArgVal 420
Db 1236 GAATATATGAAGAGATGTACATGATGTTTATACACCGTAATGAATGGCTCGAGTG 1295
QY 421 AlaGluLysAlaGlnGlyArgAspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCys 440
Db 1296 GCAGAGAAAGCTCAAGCGCGAGACACGCTCAACTATGCAAGACAGGCTTGAGGCGTGT 1355
QY 441 PheAspSerTyrMetGlnGluAlaLysTrpIleAlaThrGlyTyrLeuProThrPheGlu 460
Db 1356 TTTGATTCGTATATGACAGAACAAAGTAGATCGCCACTGGTTATCTGCCACGTTGAG 1415
QY 461 GluTyrLeuGluAsnGlyLysValSerSerAlaHisArgProCysAlaLeuGlnProIle 480
Db 1416 GAGTACTTGGAAGAACGGGAAGTTAAGCTCTGCTCATCGCCCATGCGCAACCACTT 1475
QY 481 LeuThrLeuAspIleProPheProAspHisIleLeuLysGluValAspPheProSerLys 500
Db 1476 CTGACGTTGACATCCCTTTCCTGATCACAATCCTCAAGGAAGTTGACTTCCCATCGAAG 1535
QY 501 LeuAsnAspLeuIleCysIleIleLeuArgLeuArgGlyAspThrArgCysTyrLysAla 520
Db 1536 CTCAATGACTGTATATGATCATCTTCGATTAAAGAGGTGATACACGGTGTACAAAGCA 1595
QY 521 AspArgAlaArgGlyGluGluAlaSerSerIleSerCysTyrMetLysAspAsnProGly 540
Db 1596 GACAGGGCCCGTGAGAGAAAGCTTCGCTATATCATGATTATGAAGAACAATCCTGGA 1655
QY 541 LeuThrGluGluAspAlaLeuAsnHisIleAsnPheMetIleArgAspAlaIleArgGlu 560
Db 1656 TTAAACGAAGAAGATGCTGTGATCATATCAACTTCATGATCAAGGACGAATCAGAGAA 1715
QY 561 LeuAsnTrpGluLeuLeuLysProAspAsnSerValProIleThrSerLysLysHisAla 580
Db 1716 TTAAATTGGAGCTTCTAAAGCCAGACACAGTGTCCCATCACTTCCAAGAAACACGCA 1775
QY 581 PheAspIleSerArgValTyrPheHisGlyTyrArgTyrArgAspGlyTyrSerPheAla 600
Db 1776 TTTGACATTAAGCAGAGTTTGGCATCACGGTTACAGATACCGAGATGGCTACAGCTTGGC 1835
QY 601 AsnValGluThrLysSerLeuValMetArgThrValIleGluProValProLeu 618
Db 1836 AACGTGAACAACAAAGATTGTGATGAGAACCGTCATTGAACTGTGCTTGG 1889

RESULT 2
US-09-360-545-3
; Sequence 3, Application US/09360545
; Patent No. 6429014
; GENERAL INFORMATION:
; APPLICANT: Croceau, Rodney B
; APPLICANT: Bohlmann, Jorg
; APPLICANT: Steele, Christopher L
; APPLICANT: Phillips, Michael A
; TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
; FILE REFERENCE: wslr1385
; CURRENT APPLICATION NUMBER: US/09/360,545
; CURRENT FILING DATE: 1999-07-26
; EARLIER APPLICATION NUMBER: 60/052,249
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: PCT/US98/14528
; EARLIER FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3

```

; LENGTH: 2018
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6) ..(1892)
; OTHER INFORMATION: Clone AG3.18 encoding pinene synthase
; JS-09-360-545-3

```

| | |
|------------------------|-----------|
| Alignment Scores: | |
| Pred. No.: | 3.98e-288 |
| Score: | 2453.00 |
| Percent Similarity: | 84.63% |
| Best Local Similarity: | 75.28% |
| Query Match: | 75.45% |
| DB: | 4 |
| | |
| Length: | 2018 |
| Matches: | 475 |
| Conservative: | 59 |
| Mismatches: | 81 |
| Indels: | 16 |
| Gaps: | 6 |

US-10-025-145A-65 (1-618) x US-09-360-545-3 (1-2018)

| | | | |
|----|-----|---|-----|
| Qy | 1 | MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- | 15 |
| | | ::: | |
| Db | 6 | ATGGCTTAGTTTCTACCGCACCGTTGGCTTCCAATCATGCTGCACAAATCGTTGATC | 65 |
| Qy | 16 | SerSerSerHisGluIleValaLeuArgArgThrIleProThrLeuGlyIleCysArg | 35 |
| | | ::: ::: | |
| Db | 66 | AGTTCACCCATGAGCTTAAGGCTCTCTAGAACAAATCCAGCTTAGGAATGAGTAGG | 125 |
| Qy | 36 | ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp | 55 |
| | | ::: ::: | |
| Db | 126 | CGAGGAAATCTATCACTCCTTCCATCAGCATGAGCTCTACCACCGTTGTAACCGATGAT | 185 |
| Qy | 56 | SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln | 75 |
| | | ::: ::: | |
| Db | 186 | GGTGTACGAAGACGCATGGGCGCATTTCCATTCCAACCTCTGGAGCATGATGTATACAG | 245 |
| Qy | 76 | SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle | 95 |
| | | ::: | |
| Db | 246 | TCTTTA--CCAACGGCTTATGACGAAAAATCGTACCTGGAGCGTGCTGAGAAACTGATC | 302 |
| Qy | 96 | GlyGluValLysAspIleMetPheAsnPhelySerLeuGluAspGlyGly----- | 112 |
| | | ::: | |
| Db | 303 | GGGGAAGTAAAGAAC--ATGTTCAATTGCGATGTATTAGAAGATGGAGCTTAATGAGT | 359 |
| Qy | 113 | -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle | 130 |
| | | ::: ::: | |
| Db | 360 | CCGCTCAATGATCTCATTCACGCCCTTGGATTGTGCACAGCCTTGAACGTTTGGGATC | 419 |
| Qy | 131 | AspArgHisPheLeuLysGluIleIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn | 150 |
| | | ::: ::: | |
| Db | 420 | CATAGACATTTCAAAGATGAGATAAATCGGCGCTTGATTATGTTACAGTTATTGGGCG | 479 |
| Qy | 151 | GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu | 170 |
| | | | |
| Db | 480 | GAAATGCGCATCGGATGGGGAAGAGAGTGTGTACTGATCTGAATCACTGCGCTTG | 539 |
| Qy | 171 | GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe | 190 |
| | | | |
| Db | 540 | GGGCTTCGAACCCCTACGACTACACGGATACCCGGTGCTTCAGATGTTTCAAAGCTTTC | 599 |
| Qy | 191 | LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyLeuIleArg | 210 |
| | | ::: ::: | |
| Db | 600 | AAAGGCCAAATGGGCGAGTTTCTCTGCTCTGAAATATTACAGACAGATGAAGAGATCAGA | 659 |
| Qy | 211 | GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp | 230 |
| | | ::: ::: | |
| Db | 660 | GGGTTCTGAATTTATTCGGGCTCTCCTCATTTGCCCTTCCAGGGGAGAAATATATGAT | 719 |
| Qy | 231 | GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer | 250 |
| | | ::: ::: | |
| Db | 720 | GAGGCTGAATCTTCTCTACCAATATTTAAAGAAGCCCTGCAAAAGATTCGCGTCTCC | 779 |
| Qy | 251 | SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrHisThrAsnLeuPro | 270 |
| | | | |

| | | | |
|----|------|---|------|
| Db | 780 | AGT--CTTTCGGAGAGATCGGGGACGTTTGGAAATATGGTTGGCACACATATTGGCCG | 836 |
| Qy | 271 | ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsnLysAsnAla | 290 |
| Db | 837 | CGATTGGAAGCAAGAAATTACATCCAGTCTTTGGACAGACACTGAGAACACGAAGTCA | 896 |
| Qy | 291 | -----AlaGluLysLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer | 307 |
| Db | 897 | TATGTGAAGACAAAAACTTTAGAACTCGCAAAATTGAGTTCAACATCTTCAATCC | 956 |
| Qy | 308 | LeuGlnGluArgGluLeuLysHisValSerArgTrpTrpLysAspSerGlySerProGlu | 327 |
| Db | 957 | TTACAAAAGAGGAGTTAGAAAGTGGTCAAGTGTGGAAGAATCGGGTTTCCTGAG | 1016 |
| Qy | 328 | MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe | 347 |
| Db | 1017 | ATGACCTTCTGCCGACATCGTCACGTGAATACTACACTTTGGCTTCTCGATTGGCTTC | 1076 |
| Qy | 348 | GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal | 367 |
| Db | 1077 | GAGCCTCAACATTCTGATTGAGATTGAGACTCGGCTTGGCCAAGACGTGTCACTTATCAGGTT | 1136 |
| Qy | 368 | LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluLeuPheThrAlaThr | 387 |
| Db | 1137 | CTTGACGATATGTACGACACCTTCGACAGTAGACGAGCTGGAACCTTTCACAGCGACA | 1196 |
| Qy | 388 | IleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr | 407 |
| Db | 1197 | ATGAGAGATGGGATCCGCTCGATAGATTGCTTCCAGATATATGAAGAAGTGTAC | 1256 |
| Qy | 408 | MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg | 427 |
| Db | 1257 | ATAGCGGTTTACGACACCGTAATGAATGGCTTCGAGAGGACAGAGGCGCTCAAGGCCGA | 1316 |
| Qy | 428 | AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu | 447 |
| Db | 1317 | GATACGCTCACATATGCTCGGGAAGCTTGGAGGCTTATTGATTGCTATATGCAAGAA | 1376 |
| Qy | 448 | AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys | 467 |
| Db | 1377 | GCAAGGTGATGCCACCTGTTACCTGCCCTCTTGATGAGTACTACGAGAATGGGAAA | 1436 |
| Qy | 468 | ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe | 487 |
| Db | 1437 | GTTAGCTGTGGTATCGCATATCCGATTCGACACCCATTCTGACAATGACATCCCTTT | 1496 |
| Qy | 488 | ProAspHisIleLeuLysGluValAspPheProSerLysLysLeuAsnAspLeuIleCysIle | 507 |
| Db | 1497 | CCTGATCATATCTCAAGGAAGTGACTTCCCATCAAGCTTAACGACTTGGCATGTGCC | 1556 |
| Qy | 508 | IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGlnGlu | 527 |
| Db | 1557 | ATCCTTCGATTACGAGGTGATACGGGTCTCTACAAAGCGGACAGGGCTCGTGAGAAAGA | 1616 |
| Qy | 528 | AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu | 547 |
| Db | 1617 | GCTTCTCTATATCATGTTATATGAAGACAACTCTGAGTATCAGAGGAAGATCTCTC | 1676 |
| Qy | 548 | AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys | 567 |
| Db | 1677 | GATCATATCAAGCCATGATCAGTACGTAATCAAAAGATTAAATTGGGAACCTTCAAA | 1736 |
| Qy | 568 | ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp | 587 |
| Db | 1737 | CCAGACATCAAGTTCATCCATCTCGCGGAAGAAACATGCTTTGACATCGCCAGCTTTC | 1796 |
| Qy | 588 | HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu | 607 |
| Db | 1797 | CATTACGGCTACAATAACGAGACGGCTACAGCTTGCCAACGTTGAACGAAGAGTTTG | 1856 |
| Qy | 608 | ValMetArgThrValIleGluProValProLeu 618 | |
| Db | 1857 | GTCACGAGAACCTCTTGAATCTGTGCTTTG 1889 | |

RESULT 3
US-09-398-395A-19
; Sequence 19, Application US/09398395A
; Patent No. 6468772
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64687721, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/398,395A
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 2018
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)...(1889)
; OTHER INFORMATION: pinene synthase
US-09-398-395A-19

Alignment Scores:
Pred. No.: 3,98e-288 Length: 2018
Score: 2453.00 Matches: 475
Percent Similarity: 84.63% Conservative: 59
Best Local Similarity: 75.28% Mismatches: 81
Query Match: 75.45% Indels: 16
DB: 4 Gaps: 6

US-10-025-145A-65 (1-618) x US-09-398-395A-19 (1-2018)

QY 1 MetAlaLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
DB 6 ATGGCTCTAGTTTCTACCGCACCGCTTGCCTTCCAATCATGCGTGCACAAATCGTTGATC 65
QY 16 SerSerSerHisGluIleLysAlaLeuArgThrIleProThrLeuGlyIleCysArg 35
DB 66 AGTTCTACCATGAGCTTAAGGCTCTCTAGAACATTCACAGCTCTAGGAATGAGTAGC 125
QY 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
DB 126 CGAGGGAATCTATCACTCCCTCCATCAGCATGAGCTCTACCACCGTTGTAACCGATGAT 185
QY 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75
DB 186 GGTGTACGAAGACGCGATGGCGATTTCCTCAACCTCTGGGACGATGATGTCATACAG 245
QY 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
DB 246 TCTTTA---CCAA CGGCTTATGAGGAAAAATCGTACCTGAGCGCTGCGAAGAACTGATC 302
QY 96 GlyIleValIysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly----- 112
DB 303 GGGGAAGTAAAGAAC--ATGTTCAATTGCATGTCATTAGAAGATGAGAGATTATGAGT 359
QY 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
DB 360 CCGCTCAATGATCTCATTCACGCCCTTGATGTGCGACAGCCCTTGAACGTTGGGATC 419
QY 131 AspArgHisPheLysGlyIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
DB 420 CATAGACATTTCAAAGATGAGATAAAATCGCGCTTGATTATGTTACAGTTATTGGGCC 479

QY 151 GluLysGlyIleGlyCysGlyArgGluSerValThrAspLeuAsnSerThrAlaLeu 170
DB 480 GAAATGGCATCGGATGCGGAGGAGAGAGTGTGTACTGATCTGAACCTCAACTGCGTTG 539
QY 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
DB 540 GGGCTTCGAACCCCTACGACTACACGGATACCCGGGTGCTTCAGATGTTTCAAGCTTTC 599
QY 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyIleArg 210
DB 600 AAAGGCCAAATGGGCGAGTTTCTCTGCTGAAATATTGACAGACAGATGAAGAGATCAGA 659
QY 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGlyLysValMetAsp 230
DB 660 GCGTCTGAATTATTCGGGCTCTCATTTGCCAGGGGAGAAAATTATGAT 719
QY 231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250
DB 720 GAGGCTGAATCTTCTCTACCAATATTAAAGAAGCCCTGCAGAAAAGATTCCGTCCTCC 779
QY 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrHisThrAsnLeuPro 270
DB 780 AGT---CTTCCGAGAGATCGGGGACGTTTGGATATGCTTGGCACACATATTGCGCC 836
QY 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsnLysAsnAla 290
DB 837 CGATTGGAAGCAAGGAATTACATCCAAAGTCTTTGACAGAGACACTGAGAACAAGAGTCA 896
QY 291 -----AlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307
DB 897 TATGTGAAGAGCAAAAACCTTTAGAACTCGCAAAATGGAGTTCAACATCTTCAATCC 956
QY 308 LeuGlnGluArgGluLeuLysHisValSerArgTyrTrpLysAspSerGlySerProGlu 327
DB 957 TTACAAAGAAGAGGAGTTAGAAAGTCTGTGACAGTGTGAAGAAGATCGGTTTCTCTGAG 1016
QY 328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347
DB 1017 ATGACCTCTGCGGACATCGTCACTGGAATACTACACTTGCTGCTTCCGATTCGCTTC 1076
QY 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367
DB 1077 GAGCTCAACATTTCTGATTCAGACTCGGCTTGGCCAAGAGTGTCATCTTATCAGGTT 1136
QY 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuPheThrAlaThr 387
DB 1137 CTTGACGATATGTACGACACCTTCGGCACAGTAGACGAGCTGAACTCTTCACAGCGACA 1196
QY 388 IleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407
DB 1197 ATGAGAGATGGGATCCGCTCCGATAGATTGCCCTTCAGAAATATGAAAAGAGTGTAC 1256
QY 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg 427
DB 1257 ATAGCGGTTTACGACACCGTAAATGAAATGGCTCGAGAGGCAAGAGGCTCAAGCGCGA 1316
QY 428 AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnIle 447
DB 1317 GATACGCTCACATATGCTCGGGAAGCTTGGGAGGCTTATATGATTCGTATATGCAAGAA 1376
QY 448 AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGlnGluTyrLeuGluAsnGlyLys 467
DB 1377 GCAAGGTGATCGCCACTGTTTACCTGCCCTCTTGATGAGTACTACGAGATGGGAAA 1436
QY 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
DB 1437 GTTAGCTGTGTCATCGCATATCCGCAATTGCAACCCATTGCAATGACATCCCTTTT 1496
QY 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507
DB 1497 CCTGATCATATCCTCAAGGAAGTTGACTTCCCATCAAGCTTAAAGCACTTGGCATGTGCC 1556

Qy 508 ILeuArgLeuArgGlyAspThrArgCysTyrIysAlaAspArgAlaArgGlyGlu 527
Db 1557 ATCCTCGATTACGAGGTGATACGGCGCTACAAGCGGACAGGCGCTCGAGAGAA 1616
Qy 528 AlasSerIleSerCysTyrMetIysAspAsnProGlyLeuThrGluGluAspAlaLeu 547
Db 1617 GCTTCTCTATATCATGTATATGAAAGACAATCCTGGAGTATCAGAGGAATGCTCTC 1676
Qy 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567
Db 1677 GATCATATCAACGCCATGATCAGTACGTAATCAAGGATTAAATTGGGAACTTCTCAA 1736
Qy 568 ProAspAsnSerValProIleThrSerIysLysHisAlaPheAspIleSerArgValTrp 587
Db 1737 CCAGACATCAATGTTCCTCATCTCGCGAAGAAACATGCTTTGACATCGCCAGAGCTTTC 1796
Qy 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607
Db 1797 CATACGGCTACAATATACCGAGACGGCTACGCTTGCCAAAGTTGAACGAAGAGTTTG 1856
Qy 608 ValMetArgThrValIleGluProValProLeu 618
Db 1857 GTACAGAACCTCCTCTGAATCTGTGCTTTG 1889

RESULT 4
US-09-887-586A-19
; Sequence 19, Application US/09887586A
; Patent No. 6495354
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: NO. 64953541, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/887, 586A
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/398, 395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130, 628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150, 262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for windows Version 3.0
; SEQ ID NO 19
; LENGTH: 2018
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)...(1889)
; OTHER INFORMATION: pinene synthase
US-09-887-586A-19

Alignment Scores:
Pred. No.: 3.98e-288 Length: 2018
Score: 2453.00 Matches: 475
Percent Similarity: 84.63% Conservative: 59
Best Local Similarity: 75.28% Mismatches: 81
Query Match: 75.45% Indels: 16
DB: 4 Gaps: 6

US-10-025-145A-65 (1-618) x US-09-887-586A-19 (1-2018)

Qy 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
Db 6 ATGGCTCTAGTTTCTACCGCACCGCTTGCTTCCAAATCATGCTGCACAAATCGTTGATC 65
Qy 16 SerSerSerHisGluIleLysAlaLeuArgThrIleProThrLeuGlyIleCysArg 35
Db 66 AGTTCTACCATGAGCTTAAGGCTCTCTCTAGAACAAATTCCAGGCTTACGAATGAGTAGG 125

Qy 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
Db 126 CGAGGAAATCTATCACTCCTTCCATCAAGCATGAGCTCTACACCCTGTGTAACCGATGAT 185
Qy 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75
Db 186 GGTGTACGAGACGCGATGGCGATTCATTCACACCTCTGGGACGATGATGCATACAG 245
Qy 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
Db 246 TCTTTA---CCAACGGCTTATGAGGAAATACTGTAACCTGGAGCGCTGAGAAACTGATC 302
Qy 96 GlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyIle----- 112
Db 303 GGGAGATTAAGATC--ATGTTCAATTGATGTCTATTAGAGATGAGAGATTAAATGAGT 359
Qy 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
Db 360 CCGCTCAATGATCTCATCAACGCTTGTGATGTGCAGACGCTTGAAAGTTGGGATC 419
Qy 131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
Db 420 CATAGACATTTCAAGATGAGATAAATCGCGCTGATTATGTTACAGTTATTGGGCG 479
Qy 151 GluLysGlyIleGlyCysGlyArgGluSerValThrAspLeuAsnSerThrAlaLeu 170
Db 480 GAAATGGCATCGGATGCGGAGGAGAGTGTGTTACTGATCTGAATCAACTGCGCTTG 539
Qy 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
Db 540 GGGCTTGAACCTTACGACTACACGGAATACCGGTGTCTTCAGATGTTTCAAGCTTTC 599
Qy 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGluIleArg 210
Db 600 AAAGGCCAAATGGGAGTTTCTGCTCTGAATAATTACAGACAGATGAAGAGATCAGA 659
Qy 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230
Db 660 GGCTTCTGAATTTATTCGGGCTCCTCATTCCTTCCAGGGGAGAAATATGAT 719
Qy 231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250
Db 720 GAGCTGAATCTTCTCTACCAATATTTAAAGAAGCCCTGCAAAAGATTCCGGTCTCC 779
Qy 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrPheIleThrAsnLeuPro 270
Db 780 AGT--CTTTCGGAGAGATCGGGAGCTTTTGAATATGTTGGCACACATATTTGCCG 836
Qy 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsnLysAsnAla 290
Db 837 CGATTGAACCAAGGAATTACATCAAGTCTTTGGACAGAGACACTGAGAACAGAGTCA 896
Qy 291 -----AlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307
Db 897 TATGTGAAGACCAAAAACTTTAGAACTCGCAAAATTGAGTTCAATCTTCAATCC 956
Qy 308 LeuGlnGluArgGluLeuLysHisValSerArgTrpTrpLysAspSerGlySerProGlu 327
Db 957 TTACAAGAAGGAGTAGTAAGAGTCTGTCAGATGTGAAAGAATCGGGTTTCTCTGAG 1016
Qy 328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347
Db 1017 ATGACCTTCTCGCATCATCGTCAGTAATACTACACTTTGGCTTCTGCAATGGCTTC 1076
Qy 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367
Db 1077 GAGCTCAACATCTGTGATTACAGACTCGGCTTTCACCAAGACGTGTATCTTATCACGGTT 1136
Qy 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluPheThrAlaThr 387
Db 1137 CTTGACGATATGTACGACACCTTCGACAGTAGACGAGCTGGAATCTTTCACAGCGACA 1196
Qy 388 IleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407

Db 1197 ATGAAGATGGATCCGCTCCGATGATTGCTCCAGAAATATATGAAGAAGAGTGATC 1256
QY 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg 427
Db 1257 ATAGCGGTTTACGACACCGCTAAATGAATGGCTCGAGAGCAGAGAGGCTCAAGCGCGA 1316
QY 428 AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu 447
Db 1317 GATACGCTCACATATATGCTCGGGAAGCTGGAGGCTTATATGATTGATTCGATATGCAAGAA 1376
QY 448 AlAlysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467
Db 1377 GCAAGGTGGATCGCCACTGGTTACTGCTCCCTCTTGATGAGTACTACGAGAATGGGAAA 1436
QY 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
Db 1437 GTTAGCTGTGGTATCGCATATCCGCATTGCAACCCATTCTGACAATGGACATCCCTTT 1496
QY 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspIleCysIle 507
Db 1497 CCTGATCATATCCTCAAGGAAGTGACTTCCCATCAAAAGCTTAAGCACTTGCGATGTGCC 1556
QY 508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu 527
Db 1557 ATCCTTCGATTACGAGGTGATACCGGGTCTACAAGCGGACAGGGCTCGTGAGAAGAA 1616
QY 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547
Db 1617 GCTTCTCTATATCATGTATATGAAGAACAATCCTGGAGTATCAGAGGAAGATGCTCTTC 1676
QY 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567
Db 1677 GATCATATCAACGCCCATGATGAGTAAATCAAAAGATTAAATTGGGAACCTTCTCAAA 1736
QY 568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp 587
Db 1737 CCAGACATCAATGTTCCTCCATCTCGCGCAAGAAACATGCTTTTGACATCGCCAGAGCTTTC 1796
QY 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607
Db 1797 CATTAACGGGTACAATAATACGAGACGGCTTACAGCGTTGCCAACGTTGAAGAGTTTG 1856
QY 608 ValMetArgThrValIleGluProValProLeu 618
Db 1857 GTACAGAGAACCTCCTTGATCTGTGCCTTG 1889

RESULT 5

US-09-895-752-19
; Sequence 19, Application US/09895752
; Patent No. 6559297
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 65592971, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/895,752
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 2018
; TYPE: DNA

; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)...(1889)
; OTHER INFORMATION: pinene synthase
US-09-895-752-19

Alignment Scores:
Pred. No.: 3.98e-288 Length: 2018
Score: 2453.00 Matches: 475
Percent Similarity: 84.63% Conservative: 59
Best Local Similarity: 75.28% Mismatches: 81
Query Match: 75.45% Indels: 16
DB: 4 Gaps: 6

US-10-025-145a-65 (1-618) x US-09-895-752-19 (1-2018)

QY 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
Db 6 ATGGCTTAAGTTTCTACCGCACCGTTGGCTTCCAAATCATGCTGCACAAATCGTTGATC 65
QY 16 SerSerHisGluIleLysAlaLeuArgThrIleProThrLeuGlyIleCysArg 35
Db 66 AGTTTCAACCATGAGCTTAAGGCTCTCTAGAACAAATTCGACTTAGAATGAGTAGG 125
QY 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
Db 126 CGAGGGAATCTATCACTCCTTCATCAGCATGAGCTCTACCAACCGTTGTAAACGATGAT 185
QY 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75
Db 186 GGTGTACCAAGACGCATGGGCGCATTTCCATTCCAACTCTGGAGCATGATGCATACAG 245
QY 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
Db 246 TCTTTA---CCAACGGCTTATGAGAAAATCGTACCTGGAGCGTGTGAGAACTGATC 302
QY 96 GlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly----- 112
Db 303 GGGGAATAAAGAAC--ATGTTCAATTCGATGTCAATTAGAAGTGAAGATTAAAGT 359
QY 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
Db 360 CCGTCATGATCTCATTTCAACGCTTTGGATTGTGCACAGCCTTGAACGTTTGGGATC 419
QY 131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
Db 420 CATAGCATTTCAAGATGAGATGAATAATCGCGCTTGATTTGTTTACAGTTATTTGGGCG 479
QY 151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170
Db 480 GAAATGCGATCGGATCGGGAGGAGAGTGTGTTACTGATCTGAATCTCAACTGCGCTTG 539
QY 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
Db 540 GGGCTTCGAACCTPACGACTACAGGATACCGGTTGTTTCAAGTGTTCCTTCAAGCTTTC 599
QY 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyIleArg 210
Db 600 AAAGGCCAAATGGGCGAGTTTCTGCTCTGAAATATATTGACAGATGAAGAGATCAGA 659
QY 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230
Db 660 GCGCTTGAATTTATTCGGGCTCCCTCATTTGCCCTTCCAGGGGAGAAAATATATGAT 719
QY 231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250
Db 720 GAGGCTGAATCTTCTCTACCAATATTTTAAAGAGACCCCTGCAAAAGATTCCGCTCC 779
QY 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrHisThrAsnLeuPro 270
Db 780 AGT---CTTTCGAGAGATCGGGAGCGTTTGGATATGTTGGCACACATATTTGCCG 836

Qy 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsnLysAsnAla 290
Db 837 CGATTGGAAGCAAGGAATTATACATCCAGTCTTGGACAGACACTGAGAACAGAACTCA 896
Qy 291 -----AlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307
Db 897 TATGTGAAGCAAAAACTTTAGAACTCCGCAAAATTGGAGTTCAACATCTTCAATCC 956
Qy 308 LeuGlnGluArgGluLeuLysHisValSerArgTrpTrpLysAspSerGlySerProGlu 327
Db 957 TTACAAAAGAGGAGGTAGAAAGTCTGGTCAAGATGGTGAAAGAAATCGGGTTTCTGAG 1016
Qy 328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347
Db 1017 ATGACCTTCTGCCGACATCGTCACGTGAATACACTTTGGCTTCCGATTGCGTTTC 1076
Qy 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367
Db 1077 GAGCCTCAACATTTCTGGATTCAAGACTCGGCTTGGCCAAGACGTGCTTATCACGGTT 1136
Qy 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluLeuPheThrAlaThr 387
Db 1137 CTTGACGATATGTACGACACCTTCGGCACAGTAGACGAGCTGAACTTTCACAGCGACA 1196
Qy 388 IleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407
Db 1197 ATGAAGAGATGGGATCCGCTCTCGATAGATTGCCCTTCCAGAAATATATGAAGAGTGTA 1256
Qy 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg 427
Db 1257 ATAGCGGTTTACGACACCGTAATGAATGGCTCGAGAGCGAGAGCGCTCAAGCGCGA 1316
Qy 428 AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu 447
Db 1317 GATACGCTCAATATGCTCGGAAGCTGGAGGCTTATATGATTCTGATATGCAAGAA 1376
Qy 448 AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467
Db 1377 GCAAGGTGATCGCCACTGTTACTGCCCTCTTGATGAGTACTACGAGAATGGGAAA 1436
Qy 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
Db 1437 GTTAGCTGTGTCATCGCATATCCGCATTGCAACCCATTCTGACAAATGGAATCCCTTT 1496
Qy 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507
Db 1497 CCTGATCATATCTCAAGGAAGTTGACTTCCATCAAAAGCTTAACGACTTGGCATGTGCC 1556
Qy 508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu 527
Db 1557 ATCCTTCGATTACGAGGTGATACGGGTGCTACAAAGCGGACAGGGCTCGTGGAAGAA 1616
Qy 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547
Db 1617 GCTTCCTCATATCATGTTATATGAAGCAATCCTGAGTATCAGAGAAATGCTCTTC 1676
Qy 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567
Db 1677 GATCATATCAACGCCATGATCAGTACGTAATCAAAAGATTAAATTGGAACTTCTCAA 1736
Qy 568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp 587
Db 1737 CCAGACATCAATGTTCCCATCTCGCGCGAAGAAACATGCTTTTGACATCGCCAAGAGCTTTC 1796
Qy 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607
Db 1797 CATTAAGGCTTACAAATACCGAGACGGCTTACAGCGTTGCCAACGTTGAAACGAAGAGTTTG 1856
Qy 608 ValMetArgThrValIleGluProValProLeu 618
Db 1857 GTACAGAGAACCTCTCTGAAATCTGTGCTTTG 1889

RESULT 6

US-09-903-012B-19
; Sequence 19, Application US/09903012B
; Patent No. 6569656
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 65696561, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903,012B
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 2018
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6) ..(1889)
; OTHER INFORMATION: pinene synthase
US-09-903-012B-19

Alignment Scores:
Pred. No.: 3,986-288 Length: 2018
Score: 2453.00 Matches: 475
Percent Similarity: 84.63% Conservative: 59
Best Local Similarity: 75.28% Mismatches: 81
Query Match: 75.45% Indels: 16
DB: 4 Gaps: 6

US-10-025-145A-65 (1-618) * US-09-903-012B-19 (1-2018)
Qy 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
Db 6 ATGGCTCTAGTTTCTACCGCACCGTTGCTTCCAATCATGCTGCAATCGTGATC 65
Qy 16 SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArg 35
Db 66 AGTTCTACCATGAGCTTAAAGGCTCTCTAGAACAAATTCACGCTTGAAGATGAGTAGG 125
Qy 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
Db 126 CGAGGAATCTATCACTCTCTCCATCAGCATGAGCTTACCACCGTTGTAAACCGATGAT 185
Qy 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTyrAspAspPheIleGln 75
Db 186 GGTGTACGAAGACGATGGCGATTTCATTCCAACCTCTGGAGCATGATGCATACAG 245
Qy 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
Db 246 TCTTTA---CCAACGGCTTATGAGGAAAAATCGTACCTGAGCGCTGAGAACTGATC 302
Qy 96 GlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly----- 112
Db 303 GGGGAAGTAAAGAAC--ATGTTCAATTCGATGTCTTAGAAGATGAGAGATTATGAGT 359
Qy 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
Db 360 CCGCTCAATGATCTCATTCACGCTTTGGATTGTGCAGACAGCCTTGAACGTTTGGGATC 419
Qy 131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
Db 420 CATAGACATTTCAAAAGATGAGATAAATCGCGCTTGATTATGTTTACAGTATTGGGGC 479
Qy 151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170

```
Db      480 GAAATGCGATCGATCGGAGGAGAGTGTGTACTGATCTGAACCTCACTGCGTTG 539
Qy      171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
Db      540 GGGCTTCGAACCCCTACGACTACCGGATACCCTGCTTTCAGATGTTTCAAGCTTTC 599
Qy      191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGlyGluLeuArg 210
Db      600 AAGGCGCAAAATGGGACAGTTTCTGCTCTGAAATATTTCAGACAGATGAAGAGATCAGA 659
Qy      211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGlyLysValMetAsp 230
Db      660 GCGCTTCTGAATTATTCCGGGCTCCCTCATTCCTTCCAGGGAGAAAATTATGAT 719
Qy      231 GluAlaGluThrPheSerThrIleTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250
Db      720 GAGGCTGAATCTTCTCTACCAATATTAAAGAAGCCCTGCAAAAGATTCGCGTCTCC 779
Qy      251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrHisThrAsnLeuPro 270
Db      780 AGT---CTTCCGAGAGATCGGGGACGTTTGGAAATATGGTTGGCACATATTGCGCG 836
Qy      271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsnLysAsnAla 290
Db      837 CGATTGGAAGCAAGGAATTACATCCAACTCTTGGACAGAGACACTGAGAACACGAAGTCA 896
Qy      291 -----AlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307
Db      897 TATGTGAAGAGCAAAAACCTTTGAACTCGCAAAATTGGAGTTCAACATCTTCAATCC 956
Qy      308 LeuGlnGluArgGluLeuLysHisValSerArgTyrTyrLysAspSerGlySerProGlu 327
Db      957 TTACAAGAAGAGGAGGTAGAAAGTCTGCTCAGATGCTGGAAGAATCGGGTTTCCGTGAG 1016
Qy      328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347
Db      1017 ATGACCTTCTGCGGACATCGTCACTGGAATACTACACTTGGCTTCCGATGCGGTTCC 1076
Qy      348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisIleuIleThrVal 367
Db      1077 GAGCTTCAACATCTTGATTCAGACTCGGCTTGGCCAAAGACGTGCATCTTATCACGCGTT 1136
Qy      368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluPheThrAlaThr 387
Db      1137 CTTCAGCATATGATGACGACACCTTCGGCAGTAGACGAGCTGGAACTTTCACAGCGACA 1196
Qy      388 IleLysArgTyrAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407
Db      1197 ATGAAGAGATGGGATCCGCTCGATGATGCTTCCAGAAATATGAAAGAGTGTAC 1256
Qy      408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnLysArg 427
Db      1257 ATAGCGGTTTACGACACCGTAAATGAATGGCTCGAGAGGCAAGGAGGCTCAAGGCGCA 1316
Qy      428 AspThrLeuAsnTyrAlaArgGlnAlaTyrGluAlaCysPheAspSerTyrMetGlnIle 447
Db      1317 GATACGCTCACATATGCTCGGGAAGCTTGGGAGGCTTATATGATTCGTATATGCAAGAA 1376
Qy      448 AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467
Db      1377 GCAAGGTGGATCGCCACTGGTACCTGCTCTTGTGATGATGACTACGAGAATGGGAAA 1436
Qy      468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
Db      1437 GTTAGCTGTGTCATCGCATATCCGCAATTGCAACCCCAATTCTGACAAATGGAATCCCTTT 1496
Qy      488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507
Db      1497 CCTGATCATATCTCTCAAGGAAGTGACTTCCCATCAAAAGCTTAAAGACTTGGCATGTGCC 1556
Qy      508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu 527
```

```
Db      1557 ATCCTTCGATTACGAGGTGATACCGCGGTGCTACAAAGCGGACAGGGCTCGTGAGAAAGA 1616
Qy      528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluAspAlaLeu 547
Db      1617 GCTTCCTCTATATCATGTTATATGAAAGACAATCTTGAGTATCAAGAGAGATGCTTTC 1676
Qy      548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567
Db      1677 GATCATATCAACGCCCATGATGATGACGTATCAAAAGATTAAATTGGGAACCTTCTCAA 1736
Qy      568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp 587
Db      1737 CCAGACATCAATGTTCCCATCTCGGCGAAGAAACATGCTTTGACATCGCCAGAGCTTTC 1796
Qy      588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607
Db      1797 CATTAAGGCTACAAATACCGAGACGGCTTACAGCGTTGCCCAAGTTGAACGAGAGATTGG 1856
Qy      608 ValMetArgThrValIleGluProValProLeu 618
Db      1857 GTACAGGAACCTCTGTAATCTGTGCTTGG 1889
```

RESULT 7

```
US-09-900-797-19
; Sequence 19, Application US/09900797
; Patent No. 6645762
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 66457621, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/900,797
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 2018
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)...(1889)
; OTHER INFORMATION: pinene synthase
US-09-900-797-19
```

Alignment Scores:

| Pred. No.: | 3.98e-288 | Length: | 2018 |
|------------------------|-----------|---------------|------|
| Score: | 2453.00 | Matches: | 475 |
| Percent Similarity: | 84.63% | Conservative: | 59 |
| Best Local Similarity: | 75.28% | Mismatches: | 81 |
| Query Match: | 75.45% | Indels: | 16 |
| DB: | 4 | Gaps: | 6 |

US-10-025-145A-65 (1-618) x US-09-900-797-19 (1-2018)

```
Qy      1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
Db      6 ATGGCTTAGTTTCTACCGCACCTTGGCTTCCAAATCATGCTTCACAAATCGTTGATC 65
Qy      16 SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArg 35
Db      66 AGTTTACCCATGAGCTTAAAGGCTCTCTAGAACAAATTCAGCTTAGGAATGAGTAGG 125
Qy      36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
```

Db 126 CGAGGAAATCTATCACTCTTCACATCAGCATGAGCTCTACCAACCGTTGTAACCGAT 185
QY 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75
Db 186 GGTGTAAGAAGACGCATGGCGATTCCATTCCAACCTCTGGAGCATGATGCATACAG 245
QY 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
Db 246 TCTTTA---CCAACGGCTTATGAGGAAAAATCGTACCTGAGCGTGTGAGAAACTGATC 302
QY 96 GlyGluValIysAspIleMetPheAsnPhelysSerLeuGluAspGlyGly----- 112
Db 303 GGGGAAGTAAGAAC--ATGTTCAATTGATGTCATTAGAAGATGAGAGTTAATGAGT 359
QY 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
Db 360 CCGCTCAATGATCTCATTCACACGCTTGGATTTGCACACGCTTGAACGTTGGGATC 419
QY 131 AspArgHisPheIysLysGluIleLeuThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
Db 420 CATAGACATTTCAAAGATGAGATAAATCGCGCTGATTATGTTACAGTTATTGGGCG 479
QY 151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170
Db 480 GAAATGCGATCGGATCGGAGGAGAGTGTTGTTACTGATCTGAACCTCAACTCGCGTTG 539
QY 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
Db 540 GGGCTTCGAACCTTACGACTACACGATACCCGGTGTCTTCAGATGTTTCAAAAGCTTTC 599
QY 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGlyGluIleArg 210
Db 600 AAAGGCCAAATGGGCGAGTTTCTGCTCTGAAATATTCAAGACAGATGAAGAGATCAGA 659
QY 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230
Db 660 GGGCTTCTGAATTTATTCGGGCGCTCTTCATTGCCCTTCCAGGGGAGAAATTTATGAT 719
QY 231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250
Db 720 GAGCTGAATCTTCTCTACCAATATTAAAGAAGCCCTGCAAAAGATTCCGGTCTCC 779
QY 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrHisThrAsnLeuPro 270
Db 780 AGT---CTTTCGCGAGAGATCGGGGACGTTTGGAAATATGTTGGCACACATATTGCCG 836
QY 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsnLysAsnAla 290
Db 837 CGATTGGAAGCAAGGAATTACATCAAGTCTTTGGACAGACACTGAGAAACAGAGTCA 896
QY 291 -----AlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307
Db 897 TATGTGAAGACAAAAAATTAGAACTCGCAAAATTGAGTTCAACATCTTCAATCC 956
QY 308 LeuGlnGluArgGluLeuLysHisValSerArgTyrTrpLysAspSerGlySerProGlu 327
Db 957 TTACAAAGAAGAGGAGTAGAAAGTCTGTGCAAGATGTTGAAAGAAATCGGGTTTCTGAG 1016
QY 328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347
Db 1017 ATGACCTTCTGCGCAGCATCGTCACTGGAATACTACACTTTGGCTTCTGCAATGCCGTT 1076
QY 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367
Db 1077 GAGCTCAACATTTCTGATTCAAGCTCGGCTTGGCCAAAGACGTGTCACTTATCACGGTT 1136
QY 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluPheThrAlaThr 387
Db 1137 CTTGACATATGTATGACACACTTGGGACAGTAGACAGAGCTGGAATCTTCAAGCGACA 1196
QY 388 IleLysArgTyrAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407
Db 1197 ATGAAGATGGATCCGCTCGATGATTTGCCCTTCCAGAAATATGAAGAAGAGTGTAC 1256

QY 408 MetMetValTyrHisThrValaGluMetAlaArgValAlaGluLysAlaGlnGlyArg 427
Db 1257 ATAGCGGTTTACGACACCCGTAATGAATGGCTCGAGAGGCGAGAGGAGCTCAAGGCCGA 1316
QY 428 AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu 447
Db 1317 GATACGCTCACATATGCTCGGAGAGCTGGAGGCTTATATGATTGATTGATATGCAAGAA 1376
QY 448 AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467
Db 1377 GCAAGGTGATCGGCACGTGTTACTGCCCTCTTGTGATGAGTACTACGAGAATGGGAAA 1436
QY 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
Db 1437 GTTAGCTGTGTCATCGCATATCCGCATTCGAACCCATTCTGACAAATGACATCCCTTT 1496
QY 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507
Db 1497 CCTGATCATATCTCAAGGAAGTTGACTTCCCATCAAGCTTAAAGCACTTGGCATGTGCC 1556
QY 508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu 527
Db 1557 ATCCTTCATTAACGAGGTGATACGGGTGTCTACAAAGCGGACAGGCGCTGTGAGAGAA 1616
QY 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547
Db 1617 GCTTCTCTATATCATGTTATATGAAGAACAATCCTGAGTATCAGAGAAAGATGCTTTC 1676
QY 548 AsnHisIleAsnPhenMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567
Db 1677 GATCATATCAAGCCATGATGATGACGTAATCAAAAGATTAATGGAACTTCTCAA 1736
QY 568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp 587
Db 1737 CCAGACATCAATGTTCCCATCTCGGCGAAGAAACATGCTTTGACATCGCCAGAGCTTTC 1796
QY 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607
Db 1797 CATTAAGCTACAAATACCAGAGCGCTACAGCGTTGCCAACGTTGAAACGAAGATTGG 1856
QY 608 ValMetArgThrValIleGluProValProLeu 618
Db 1857 GTACGAGAACCTCTCTGAATCTGTGCTTTG 1889

RESULT 8
US-09-360-545-66
; Sequence 66, Application US/09360545
; Patent No. 6429014
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B
; APPLICANT: Bohlmann, Jorg
; APPLICANT: Steele, Christopher L
; APPLICANT: Phillips, Michael A
; TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
; FILE REFERENCE: wsur13885
; CURRENT APPLICATION NUMBER: US/09/360,545
; EARLIER APPLICATION NUMBER: 1999-07-26
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: PCT/US98/14528
; EARLIER FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: Patencin Ver 2.0
; SEQ ID NO 66
; LENGTH: 2186
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (34)..(1923)
US-09-360-545-66

Alignment Scores:

| | | | |
|------------------------|-----------|---------------|------|
| Pred. No.: | 4,75e-265 | length: | 2186 |
| Score: | 2264.00 | Matches: | 435 |
| Percent Similarity: | 80.53% | Conservative: | 78 |
| Best Local Similarity: | 68.29% | Mismatches: | 98 |
| Query Match: | 69.64% | Indels: | 26 |
| DB: | 4 | Gaps: | 9 |

US-10-025-145A-65 (1-618) x US-09-360-545-66 (1-2186)

| | | | |
|----|-----|---|-----|
| QY | 1 | MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- | 15 |
| Db | 34 | ATGGCTCTGGTTCTTCCGCACC-----AAATCCGCTGCACAAATCGTTGATC | 84 |
| QY | 16 | ---SerSerSerHisGluIleLeuValaLeuArgArgThrIleProThrLeuGlyIleCys | 34 |
| Db | 85 | AGGTCTACTCATCATGAGCTCAAGCCTCTGCGCAGAACCATCCCAACTCTTGGAATGTGT | 144 |
| QY | 35 | ArgProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThr | 54 |
| Db | 145 | AGCGAGGGAATCTTTCACACCTTCTGTGACATGAGTTTGACCACCGCTGTATCTGAT | 204 |
| QY | 55 | AspSerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIle | 74 |
| Db | 205 | GATGCTCTACAAAGACGCATAGTGACTATCATTTCCAATCTCTGGACGACGATTCATA | 264 |
| QY | 75 | GlnSerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeu | 94 |
| Db | 265 | CAGTCTCTA---TCAACGCCCTTATGGGAGCCTTCTTACCAGAGACGTGCTGAAGAACTG | 321 |
| QY | 95 | IleGlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly----- | 112 |
| Db | 322 | ATTGGGGAAGTGAAGAG--ATGTTCAATTCAATGCCATCGGAAGATGAGAAATCAATG | 378 |
| QY | 113 | -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGly | 129 |
| Db | 379 | AGTCCCTCAATGATCTTATGAAACGACTTTGGATGCTGATAGCGTTGAACGTTTGGGG | 438 |
| QY | 130 | IleAspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrp | 149 |
| Db | 439 | ATTGATAGACATTTCAAAAAAGAGATMAATCAGCCCTGATTATGTTACAGTATTTGG | 498 |
| QY | 150 | AsnGluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAla | 169 |
| Db | 499 | AACGAAAAAGGTATTGGATGCGGTAGAGATAGCTTTTCTCGATGTCAACTCGACTGCC | 558 |
| QY | 170 | LeuGlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnVal | 189 |
| Db | 559 | TCGGGGTTTCGAACCTCTTCGCCCTACACGGATACAGTGTCTCTCAGAGGTTTGAAGTA | 618 |
| QY | 190 | PheLysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGlyGluIle | 209 |
| Db | 619 | TTTCAAGAACCAAAATGGGCAGTTTGCAATCTCTCTAGTACAAAA--GAGAGAGACATC | 675 |
| QY | 210 | ArgGlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMet | 229 |
| Db | 676 | AGAACCGTTCTGAATTATATCGGGCTTCTTTCATTCCTTCCGCGGAGAAAGTTATG | 735 |
| QY | 230 | AspGluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAla | 249 |
| Db | 736 | GAAGAGCGCTGAATAATTTCTCTTCAAGATATTGAAAGAACCCGTGCAAAAGATCCGCTC | 795 |
| QY | 250 | SerSerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTrpHisThrAsnLeu | 269 |
| Db | 796 | TCGAGT---CTTTCACAAGAATAAGACTACACTTTGGAATATGTTGGCACACAATATAG | 852 |
| QY | 270 | ProArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThr----- | 285 |
| Db | 853 | CCAAGATTGGAAACAAGGAATTACTAGATGATATTGGACATCTCCATCCATGGCTC | 912 |
| QY | 286 | LysAsnLysAsnAla-----AlaGluLysLeuLeuGluLeuAlaLysLeuGlu | 301 |
| Db | 913 | AAGAAGAAAAAGACGCAATATCTGACACGCGAAAAAGCTTTTAGAACTCGCAAAATTGGAG | 972 |

| | | | |
|----|------|--|------|
| QY | 302 | PheAsnIlePheHisSerLeuGlnGluArgGluLeuLysHisValSerArgTrpTrpLys | 321 |
| Db | 973 | TTCAACATCTTTCACTCCCTTCAACAGAGAGTTACAGTATCTCTCCAGATGTTGATA | 1032 |
| QY | 322 | AspSerGlySerProGluMetThrPheCysArgHisArgHisValGluTyrTyrAlaLeu | 341 |
| Db | 1033 | CATTGGGTTTGCTGAACGTACCTTTGGTCGGCATCGTCACGTGGAAATACACACCTG | 1092 |
| QY | 342 | AlaSerCysIleAlaPheGluProGlnHisSerGlyPheArgLeuGlyPheThrLysMet | 361 |
| Db | 1093 | AGCTCTTGCAATGGCACTGAGCCCAACATCTGCATTGAGATTGGCTTGGCCAAAACG | 1152 |
| QY | 362 | SerHisLeuIleThrValLeuAspAspMetTyrAspValPheGlyThrValAspGluLeu | 381 |
| Db | 1153 | TGTCATCTTATCAACGGTTCTGACGATATCTACGACACTTTCGAAACGATGGTGAATC | 1212 |
| QY | 382 | GluLeuPheThrAlaThrIleLysArgTrpAspProSerAlaMetGluCysLeuProGlu | 401 |
| Db | 1213 | GAACTCTTCAACGACGACGAGTTAGAGATGGAAATCCGTCGGAAGAAGAACGCTCCAGAA | 1272 |
| QY | 402 | TyrMetLysGlyValTyrMetMetValTyrHisThrValAsnGluMetAlaArgValAla | 421 |
| Db | 1273 | TATATGAAGAAATCTTACATGGCACCTTACGAAAGCTTAACTGCATGGCGGAGAGCA | 1332 |
| QY | 422 | GluLysAlaGlnGlyArgAspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPhe | 441 |
| Db | 1333 | GAGAAACACAGGCCGAGACACGCTCAATTATGCTAGAAAGCCTTGGGAGTTTATCTT | 1392 |
| QY | 442 | AspSerTyrMetGlnGluAlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGlu | 461 |
| Db | 1393 | GATTGTTATACACAAGAACAAGTGATCGCACGCGTTATCTGCCAATTCTTGAGAGAG | 1452 |
| QY | 462 | TyrLeuGluAsnGlyLysValSerSerAlaHisArgProCysAlaLeuGlnProIleLeu | 481 |
| Db | 1453 | TACTTAGAGAACGCGAAGTTAGCTCTGGTCATCGTGACGCGCATTGACACCCTCCTG | 1512 |
| QY | 482 | ThrLeuAspIleProPheProAspHisIleLeuLysGluValAspPheProSerLysLeu | 501 |
| Db | 1513 | ACATTGGACGTACCGCTTCTGATGACGCTTGAAGGGAATAGATTTTCCATCGAGATTT | 1572 |
| QY | 502 | AsnAspLeuIleCysIleIleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAsp | 521 |
| Db | 1573 | AATGATTTGGCATCTTCTTCTTGACTAAGAGGTGACACACGATGCTTACAGCGCAGAC | 1632 |
| QY | 522 | ArgAlaArgGlyGluGluAlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeu | 541 |
| Db | 1633 | AGGAGCCGAGGAGAAAGCGTCAAGCATATCGTGTTCATGAAAGACAATCCGGATTTA | 1692 |
| QY | 542 | ThrGluGluAspAlaLeuAsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeu | 561 |
| Db | 1693 | ACAGAGGAAGATGCTCTCAATCATATCATATGATCCATGATCAACGACATTAATCAAGAA | 1752 |
| QY | 562 | AsnTrpGluLeuLeuLysProAspAsnSerValProIleThrSerLysLysAlaPhe | 581 |
| Db | 1753 | AATTGGAACTTCTCAAAACCCGATAGCAATATTCGAATGACTGCACGGAACATGCTTAT | 1812 |
| QY | 582 | AspIleSerArgValTrpHisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsn | 601 |
| Db | 1813 | GAGATTAACCAAGCTTTCACCACTTACAAATATAGAGATGGCTTACAGCGTTGCCACT | 1872 |
| QY | 602 | ValGluThrLysSerLeuValMetArgThrValIleGluProValProLeu | 618 |
| Db | 1873 | CAAGAAACGAAAGTTTGGTGAAGAGAACGGTCTTGAACCAAGTGCCTCTT | 1923 |

RESULT 9

US-09-360-545-1
; Sequence 1, Application US/09360545
; Patent No. 6429014
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B
; APPLICANT: Bohmann, Jorg
; APPLICANT: Steele, Christopher L

QY 568 ProaspasnservalProilethrSerlyslyshisAlapheaspilleSerArgvalTrp 587
Db 1797 TCCAACGACATATATTCATGCTGCGCAAGAACATGCTTTGACATACAGAGAGCTCTC 1856
QY 588 HishisglyTyrArgTyrArgAspGlyTyrSerpheAlaasnValGluThrlysserleu 607
Db 1857 CACCATCTCTACATATATTCGAGATGCGCTTAACTGTGCGCAACAGAAACAAAAATTG 1916
QY 608 ValmetArgThrValileGlu 614
Db 1917 GTTATGGAACACTCCTTGAA 1937
RESULT 10
US-09-398-395A-29
; Sequence 29, Application US/09398395A
; Patent No. 6468772
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64687721, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/398,395A
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (69)...(1949)
; OTHER INFORMATION: myrcene synthase
US-09-398-395A-29
Alignment Scores:
Pred. No.: 2.59e-257 Length: 2196
Score: 2200.50 Matches: 427
Percent Similarity: 80.38% Conservative: 77
Best Local Similarity: 68.10% Mismatches: 106
Query Match: 67.69% Indels: 17
DB: 4 Gaps: 7
US-10-025-145A-65 (1-618) x US-09-398-395A-29 (1-2196)
QY 1 MetAlaleuleuSerilethrProleuValSerArgserCysleu----- 15
Db 69 ATGGCTCTGTTTCTATCTCACCGTTGGCTTGAATCTTGCTGCGCAAGTCGTTGATC 128
QY 16 SerSerSerHisGluileLysAlaleuArgThrileProthrleuGlyleCysArg 35
Db 129 AGTTCAATTCAATGAACATTAAGCCTCCCTATAGAACAAATCCCAAATCTTGGAATGCGTAGG 188
QY 36 ProGlyLysSerValAlaHisSerileAsnMetCysleuThrSerValAlaserThrAsp 55
Db 189 CGAGGGAATCTGTCAAGCCTTCATGAGCATCAGTTTGGCCACCGCTGCACCTGATGAT 248
QY 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnleuTrpAspAspPheileGln 75
Db 249 GGTTGACAAAGACGATAGTGTACATTCATTCATATCTGGGACGATGATTCATACAG 308
QY 76 SerleuileSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgleuile 95
Db 309 TCTCTA---TCAACGCCCTTATGGGGAACCTCTTACCAGGAACGCTGAGAGATTAAATT 365

QY 96 GlyGluValLysAspIleMetPheAsnPhelysSerleuGluAspGlyGly----- 112
Db 366 GTGAGAGTAAGAAGATA---TTCATTCATGATGATCCTGATGATGAGATTAATGACT 422
QY 113 -----AsnAspLeuLeuGlnArgleuLeuValAspAspValGluArgleuGlyle 130
Db 423 TCCCTTAATGATCTCATGCAACGCCCTTGATAGTCGATACCGTTGAACGTTGGGATA 482
QY 131 AspArgHisPheLysLysGluileLysThrAlaleuAspTyrValAsnSerTyrTrpAsn 150
Db 483 GCTAGACATTTCAAGAACGAGATTAACATCAGCTCTGGATTATGTTTCCGTTACTGGAG 542
QY 151 GluLysGlyIleGlyCysGlyArgGluSerValThrAspLeuAsnSerThrAlaleu 170
Db 543 GAAACGCGCATTTGATGCGGAGAGACAGTATTGTTACTGATCTCAACTCAACTGCGTTG 602
QY 171 GlyLeuArgThrLeuArgleuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
Db 603 GGGTTTCAACTCTTCGATTCACGGGTACACTGATCTCCAGAGCTTTTAAAGCTTTT 662
QY 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyLyleArg 210
Db 663 CACAGATCAAAATGACAGAGTTGTATGCTCCCGCGT---CAGACAGAGGTGAGATCAGA 719
QY 211 GlyValLeuAsnLeuPheArgAlaserleuValAlapheProGlyGlyLysValMetAsp 230
Db 720 AGCGTTCTTAATTAATATCGGCTTCCCTCATTTGCCCTGCGTGAAGAACTTATGGA 779
QY 231 GluAlaGluThrPheSerThrlySTyrLeuArgGluAlaleuGlnLysileProAlaser 250
Db 780 GAAGCTGAATCTTCTCCACAGATATTTGAAAGAGCTCTTACAAAGATTCCAGTCTCC 839
QY 251 SerileuSerleuGluileArgAspValLeuGluTyrGlyTyrHisThrAsnleuPro 270
Db 840 GCT---CTTTCACAGAGATTAAGTTGTTATGAAATAGCTGCGCACACAAATTTGCCA 896
QY 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLys-----Asn 287
Db 897 AGATTGGAAGCAAGAATTAATACATAGACACACTTGAGAAAGACACCAGTCATGCTCAAT 956
QY 288 LysAsnAlaAlaGluLysleuLeuGluLeuAlaleuLysleuGluPheAsnIlePheHisSer 307
Db 957 AAAATGCTGGGAGAGAGCTTTTGAAGACTTGCAAAATTGAGCTTCATATATTAACTCC 1016
QY 308 LeuGlnGluArgGluLeuLysHisValSerArgTyrTrpLysAspSerGlySerProGlu 327
Db 1017 TTACAACAAAAGAAATTACATATCTTTTGAGATGCTGGAAGAAGATTCGATTCCTTAA 1076
QY 328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaleuAlaserCysileAlaphe 347
Db 1077 TTGACATTTGCTCGGCATCGTCATGTGGAATTTCTACACTTTGGCCTCTTGATTTGCCATT 1136
QY 348 GluProGlnHisSerGlyPheArgleuGlyPheThrLysMetSerHisleuileThrVal 367
Db 1137 GACCCAAACATTTCTGCATTCAGACTAGGCTTCCGCAAAATGTGTCACTTGTACAGATT 1196
QY 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluPheThrAlaThr 387
Db 1197 TTGACGATATTATGACACACTTTTGAACGATTGACGAGCTTGAACCTTTCACATCTGCA 1256
QY 388 IleLysArgTrpAspProSerAlaMetGluCysleuProGluTyrMetLysGlyValTyr 407
Db 1257 ATTAAGAGATGGAATTCATCAGAGATAGAACACCTTCCGAATATATGAATGTGTGTCAC 1316
QY 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg 427
Db 1317 ATGTCGTGTTTGAACGTGAATGAAGTACGACAGAGGCGGAGAAAGACTCAAGGGAGA 1376
QY 428 AspThrLeuAsnTyrAlaArgGlnAlaTyrGluAlaCysPheAspSerTyrMetGlnGlu 447
Db 1377 AACACTCTCAACTATGTTGAAAGGCTTGGAGGCTTATTTGATTCATATATGAAGAA 1436

Qy 448 AlAlYrETrPLeAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467
Db 1437 GCAAAATGGATCTCTAATGTTATCTGCCAATGTTGAAGAGTACCATGAGAATGGAAA 1496
Qy 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
Db 1497 GTGAGCTCTGCATATCGCGTAGCAACATGGCAACCATCTCATCTTGAATGCATGGCTT 1556
Qy 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507
Db 1557 CCTGATTACATCTTGAAGGGAATTGATTTCCATCCAGGTTCAATGATTTGGCATCGTCC 1616
Qy 508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu 527
Db 1617 TTCCTTCGGCTACGAGGTGACACACGCTGCTACAAGCCGATAGGATCGTGGAAGAA 1676
Qy 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547
Db 1677 GCTTCGTATATCATGTTATATGAAGAATCCTGGATCAACCGAAGAAGATGCCCTC 1736
Qy 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567
Db 1737 AATCATATCAATGCCATGTCATGACATGACATTAATGAATTAATGGAACTTCTAAGA 1796
Qy 568 ProAspAsnSerValProIleThrSerLysHisAlaPheAspIleSerArgValTrp 587
Db 1797 TCCACGACAAATATTCCAATGCTGCCAAGAAACATGCTTTGACATTAACAAGAGCTCTC 1856
Qy 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607
Db 1857 CACCATCTCTACATATATCGAGATGCGTTAGTGTGCCAACAAGAAACAAAAAATTG 1916
Qy 608 ValMetArgThrValIleGlu 614
Db 1917 GTTATGGAACAACCTCCTTGAA 1937

RESULT 11
US-09-887-586A-29
; Sequence 29, Application US/09887586A
; Patent No. 6495354
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 64953541, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/887, 586A
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/398, 395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130, 628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150, 262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (69)...(1949)
; OTHER INFORMATION: myrcene synthase
; US-09-887-586A-29

Alignment Scores:
Pred. No.: 2.59e-257 Length: 2196
Score: 2200.50 Matches: 427
Percent Similarity: 80.38% Conservative: 77
Best Local Similarity: 68.10% Mismatches: 106
Query Match: 67.69% Indels: 17

DB: 4 Gaps: 7
US-10-025-145A-65 (1-618) x US-09-887-586A-29 (1-2196)
Qy 1 MetalAlaLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
Db 69 ATGGCTCTGGTTCTATCTCACCGCTTGCTTGAATCTTCCCTGGCAAGTCGTGATC 128
Qy 16 SerSerSerHisGluIleLysAlaLeuArgThrIleProThrLeuGlyIleCysArg 35
Db 129 AGTTCAATTCAATGACATTAAGCCCTCCTATAGAACAAATCCCAATCTTGAATGCGTAGG 188
Qy 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
Db 189 CGAGGAAATCTGTACCGCTTCATGACATCAGTTGGCCACCGCTGACCTGATGAT 248
Qy 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75
Db 249 GGTGTACAAGACCGCATAGGTGACATCAATCAATATCTGGAGCATGATTCATACAG 308
Qy 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
Db 309 TCTCTA--TCAAGCCTTATGGGGAACCTCTTACCAGGAACGTGAGAGATTAAAT 365
Qy 96 GlyGluValLysAspIleMetPheAsnLysSerLeuGluAspGlyIle----- 112
Db 366 GTGAGGTAAAGAGATA--TTCAATTCAATGTACCTGATGATGGAAGATTATGAGT 422
Qy 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
Db 423 TCCTTTAATGATCTCATGCAACGCCCTTGGATAGTCGATAGCGTTGAACGTTGGGATA 482
Qy 131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
Db 483 GCTAGACATTTCAAGAAGAGATTAACATCAGCTCGATTATGTTTCCGTTACTGGAG 542
Qy 151 GluLysGlyIleGlyCysGlyArgGluSerValThrAspLeuAsnSerThrAlaLeu 170
Db 543 GAAACGGCATGTGATGTGGAGACAGATATGTTACTGATCTCAACTCAGCTTG 602
Qy 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
Db 603 GGGTTCCAACTCTTCGATTACACGGGTACACTGATCTCCAGAGGTTTAAAGCTTT 662
Qy 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyIleArg 210
Db 663 CAAGATCAAAATCGACAGTTGTATGCTCCCGGCT--CAGACAGAGGTGAGATCAGA 719
Qy 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230
Db 720 AGCGTTCTTAACCTATATCGGCTTCCCTCATTTCCCTCGTGAGAAAAGTTATGGA 779
Qy 231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250
Db 780 GAAGCTGAATCTTCTCCACAAGATTTGAAGAAGCTCTACAAGAAAGATTCAGTCTCC 839
Qy 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrPheIleThrAsnLeuPro 270
Db 840 GCT---CTTCCACAAGAGATAAGTTGTTATGGAATATGGCTGCAACAATTTGCCA 896
Qy 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLys-----Asn 287
Db 897 AGATTGGAAGCAAGAAATTACATAGACACACTTGAGAAAGACACAGTCATGGCTCAAT 956
Qy 288 LysAsnAlaAlaGluLysLeuLeuGluValAlaLysLeuGluPheAsnIlePheHisSer 307
Db 957 AAAAATGCTGGGAAGAGCTTTGAACCTTGCAAAATTGGAGTTCAATATATTAACTCC 1016
Qy 308 LeuGlnGluArgGluLeuLysHisValSerArgTyrTrpLysAspSerGlySerProGlu 327
Db 1017 TTACAACAAGAAAGGAATTACATATCTTTGAGATGTGGAAAGATCGGATTTGCCATAA 1076
Qy 328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347

Db 1077 TTGACATTGCTCGGCATCGTCATGGAATTCTACACCTTGGCCTCTGTATGGCATT 1136
Qy 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367
Db 1137 GACCCAACAACATCTGCATTCAGACTAGGCTTCGCCAAAATGTGCATCTGTCAAGTT 1196
Qy 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluPheThrAlaThr 387
Db 1197 TTGGACGATATTATTCAGACACTTTTGAACGATTGACGAGCTGAACTCTTCACATCTGCA 1256
Qy 388 IleLysArgTTrpAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407
Db 1257 ATTAAGAGATGGAATTCATCAGAGATAGAACACCTTCAGAAATATATGAATGTGTAC 1316
Qy 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg 427
Db 1317 ATGGTCGTGTTGAACCTGTAATGAAGCTGACACGAGAGGCGGAGAGACTCAAGGGAGA 1376
Qy 428 AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu 447
Db 1377 AACACTCTCAACTATGTTGGAAGGCTTGGAGGCTTATTTGATTCATATATGAAGAA 1436
Qy 448 AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467
Db 1437 GCAAAATGATCTCTAATGGTTATCTGCCAATGTTGAAGAGTACCATGAGATGGGAA 1496
Qy 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
Db 1497 GTGAGCTCTGCATATCGCGTAGCAACATTGCCAACCCATCCTCATTGAAATGCATGGCTT 1556
Qy 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507
Db 1557 CCTGATTACATCTTGAAAGGGAATGATTTTCCATCCAGGTTCAATGATTTGGCATCGTCC 1616
Qy 508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu 527
Db 1617 TTCTCTCGGCTACGAGGTGACACACGCTGTACAAGGCCGATGGGATCGGTGAAGAA 1676
Qy 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547
Db 1677 GCTTCGTATATCATGTTATATGAACAACATCCTGATCAACGAGAAGATGCCCTC 1736
Qy 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567
Db 1737 AATCATATCAATGCCATGGTCAATGACATAATCAAGAATTAAATGGGAATCTTAAGA 1796
Qy 568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTyr 587
Db 1797 TCCAACGACAATATTCCAATGCTGGCCAAAGAAACATGCTTTGACATTAACAAGAGCTTC 1856
Qy 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607
Db 1857 CACCATCTCTACATATATCGAGATGCTTTAGTGTGCCAACAGGAAACAAAAAATTG 1916
Qy 608 ValMetArgThrValIleGlu 614
Db 1917 GTTATGGAACAACCTCCTTGAA 1937

RESULT 12
US-09-895-752-29
; Sequence 29, Application US/09895752
; Patent No. 6559297
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 65592971, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/895,752
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/398,395

; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (69)...(1949)
; OTHER INFORMATION: myrcene synthase
US-09-895-752-29

Alignment Scores:
Pred. No.: 2.59e-257 Length: 2196
Score: 2200.50 Matches: 427
Percent Similarity: 80.38% Conservative: 77
Best Local Similarity: 68.10% Mismatches: 106
Query Match: 67.69% Indels: 17
DB: 4 Gaps: 7

US-10-025-145A-65 (1-618) x US-09-895-752-29 (1-2196)

Qy 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
Db 69 ATGGCTCTGTTCTTCTATCTCACCGTTGGCTTGAAATCTTGCCCTGCCGAAGTCGTGATC 128
Qy 16 SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArg 35
Db 129 AGTTCAATTCATGAACATAAGCCTCCCTATAGAACAAATCCAAATCTTGAAATGCGTAGG 188
Qy 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
Db 189 CGAGGGAATCTGTACGCGCTTCCATGAGCATGATTGGCCACCGCTGCACCTGATGAT 248
Qy 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75
Db 249 GGTGACAAAGACGATAGGTGACTACCATTCCAATATCTGGAGCATGATTCTATACAG 308
Qy 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
Db 309 TCTCTA---TCAACGCCCTTATGGGAAACCTCTTACCAGGAACGTGCTGAGAGATTAA 365
Qy 96 GlyIleValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyIle----- 112
Db 366 GTGAGAGTAAAGAGATA--TTCAATTCAATGTACCTGGATGATGGAAGATTATAGAT 422
Qy 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
Db 423 TCTTTAATGATCTCATGCAACGCCCTTGGATAGTCGATAGCGTTGAACGTTGGGATA 482
Qy 131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
Db 483 GCTAGACATTTCAAGAACGAGATTAACATCAGCTCTGGATTATGTTTCCGTTACTGGAG 542
Qy 151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170
Db 543 GAAACGGCATTTGATGTGGAGAGACAGATATTGTACTGATCTCAACTCAACTGCGTTG 602
Qy 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
Db 603 GGGTTTGAACCTCTTCGATTACACGGGTACACTGTATCTCAGAGGTTTAAAGCTTTT 662
Qy 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyGluIleArg 210
Db 663 CAAGATCAAAATGACAGATTGTATGCTCCCGCGT--CAGACAGAGGGTGAGATCAGA 719

```
Qy 211 G1yValIeuAenLeuPheArgAlaSerIeuValAlaPheProGluGluIysValMetAsp 230
Db 720 AGCGTCTTAACCTATATATCGGCGCTCCCTCATGCTCCCTGCTGAGAAAGTATGAA 779
Qy 231 G1uAlaGluThrPheSerThrIleuArgGluAlaLeuGlnIleProAlaSer 250
Db 780 GAAGCTGAATCTTCTCCACAAGATATTTGAAAAGAGCTTACAAAAGATTCCAGTCTCC 839
Qy 251 SerIleuSerLeuGluIleArgAspValIleuGluTyrGluTyrHisThrAsnLeuPro 270
Db 840 GCT--CTTCAACAAGAGATTAAGTTGTTGATGAAATATGGCTGCACACAATTTGCCA 896
Qy 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGluGlnHisThrLys-----Asn 287
Db 897 AGATTGGAAGCAAGAATATACATAGACACACTTGAGAAGACACACAGTCATGCTCAAT 956
Qy 288 LysAsnAlaAlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307
Db 957 AAAAATGCTGGGAAGAAGCTTTAGAACTTGCAAAATTGAGTTCATATATTAATCTCC 1016
Qy 308 LeuGlnGluArgGluLeuLysHisValSerArgTyrTrpLysAspSerGlySerProGlu 327
Db 1017 TTACAACAAGGAATTAACAATATCTTTGAGATGCTGGAAGAGTCGGATTGCTTAA 1076
Qy 328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347
Db 1077 TTGACATTGCTCGGCATCGTCATGGAATTTCACTTTGGCTCTTGATTTGCCATT 1136
Qy 348 GluProGlnHisSerGlyPheArgLeuGluPheThrLysMetSerHisLeuIleThrVal 367
Db 1137 GACCCAAACATTTGTCATTCAGACTGAGCTTGCACAAATGTGTCTTCTTGCACAGTT 1196
Qy 368 LeuAspAspMetTyrAspValPheGluThrValAspGluLeuGluPheThrAlaThr 387
Db 1197 TTGAGAGATATTACGACACTTTGGAACGATGACGAGCTTGAACCTTCACATCTGCA 1256
Qy 388 IleLysArgTyrAspProSerAlaMetCysLeuProGluTyrMetLysGluValTyr 407
Db 1257 ATTAAGAGATGGAATTCATCAGAGATAGAACACCTTCCAGATATATGAATGTGTAC 1316
Qy 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGluArg 427
Db 1317 ATGGTGTGTTGAAACTGTAATGAATGACACGAGAGCGGAGAACTCAAGGAGAA 1376
Qy 428 AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu 447
Db 1377 AACACTCTCAACTATGTTGAAAGGCTTGGAGGCTTATTTGATTCATATATGAGAGAA 1436
Qy 448 AlaLysTrpIleAlaThrGluTyrLeuProThrPheGluGluTyrLeuGluAsnGluLys 467
Db 1437 GCAAAATGATCTCTAATGTTATCTGCAATGTTGAAGAGTACCATGAGAATGGAAA 1496
Qy 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
Db 1497 GTGAGCTGTCATATCGCGTAGCAACATTGCCATCCTCACTTGAATGCATGCGCTT 1556
Qy 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507
Db 1557 CCTGATTACATCTTGAAGGGAATTTTCCATCCAGGTTCAATGATTTGGCATCGTCC 1616
Qy 508 IleLeuArgLeuArgGluAspThrArgCysTyrLysAlaAspArgAlaArgGluGluGlu 527
Db 1617 TTCTTCGCTACGAGGTGACACACGCTGCTACAAAGCCGATAGGATCGTGTGAAGAA 1676
Qy 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGluLeuThrGluGluAspAlaLeu 547
Db 1677 GCTTCGTATATCATGTTATATGAAGCAATCTGATCAACCGAAGAAAGATGCCCTC 1736
Qy 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567
Db 1737 AATCATATCAATGCATGTCATGACATTAACAAGAAATTAATGGGAATCTTAAGA 1796
Qy 568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTyr 587
```

```
Db 1797 TCCAACGACAATATTTCCAAATGCTGCGCCAGAAACATGCTTTTGACATTAACAAGAGCTCTC 1856
Qy 588 HisIleGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607
Db 1857 CACCATCTCAATATATATGAGATGGCTTAGTGTGCCAACAGGAACAAAAAATTG 1916
Qy 608 ValMetArgThrValIleGlu 614
Db 1917 GTTATGGAACAACCTCCTTGAA 1937

RESULT 13
US-09-903-012B-29
; Sequence 29, Application US/09903012B
; Patent No. 6569656
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. 6569656, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903, 012B
; PRIORITY FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (69)...(1949)
; OTHER INFORMATION: myrcene synthase
; US-09-903-012B-29

Alignment Scores:
Pred. No.: 2,59e-257 Length: 2196
Score: 2200.50 Matches: 427
Percent Similarity: 80.38% Conservative: 77
Best Local Similarity: 68.10% Mismatches: 106
Query Match: 67.69% Indels: 17
DB: 4 Gaps: 7

US-10-025-145A-65 (1-618) x US-09-903-012B-29 (1-2196)
Qy 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
Db 69 ATGGCTCTGCTTCTATCTCACCGCTTGCTTGAATCTTGCGCAAGTGTGATC 128
Qy 16 SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGluLysCysArg 35
Db 129 AGTTCAATTCATGACATTAAGCCCTCCATAGACAAATCCCAATCTTGAATGCGTAGG 188
Qy 36 ProGluLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
Db 189 CGAGGGAATGTGTACGCGCTTCCATGAGCATCAAGTTGGCCACCGCTGCACCTGATGAT 248
Qy 56 SerValGlnArgArgValGluAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75
Db 249 GGTTGACAAAGACGATAGGTAACAATCCATTCATATCTGGAGCGATGATTTCATACAG 308
Qy 76 SerLeuIleSerThrProTyrGluAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
Db 309 TCTCTA--TCAACGCCCTTATGGGAACCTCTTACACGAGAACGTGTCAGAGATTAAAT 365
Qy 96 GlyGluValLysAspIleMetPheAsnPhelySerLeuGluAspGluGly----- 112
```


Db 366 GTGAGCTAAAGAGATA---TTCAATTCATGTACCTGGATGATGGAAGATTAAATGAGT 422
Qy 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGlnArgLeuGlyIle 130
Db 423 TCCTTAATGATCTCATGCAACGCCCTTGGATAGTCGATAGCGTTGAACGTTGGGGATA 482
Qy 131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
Db 483 GCTAGACATTTCAAGAACGAGATTAACATCACTCTGGATTATGTTTCCGTTACTGGGAG 542
Qy 151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170
Db 543 GAAACCGCATTTGATGTGGAGAGACATATTGTTACTGATCTCAACTCAACTGCGTTG 602
Qy 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
Db 603 GGGTTTCGAACCTCTTCGATTACACGGGTACACTGTATCTCCAGAGCTTTAAAGCTTTT 662
Qy 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyLuiLeArg 210
Db 663 CAAGATCAAAATGACAGTTTGTATGCTCCCCGGT---CAGACAGAGGGTGAGATCAGA 719
Qy 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230
Db 720 AGCGTTCTTAATTTATATCGGGCTTCCTCATTCCTTCCCTGGTGAGAAAGTTATGGAA 779
Qy 231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250
Db 780 GAAGCTGAAATCTTCTCCACAGATATTGAAAGAAAGCTCTACAAAAGATTCCAGTCTCC 839
Qy 251 SerIleuSerLeuGluIleArgAspValLeuGluTyrGlyTyrPheIsthAsnLeuPro 270
Db 840 GCT---CTTTCAACAAGATTAAGTTTGTATGGAATATGGCTGGCACACAATTTGCCA 896
Qy 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLys-----Asn 287
Db 897 AGATTGGAAGCAAGAAATTACATAGACACACTTGAGAAAGACACCAGTCATGGCTCAAT 956
Qy 288 LysAsnAlaAlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307
Db 957 AAAAATGCTGGGAAGAAGCTTTTAGAAGCTTGAACAATTTGAGTTGATATATTAATCC 1016
Qy 308 LeuGlnGluArgGluLeuLysHisValSerArgTyrTrpLysAspSerGlySerProGlu 327
Db 1017 TTACAACAAGGAATTACAATATCTTTGAAGATGCTGGAAGAGCTCGAATTTGCCATAA 1076
Qy 328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347
Db 1077 TTGACATTTGCTCGGCATCGTCATGTGAATTCTACACTTTGGCCTCTTGATTTGCCATT 1136
Qy 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367
Db 1137 GACCCAAAACATTTGCATTCAGACTAGCTTGCACAAAATGTGTCAATCTTGTACAGATT 1196
Qy 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluLeuPheThrAlaThr 387
Db 1197 TTGGAGCATATTTCAGACACTTTTGAACGATTGACGAGCTTGAACCTTTCACATCTGCA 1256
Qy 388 IleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407
Db 1257 ATTAAGAGATGGAATTCATCAGAGATGAACACCTTCCGAATATATGAATGTGTGTAC 1316
Qy 408 MetMetValTyrHisIsthValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg 427
Db 1317 ATGGTCGTGTTGAAACTGTAAATGAATGACACGAGAGGCCGAGAGAAGACTCAAGGGAGA 1376
Qy 428 AspThrLeuAsnTyrAlaArgGlnAlaTyrGluAlaCysPheAspSerTyrMetGlnGlu 447
Db 1377 AACACTCTCAACTATGTTGAAAGGCTTGGAGGCTTATTTGATTCATATATGGAAGAA 1436
Qy 448 AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467

Db 1437 GCAAAATGGATCTCTAATGCTTATCTGCCAATGTTTGAAGAGTACCATGAGATGGGAA 1496
Qy 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
Db 1497 GTGAGCTCTGCATATCGCTAGCAACATTTGCAACCCATCTTCACTTTGAATGCATGGCTT 1556
Qy 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507
Db 1557 CCTGATTACATCTTGAAGGAATTGATTTTCCATCCAGGTTCAATGATTGGCATCGTCC 1616
Qy 508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu 527
Db 1617 TTCCTTCGGCTACGAGGTGACACGCTGCTACAAAGGCCGATAGGGATCGTGTGAAGAA 1676
Qy 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547
Db 1677 GCTTCGTATATCATGTTATATGAACAATCCTGATCAACCGAAGAGATGCCCTC 1736
Qy 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567
Db 1737 AATCATATCAATGCCATGCTCATGACATTAATCAAGAATTAAATTGGAACTTCTAGA 1796
Qy 568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp 587
Db 1797 TTCAACGACAAATATTCCAATGCTGGCCCAAGAAACATGCTTTTGACATAACAAGAGCTTC 1856
Qy 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607
Db 1857 CACCAATCTCTACATATATCGAGTGGCTTTAGTGTGCCAACAAGAAACAAAAAATTG 1916
Qy 608 ValMetArgThrValIleGlu 614
Db 1917 GTTATGGAACACTCCTTGAA 1937

RESULT 14

US-09-900-797-29
; Sequence 29, Application US/09900797
; Patent No. 6645762
; GENERAL INFORMATION:
; APPLICANT: Chappel, Joseph
; APPLICANT: No. 66457621, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/900,797
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (69)...(1949)
; OTHER INFORMATION: myrcene synthase
; US-09-900-797-29

Alignment Scores:
Pred. No.: 2.59e-257 length: 2196
Score: 2200.50 Matches: 427
Percent Similarity: 80.38% Conservative: 77
Best Local Similarity: 68.10% Mismatches: 106
Query Match: 67.69% Indels: 17
DB: 4 Gaps: 7

US-10-025-145A-65 (1-618) x US-09-900-797-29 (1-2196)

```
OY      1 MetAlaleuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
DB      69 ATGGCTCTGGTTTCTATCTCACCCGTTGGCTTCAAATCTTGCCCTGCCGAAGCTGTTGATC 128
OY      16 SerSerSerHisGluIleLysAlaLeuArgThrIleProThrLeuGluIleCysArg 35
DB      129 AGTTCAATTGATGAACATTAAGCCCTCCCTATGAAACAATCCCAATCTTGGAAATGCGTAGG 188
OY      36 ProGluLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
DB      189 CGAGGAAATCTGTCAAGCCTTCCATGAGCATGTTGGCCACCGCTGCACCTGATGAT 248
OY      56 SerValGlnArgArgValGluAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75
DB      249 GGTGTACAAGAAGCATAGTACTACCATCCAAATATCTGGAGACGATTTTCATACAG 308
OY      76 SerLeuIleSerThrProTyrGluAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
DB      309 TCTCTA---TCAACGCCCTTATGGGGAACCCCTCTTACCAGGAACGTGCTGAGATTATTT 365
OY      96 GlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly----- 112
DB      366 GTGGAGGTAAAGAGATA--TTCAATTCAATGTAACCTGGATGATGAGATTAAATGAGT 422
OY      113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
DB      423 TCCTTTAATGATCTCATGCAACGCCCTTGGATGATGATAGCGTTGAACGTTTGGGGATA 482
OY      131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
DB      483 GCTAGACATTTCAAGAAGAGATTAACATCAGCTCTGATTATGTTTCCGTTACTGGAG 542
OY      151 GluLysGlyIleGlyCysGlyArgGluSerValIleThrAspLeuAsnSerThrAlaLeu 170
DB      543 GAAAACGGCATTTGGATGTGGAGAGACAGATTGTTACTGATCTCACTCAACTGCGCTTG 602
OY      171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
DB      603 GGGTTTCCAACTCTTCGATTACACGGGTACACTGTATCTCCAGAGGTTTAAAGCTTTT 662
OY      191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGluIleArg 210
DB      663 CAAGATCAAAAATGGACAGTTGTATGCTCCCGCGGT--CAGACAGAGGGTGAGATCAGA 719
OY      211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGluGluLysValMetAsp 230
DB      720 AGCGTTCTTAATCTATATCGGGCTTCCCTCATGCTCCCTGCTGTAAGAACTTATGAA 779
OY      231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250
DB      780 GAAGCTGAATCTTCTCCACAGATATTGAAAGAAAGCTCTACAAAGATTTCCAGTCTCC 839
OY      251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrPheIleThrAsnLeuPro 270
DB      840 GCT---CTTCAACAAGAGATAAAGTTGTATGGAATATGCTGGCAGACAATTTGCCA 896
OY      271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLys-----Asn 287
DB      897 AGATTGGAAAGCAAGAAATTACATAGACACACTTGAAGAAAGACACAGTGGCTCAAT 956
OY      288 LysAsnAlaAlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307
DB      957 AAAAATGCTGGGAAGAGCTTTTGAACCTTGCAAAATTTGAGATTCAATATATTAACTCC 1016
OY      308 LeuGlnGluArgGluLeuLysHisValSerArgTrpTrpLysAspSerGlySerProGlu 327
DB      1017 TTACAACAAAGAAATTACATATCTTTTGAAGATGTTGAAAGAGTCGATTTGCCCTAAA 1076
OY      328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347
DB      1077 TTGACATTTGCTCGGCATCGTCATGTGAATTCTACACTTTGGCCTCTTGTATTGCCATT 1136
```

```
OY      348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367
DB      1137 GACCCAAAACATTCGCATTTCAGACTAGGCTTCCCAAAATGTGTCTTGTTCACAGTT 1196
OY      368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluPheThrAlaThr 387
DB      1197 TTGACAGATATTACAGACACTTTTGAACGATTGACGAGCTTGAATCTTCACATCTGCA 1256
OY      388 IleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyrMetLysGluValTyr 407
DB      1257 ATTAAGAGATGAATTCATCAGAGATGAAACACCTTCCAGATATGAAATGTGTGAC 1316
OY      408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg 427
DB      1317 ATGCTCGTGTGAAACTGTAAATGAACTGACACAGAGAGCGGAGAAAGACTCAAGGAGA 1376
OY      428 AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu 447
DB      1377 AACACTCTCAACTATGTTCCAAAGGCTTGGAGGCTTATTTGATTATATGGAAGAA 1436
OY      448 AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467
DB      1437 GCAAAATGGAATCTTAATGTTATGTTCCCAATGTTGAAGAGTACATGAAATGGGAAA 1496
OY      468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
DB      1497 GTGAGCTGTGATATCGCGTAGCAACATTTGCAACCATCTCACTTGAATGCATGCTT 1556
OY      488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507
DB      1557 CCTGATTACATCTTGAAGGGAATGATTTTCCATCCAGGTTCAATGATTTGGCATGCTCC 1616
OY      508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGlu 527
DB      1617 TTCTTGGCTTAGAGGTGACACAGCTGCTCAAGGCCGATAGGGATCGTGGAAGAA 1676
OY      528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547
DB      1677 GCTTGTGATATCATGATTATATGAAGACAATCTGTGATCAACCGAAGAGATGCCCTC 1736
OY      548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567
DB      1737 AATCATATCAATGCCATGTCAATGACATAATCAAGAATTAATGGGAATTTCTAAGA 1796
OY      568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp 587
DB      1797 TCCAACGACAAATATCCAAATGCTGGCCAAGAAACATGCTTTGACATTAACAAGACTCTC 1856
OY      588 HisIleGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607
DB      1857 CACCATCTCTATATATATGAGATGGCTTTAGTGTGCCAACAAGAAACAAAATTTG 1916
OY      608 ValMetArgThrValIleGlu 614
DB      1917 GTTATGAAACACTCCTTGA 1937
```

RESULT 15

```
US-09-360-545-31
; Sequence 31, Application US/09360545
; Patent No. 6429014
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B
; APPLICANT: Bohlmann, Jorg
; APPLICANT: Steele, Christopher L
; APPLICANT: Phillips, Michael A
; TITLE OF INVENTION: MONOTERPENE SYNTHASES FROM GRAND FIR (ABIES GRANDIS)
; FILE REFERENCE: wau13885
; CURRENT APPLICATION NUMBER: US/09/360, 545
; CURRENT FILING DATE: 1999-07-26
; EARLIER APPLICATION NUMBER: 60/052, 249
; EARLIER FILING DATE: 1997-11-07
; EARLIER APPLICATION NUMBER: PCT/US98/14528
```


Tue Jul 27 08:32:48 2004

us-10-025-145a-65.rni

Qy 608 ValMeCArgThrValIleGlu 614
Db 1905 GTATGGAAACACTCCTTGAA 1925

Search completed: July 26, 2004, 20:38:40
Job time : 180 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 26, 2004, 19:38:30 ; Search time 684 Seconds
(without alignments)
4416.621 Million cell updates/sec

Title: US-10-025-145A-65
Perfect score: 3251
Sequence: 1 MALLSTPLVSRSLSSSHE.....FANVETKSLVMRTVIEPVPL 618

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delep 6.0 , Delext 7.0

Searched: 3216467 seqs, 2444149694 residues

Total number of hits satisfying chosen parameters: 6432934

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame_plus_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO.spool_p/US10025145/runat_23072004_092625_23002/app_query.fasta_1.775
-DB=Published_Applications_NA-QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=biosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10025145_@CCN_1_1_723_@runat_23072004_092625_23002
-NCPUL=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA.*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
|------------|-------|-------------|--------|-------|-------------|

| | | | | | | |
|----|--------|-------|------|----|-------------------|-------------------|
| 1 | 3251 | 100.0 | 2013 | 15 | US-10-025-145A-64 | Sequence 64, Appl |
| 2 | 2453 | 75.5 | 2018 | 9 | US-09-887-586A-19 | Sequence 19, Appl |
| 3 | 2453 | 75.5 | 2018 | 9 | US-09-903-012-19 | Sequence 19, Appl |
| 4 | 2453 | 75.5 | 2018 | 10 | US-09-900-797-19 | Sequence 19, Appl |
| 5 | 2453 | 75.5 | 2018 | 13 | US-09-893-820-19 | Sequence 19, Appl |
| 6 | 2453 | 75.5 | 2018 | 14 | US-10-041-007-21 | Sequence 21, Appl |
| 7 | 2453 | 75.5 | 2018 | 15 | US-10-025-145A-3 | Sequence 3, Appl |
| 8 | 2264 | 69.6 | 2186 | 15 | US-10-025-145A-66 | Sequence 66, Appl |
| 9 | 2200.5 | 67.7 | 2196 | 9 | US-09-887-586A-29 | Sequence 29, Appl |
| 10 | 2200.5 | 67.7 | 2196 | 9 | US-09-903-012-29 | Sequence 29, Appl |
| 11 | 2200.5 | 67.7 | 2196 | 10 | US-09-900-797-29 | Sequence 29, Appl |
| 12 | 2200.5 | 67.7 | 2196 | 13 | US-09-893-820-29 | Sequence 29, Appl |
| 13 | 2200.5 | 67.7 | 2196 | 14 | US-10-041-007-25 | Sequence 25, Appl |
| 14 | 2200.5 | 67.7 | 2196 | 15 | US-10-025-145A-1 | Sequence 1, Appl |
| 15 | 2197.5 | 67.6 | 2205 | 15 | US-10-025-145A-31 | Sequence 31, Appl |
| 16 | 2137 | 65.7 | 1890 | 15 | US-10-025-145A-77 | Sequence 27, Appl |
| 17 | 2084.5 | 64.1 | 2429 | 14 | US-10-041-007-27 | Sequence 27, Appl |
| 18 | 2084.5 | 64.1 | 2429 | 15 | US-10-025-145A-68 | Sequence 68, Appl |
| 19 | 2031.5 | 62.5 | 2089 | 9 | US-09-887-586A-57 | Sequence 57, Appl |
| 20 | 2031.5 | 62.5 | 2089 | 9 | US-09-903-012-57 | Sequence 57, Appl |
| 21 | 2031.5 | 62.5 | 2089 | 10 | US-09-900-797-57 | Sequence 57, Appl |
| 22 | 2031.5 | 62.5 | 2089 | 13 | US-09-893-820-57 | Sequence 57, Appl |
| 23 | 2031.5 | 62.5 | 2089 | 14 | US-10-041-007-23 | Sequence 23, Appl |
| 24 | 2031.5 | 62.5 | 2089 | 15 | US-10-025-145A-5 | Sequence 5, Appl |
| 25 | 1295.5 | 39.8 | 1865 | 9 | US-09-887-586A-47 | Sequence 47, Appl |
| 26 | 1295.5 | 39.8 | 1865 | 9 | US-09-903-012-47 | Sequence 47, Appl |
| 27 | 1295.5 | 39.8 | 1865 | 10 | US-09-900-797-47 | Sequence 47, Appl |
| 28 | 1295.5 | 39.8 | 1865 | 13 | US-09-893-820-47 | Sequence 47, Appl |
| 29 | 1295.5 | 39.8 | 1865 | 14 | US-10-041-007-17 | Sequence 17, Appl |
| 30 | 1250.5 | 38.5 | 1967 | 15 | US-10-025-145A-17 | Sequence 17, Appl |
| 31 | 1240.5 | 38.2 | 2700 | 9 | US-09-887-586A-43 | Sequence 43, Appl |
| 32 | 1240.5 | 38.2 | 2700 | 9 | US-09-903-012-43 | Sequence 43, Appl |
| 33 | 1240.5 | 38.2 | 2700 | 10 | US-09-900-797-43 | Sequence 43, Appl |
| 34 | 1240.5 | 38.2 | 2700 | 12 | US-10-041-018-363 | Sequence 363, App |
| 35 | 1240.5 | 38.2 | 2700 | 13 | US-09-893-820-43 | Sequence 43, Appl |
| 36 | 1231 | 37.9 | 1785 | 9 | US-09-887-586A-49 | Sequence 49, Appl |
| 37 | 1231 | 37.9 | 1785 | 9 | US-09-903-012-49 | Sequence 49, Appl |
| 38 | 1231 | 37.9 | 1785 | 10 | US-09-900-797-49 | Sequence 49, Appl |
| 39 | 1231 | 37.9 | 1785 | 13 | US-09-893-820-49 | Sequence 49, Appl |
| 40 | 1231 | 37.9 | 1785 | 14 | US-10-041-007-19 | Sequence 19, Appl |
| 41 | 1187 | 36.5 | 2424 | 9 | US-09-887-586A-45 | Sequence 45, Appl |
| 42 | 1187 | 36.5 | 2424 | 9 | US-09-903-012-45 | Sequence 45, Appl |
| 43 | 1187 | 36.5 | 2424 | 10 | US-09-900-797-45 | Sequence 45, Appl |
| 44 | 1187 | 36.5 | 2424 | 13 | US-09-893-820-45 | Sequence 45, Appl |
| 45 | 1187 | 36.5 | 2424 | 14 | US-10-041-007-14 | Sequence 14, Appl |

ALIGNMENTS

RESULT 1
US-10-025-145A-64
; Sequence 64, Application US/10025145A
; Publication No. US20030175861A1
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B.
; APPLICANT: Bohlmann, Joerg
; APPLICANT: Steele, Christopher L.
; APPLICANT: Phillips, Michael A.
; TITLE OF INVENTION: Monoterpene Synthases from Grand Fir (Abies Grandis)
; FILE REFERENCE: WSR118414
; CURRENT APPLICATION NUMBER: US/10/025,145A
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 09/360,545
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: PCT/US98/14528
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: US 60/052,249
; PRIOR FILING DATE: 1997-07-11
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 2013


```

; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20020094556A11, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/887,586A
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 2018
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)...(1889)
; OTHER INFORMATION: pinene synthase
; US-09-887-586A-19

Alignment Scores:
Pred. No.:      8.17e-279      Length:      2018
Score:          2453.00        Matches:      475
Percent Similarity: 84.63%      Conservative: 59
Best Local Similarity: 75.28%      Mismatches:  81
Query Match:    75.45%          Indels:      16
DB:              9              Gaps:        6

US-10-025-145A-65 (1-618) x US-09-887-586A-19 (1-2018)
QY      1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
Db      6 ATGGCTCTAGTTTCTACCGCACCGTGGCTTCCAATCATGCGTGCACAAATCGTTGATC 65
QY      16 SerSerSerHisGluIleLysAlaLeuArgThrIleProThrLeuGlyIleCysArg 35
Db      66 AGTTCACCATGAGCTTAAGGCTCTCTGAACAATTCACGCTTGAAGAATGAGTAGG 125
QY      36 ProGlySerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
Db      126 CGAGGGAATCTATCACTCCTTCATCATGAGCTTACCACCGCTTGTAAACGATGAT 185
QY      56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTyrAspAspAspPheIleGln 75
Db      186 GGTGTACGAAGACCGCATGGCGGATTTCCAACTCTGGGACGATGATCATACAG 245
QY      76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
Db      246 TCTTTA---CCAAACGGCTTATGAGAAATAATCGTACCTGAGCGTGTGAGAAACTGATC 302
QY      96 GlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly----- 112
Db      303 GGGGAAGTAAAGAAC--ATGTTCAATTCGATGTCATTAGAAGATGAGAGTTAATGAGT 359
QY      113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
Db      360 CCGCTCATGATCTCATTCACGCGCTTGGATTTGCGACAGCCTTGAACGTTTGGGATC 419
QY      131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
Db      420 CATAGACATTTTCAAGAATGAGATAAATCGCGCTTGATTTATGTTACAGATTATGGGCG 479
QY      151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170
Db      480 GAAATATGGCATCGGATCGGGAGGGAGAGTGTGTTACTGATCTGAACCTCAACTGCGTTG 539
```

```

QY      171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
Db      540 GGGCTTGAACCCCTACGACTACAGGATACCCGGTGTCTTCAAGTCTTTCAAAGCTTTC 599
QY      191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyIleArg 210
Db      600 AAAGGCCAAAATGGGACAGTTTCTCGCTCTGAAATATATTACAGACAGATGAAGATCAGA 659
QY      211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230
Db      660 GGGCTTGAATTATTCCGGGCTTCCCTCATTTGCCCTTCCAGGGAGAAAATTATGAT 719
QY      231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250
Db      720 GAGGCTGAATCTTCTACCAATATTTAAAGAACCCCTGCAAAAGATTCCGGTCTCC 779
QY      251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrPheIsthrAsnLeuPro 270
Db      780 AGT---CTTTCGCGAGAGATCGGGACGTTTGGATATAGTTGGCACACATATTGCCG 836
QY      271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsnLysAsnAla 290
Db      837 CGATTGGAACGAAGAATTACATCCAGTCTTTGGACAGACACTGAGAACAACGAAGTCA 896
QY      291 -----AlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307
Db      897 TATGTGAAGACCAAAAACCTTTAGAACTCCGAAAATTGGAGTTCAACATCTTCAATCC 956
QY      308 LeuGlnGluArgGluLeuLysHisValSerArgTyrTrpLysAspSerGlySerProGlu 327
Db      957 TTACAAAGAGGGAGATTAGAAAGTGTGTCAGATGTGTGAAGAAATCGGGTTTCTCTGAG 1016
QY      328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347
Db      1017 ATGACCTTTCGCCGACATCGTACAGTGAATACTACACTTTGGCTTCCTGCAATGCGTTC 1076
QY      348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367
Db      1077 GAGCCTCAACATTTCTGATTCAAGCTCGGCTTGGCCAAGACGTGCATCTTATCACGCTT 1136
QY      368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluPheThrAlaThr 387
Db      1137 CTTGACGATATGTAGACACACCTTCGACAGAGTACAGACGAGTCTTACACAGCACA 1196
QY      388 IleLysArgTyrAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407
Db      1197 ATGAAGACATGGGATCCGCTCGATGATGCTTCCAGATATATGAAGAGAGTGTAC 1256
QY      408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnIleArg 427
Db      1257 ATAGCGGTTTACGACACCGTTAAATGAATGGCTCGAGAGGCGAGAGGCTCAAGGCCGA 1316
QY      428 AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu 447
Db      1317 GATACGCTCACATATGCTCGGAGAGCTTGGGAGGCTTATATGATGATTCGATATGCAAGAA 1376
QY      448 AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467
Db      1377 GCAAGGTGATCGCCACTGTGTTACCTCCCTCTTGATGAGTACTACGAGAATGGGAAA 1436
QY      468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
Db      1437 GTTAGCTGTGTCATCGCATATCCGCAATTGCAACCATTTCTGACAAATGACATCCCTTT 1496
QY      488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507
Db      1497 CCGATCATATCTCAAGGAAGTTGACTTCCATCAAAAGCTTAAAGACTTGGCATGTGCC 1556
QY      508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu 527
Db      1557 ATCCTTGATTTACGAGGTGATACGGGTGTCTACAAGGCGGACAGGGCTCGTGAAGAGAA 1616
QY      528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547
```

Db 1617 GCTTCCTATATCATGTATATGAAGACAATCCTGAGATATCAGAGGAGATGCTCTC 1676
Qy 548 AsnHisIleasnPhemetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLeuLys 567
Db 1677 GATCATATCAACGCCCATGATCAGTACGCTAATCAAGGATTAAATTGGGAACCTCTCAAA 1736
Qy 568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAsnIleSerArgValTrp 587
Db 1737 CCAGACATCAATGTTCCCATCTCGGCGAAGAAACATGCTTTGACATCGCCAGAGCTTTC 1796
Qy 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607
Db 1797 CATTAACGCTAACAAATACCGAGACGGCTAACAGCGTTGCCAACGTTGAAACGAAGATTGG 1856
Qy 608 ValMetArgThrValIleGluProValProLeu 618
Db 1857 GTCACGAGAACCTCCTTGAATCTGTGCTTTG 1889

RESULT 3

US-09-903-012-19
; Sequence 19, Application US/09903012
; Patent No. US20020094557A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20020094557A1, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903,012
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for windows Version 3.0
; SEQ ID NO 19
; LENGTH: 2018
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)...(1889)
; OTHER INFORMATION: pinene synthase
US-09-903-012-19

Alignment Scores:
Pred. No.: 8.17e-279 Length: 2018
Score: 2453.00 Matches: 475
Percent Similarity: 84.63% Conservative: 59
Best Local Similarity: 75.28% Mismatches: 81
Query Match: 75.45% Indels: 16
DB: 9 Gaps: 6

US-10-025-145A-65 (1-618) x US-09-903-012-19 (1-2018)

Qy 1 MetAlaIleuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
Db 6 ATGGCTCTAGTTTCTTACCGCACCGTGGCTTCCAATCATGCGTGCACAAATCGTTGATC 65
Qy 16 SerSerSerHisGluIleLysAlaLeuArgThrIleProThrLeuGlyIleCysArg 35
Db 66 AGTCTTACCATGAGCTTAAGGCTCTCTTGAACAATTCACGCTTGAAGATGAGTAGG 125
Qy 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
Db 126 CGAGGGAAATCTATCACTCCTTCATCAGCATGAGCTTACCAACCGTTGTAAACGATGAT 185

Qy 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75
Db 186 GGTGTACGAAGACGCATGGGGCATTTCCATTCCACCTCTGGAGCATGATGTCATACAG 245
Qy 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
Db 246 TCTTTA---CCAACGGCTTATAGGAAAAATCGTACCTGGAGCGTCTGAGAAACTGATC 302
Qy 96 GlyGluValLysAspIleMetPheAsnPhelysSerLeuGluAspGlyGly----- 112
Db 303 GGGGAAGTAAAGAAC--ATGTTCAATTGATGTCATTAGAGATGAGAGTTAATGAGT 359
Qy 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
Db 360 CCGCTCAATGATCTCATTCACGCTTTGGATTGTCCAGACGCTTGAACGTTGGGATC 419
Qy 131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
Db 420 CATAGCATTTCAAGATGAGATAAATCGGCGCTGATTAATTACAGTTATGGGGC 479
Qy 151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170
Db 480 GAAATGSCATCGGATCGGGAGGAGAGAGTGTTGTTACTGATCTGAACCTCACTCGCTTG 539
Qy 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
Db 540 GGGCTTCGAACCTACGACTACGAGTACCAGGAGTGTTCAGATGTTTCAAGCTTTC 599
Qy 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyGluIleArg 210
Db 600 AAAGGCCAAATGGGAGTTTCTCTGTAATAATATTCAGACAGATGAAGAGATCAGA 659
Qy 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230
Db 660 GGGCTTGAATTATTCCGGGCTCCCTCATTCCTTCCAGGGGAGAAATATGATGAT 719
Qy 231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250
Db 720 GAGGCTGAATCTTCTCTACCAATATTTAAAGAGCCCTGCAGAAAGATTCCGCTCC 779
Qy 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrPheIstThrAsnLeuPro 270
Db 780 AGT---CTTCCGAGAGATCGGGAGCGTTTGGATATGGTTGGCACACATATTGGCCG 836
Qy 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsnLysAsnAla 290
Db 837 CGATTGGAAGCAAGGAATTACCAAGTCTTTGGACAGAGACACTGAGAACACGAAGTCA 896
Qy 291 -----AlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307
Db 897 TATGTGAAGAGCAAAAACTTTTGAACCTCGCAAAATTTGAGTTCAACATCTTCAATCC 956
Qy 308 LeuGlnGluArgGluLeuLysHisValSerArgTyrTrpLysAspSerGlySerProGlu 327
Db 957 TTACAAGAAGAGGAGTTAGAAGTCTGTCAGATGTGGAAGAATCGGGTTTCTCTGAG 1016
Qy 328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347
Db 1017 ATGACTTCTGCCGACATCGTCACTGGAATACTACACTTGCGCTTCCGATGCGTTC 1076
Qy 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367
Db 1077 GAGCTTCAACATTCTGATTACAGACTCGGCTTGCCAGAGCGTGTCACTTATCACGGTT 1136
Qy 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluLeuPheThrAlaThr 387
Db 1137 CTTGAGATATGTACGACACTTGGCACAGTAGACGAGCTGAACTCTTACACAGCGACA 1196
Qy 388 IleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407
Db 1197 ATGAAGAGATGGGATCCGCTCGATATGATTGCCCTTCCAGAAATATATGAAGAGTGTAC 1256


```

Oy 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg 427
Db 1257 ATAGCGGTTTACGACACCCGTAATGAATGGCTCGAGAGCAGAGAGGCTCAAGGCCGA 1316
Oy 428 AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnIu 447
Db 1317 GATACGCTCACATATAGCTCGGGAAGCTTGGAGGCTTATATGATTCGTATATGCAAGAA 1376
Oy 448 AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGlyTyrLeuGluAsnGlyLys 467
Db 1377 GCAAGGTGATCGCCACTGGTTACCTGCCCTCTTGATGAGTACTACGAGATGGGAA 1436
Oy 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
Db 1437 GTTAGCTGTGTGCATCGCATATCCGCATTGCAACCCATTCTGACAAATGCACATCCCCTTT 1496
Oy 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507
Db 1497 CCTGATCATATCCTCAAGGAAGTTGACTTCCCATCAAGCTTAAAGCACTTGCGATGTGCC 1556
Oy 508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGly 527
Db 1557 ATCCTTCGATTACGAGGTGATACGGGTGCTACAAAGCGGACGAGGCTCGTGAGAAGAA 1616
Oy 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547
Db 1617 GCTTCCTCTATATCATGTTATATGAAGAACAATCCTGGAGTATCAGAGGAAGATGCTCTC 1676
Oy 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLeuLys 567
Db 1677 GATCATATCAACGCCCATGATGATGACGTAATCAAAAGGATTAATTGGGAATCTCTCAA 1736
Oy 568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp 587
Db 1737 CCAGACATCAATGTTCCCATCTCGGCGAAGAAACATGCTTTGACATCGCCAGAGCTTTC 1796
Oy 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607
Db 1797 CATTAACGGCTACAAATACCGAGACGGCTTACAGCGTTGCCAAAGTTGAAACGAAGAGTTTG 1856
Oy 608 ValMetArgThrValIleGluProValProLeu 618
Db 1857 GTCACGAGAACCTCCTGTAATCTGTGCTTTTG 1889

RESULT 4
US-09-900-797-19
; Sequence 19, Application US/09900797
; Publication No. US20030087406A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: NO. US20030087406A1, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/900,797
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 2018
; TYPE: DNA
; ORGANISM: Adies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)...(1889)
; OTHER INFORMATION: pinene synthase

```

US-09-900-797-19

Alignment Scores:

| Pred. No.: | 8.176-279 | Length: | 2018 |
|------------------------|-----------|---------------|------|
| Score: | 2453/100 | Matches: | 475 |
| Percent Similarity: | 84.63% | Conservative: | 59 |
| Best Local Similarity: | 75.28% | Mismatches: | 81 |
| Query Match: | 75.43% | Gaps: | 16 |
| DB: | 10 | | 6 |

US-10-025-145A-65 (1-618) x US-09-900-797-19 (1-2018)

```

Qy      1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
Db      6 ATGGCTCTAGTTTCTACCGCACCGCTTGCTTCCAATCATGCTCGACAAATCGTTGATC 65
Qy      16 SerSerHisGluIleLeuValAlaLeuArgArgThrIleProThrLeuGluIleCysArg 35
Db      66 AGTTCTTACCCTAGTACGCTTAAAGGCTCTCTTGAACAATTCCAGCTCTAGGAATGAGTAGG 125
Qy      36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
Db      126 CGAGGGAATCTATACCTCCCTTCCATCAGCATGAGCTCTACCAACCGTTGTAAACGATGAT 185
Qy      56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75
Db      186 GGTGTACGAAGACGCGATGGCGATTCCATTCCAACCTCTGGAGACGATGATCATACAG 245
Qy      76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
Db      246 TCTTTA---CCAACGGCTTATGAGAAATAATCGTACTGGAGCGTGTGAAGAACTGATC 302
Qy      96 GlyGluValLysAspIleMetPheAsnPhelySerLeuGluAspGlyIle----- 112
Db      303 GGGGAAGTAAGAAC--ATGTTCAATTCCATGTCATTAGAAGATGGAGAGTTAATGAGT 359
Qy      113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
Db      360 CCGCTCAATGATCTCATTCACACGCTTTGGATTGTGCACAGCCCTGAACGTTTGGGGATC 419
Qy      131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
Db      420 CATGACATTTCAAGATGAGATTAATCGCGCTTGATTATGTTTACAGTTATTGGGGC 479
Qy      151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170
Db      480 GAATATGCGATCGGATGCGGAGGAGAGTGTGTACTGATCTGAACCTCACTGCGGTG 539
Qy      171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
Db      540 GGGCTTCGAACCTACGACTACACGGATACCCGGTGCTTCAGATGTTTCAAAAGCTTTC 599
Qy      191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyLeuLeuArg 210
Db      600 AAAAGGCCAAATGGCGAGTTTCTGCTCTGAAATAATTCAAGACAGATGAAGATCAGA 659
Qy      211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230
Db      660 GGCCTTCTGAATTTATTCGGGCTCCCTCATTTGCCCTTCCAGGGGAGAAATTATGGAT 719
Qy      231 GluAlaGluThrPheSerThrTyrTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250
Db      720 GAGGCTGAATCTTCTCTACCAATAATTAAAGAAGCCCTGCAAAAGATTCCGGTCTCC 779
Qy      251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrHisThrAsnLeuPro 270
Db      780 AGT---CTTTCGCGAGAGATCGGGGACGTTTGGATATGTTGGACACATATTGGCG 836
Qy      271 ArgLeuGluAlaLeuArgAsnTyrMetAspValPheGlyGlnHisThrLysAsnLysAsnAla 290
Db      837 CGATTGGAAGCAAGGAATTACATCCAGTCTTTGGACAGGACACTGAGAACACGAAAGTCA 896
Qy      291 -----AlaGluLysLeuLeuGluLeuAlaLysLeuGluIlePheAsnIlePheHisSer 307
  
```

Db 897 TATGTGAAGAGCAAAAACCTTTAGAACTCGCAAAATTGGAGTTCAACATCTTCAATCC 956
Qy 308 LeuGlnGluArgGluLeuLysHisValSerArgTrpTrpLysAspSergLysSerProGlu 327
Db 957 TTACAAAGAAGGAGGTAGAAAGTCTGCTCAGATGCTGGAAGAATCGGGTTTCCTGAG 1016
Qy 328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347
Db 1017 ATGACCTTCTGCCGACATCGTCACGTGAATACTACACTTTGGCTTCTTCATTCGCTTC 1076
Qy 348 GluProGlnHisSergLysPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367
Db 1077 GAGCCTCAACATTCTGATTCAAGCTCGCTTCCCAAGACGTGATCTTATCACGGTT 1136
Qy 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluLeuPheThrAlaThr 387
Db 1137 CTGACGATATGTACGACACCTTCGGCAGTAGACGAGCTGGAATCTTCACAGCGACA 1196
Qy 388 IleLysArgTrpAspProSergAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407
Db 1197 ATGAAGACATGGGATCCGTCCTCGATAGATTGCCCTTCCAGAATATATGAAGAAGAGTGATAC 1256
Qy 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg 427
Db 1257 ATAGCGGTTTACGACACCGTAATGAATGGCTCGAGAGCGCAGAGGAGGCTCAAGGCCGA 1316
Qy 428 AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSergTyrMetGlnGlu 447
Db 1317 GATACGCTCACATATGCTCGGGAAGCTTGGAGGCTTATATGATTGATTCGATATGCAAGAA 1376
Qy 448 AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467
Db 1377 GCAAGGTGAGTCGCCACTGTTACTGCTCCCTCTTGATGAGTACTACGAGAATGGGAAA 1436
Qy 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
Db 1437 GTTAGCTGTGGTCATCCGATATCCGCAATTGCAACCCATTCTGACAAATGACATCCCTTT 1496
Qy 488 ProAspHisIleLeuLysGluValAspPheProSergLysLeuAsnAspLeuIleCysIle 507
Db 1497 CCTGATATATCTCTCAAGGAGTTGACTTCCCATCAAGCTTAACGACTTGGCATGTGCC 1556
Qy 508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu 527
Db 1557 ATCCTTGCAATTAAGAGGTGATACGCGGTGCTTACAAGCGGACAGGCGCTCGTGAGAAAGAA 1616
Qy 528 AlaSerSerIleSergCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547
Db 1617 GCTTCTCTATATCATGTTATATGAACAATCCTGAGTATCAGAGGAATGCTCTTC 1676
Qy 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567
Db 1677 GATCATATCAACGCCATGATCAGTGAAGTAATCAAGGATTAATTGGGAATCTTCTCAA 1736
Qy 568 ProAspAsnSerValProIleThrSergLysHisAlaPheAspIleSergArgValTrp 587
Db 1737 CCAGACATCAATGTTCCTCCATCTCGCGCAAGAACAATGCTTTGACATCGCCAGAGCTTTC 1796
Qy 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607
Db 1797 CATTAACGCTACAAATACCGAGACGGCTACAGCGTTGCCAACGTTGAACGAAGAGTTTG 1856
Qy 608 ValMetArgThrValIleGluProValProLeu 618
Db 1857 GTACAGAAACCCTCTGAAATCTGTGCTTTG 1889

RESULT 5
US-09-893-820-19
; Sequence 19, Application US/09893820
; Publication No. US20040053386A1
; GENERAL INFORMATION:
*; APPLICANT: Chappell, Joseph

; APPLICANT: No. US20040053386A11, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/893, 820
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US/09/398, 395A
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100, 993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130, 628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150, 262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 2018
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)...(1889)
; OTHER INFORMATION: pinene synthase
US-09-893-820-19

Alignment Scores:
Pred. No.: 8.17e-279 Length: 2018
Score: 2453.00 Matches: 475
Percent Similarity: 84.63% Conservative: 59
Best Local Similarity: 75.28% Mismatches: 81
Query Match: 75.45% Indels: 16
DB: 13 Gaps: 6

US-10-025-145A-65 (1-618) x US-09-893-820-19 (1-2018)

Qy 1 MetAlaLeuLeuSerIleThrProLeuValSergSerCysLeu----- 15
Db 6 ATGGCTCTAGTTCTTACCGCACCGTTGGCTTCCAATCATGCCCTGCACAAATCGTTGATC 65
Qy 16 SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArg 35
Db 66 AGTTCTAACCATGAGCTTAAGGCTCTCTAGAACAAATTCACGCTCTAGGAATGAGTAGG 125
Qy 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
Db 126 CGAGGGAATCTATCACTCTTCCATCAGCATGAGCTCTTACCAACCGTTGTAACCGATGAT 185
Qy 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75
Db 186 GGTTAGCAAGACGATGGGATTTCCATTCCAACCTTGGGACGATGATGTCATACAG 245
Qy 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
Db 246 TCTTTA---CCAACGGCTTTAGAGAAAATCGTACCTGGAGCGCTGAGAAACTGATC 302
Qy 96 GlyLysValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly----- 112
Db 303 GGGGAAGTAAAGAAC--ATGTTCAATTGCGATGTCATAGAGATGAGAGTTAATGAGT 359
Qy 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
Db 360 CCGCTCAATGATCTCATTCACCGCTTTGGATTGTCCGACGCCCTTGAACGTTGGGGATC 419
Qy 131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSergTyrTrpAsn 150
Db 420 CATAGACATTCAAAGATGAGATTAATCGCGCTTGATTATGTTTACAGTATTGGGGC 479
Qy 151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSergThrAlaLeu 170
Db 480 GAAATGGCATCGGATGCGGAGGAGAGAGTGTGTACTGATCTGAACCTCAACTGCGGTG 539

| | | | |
|----|------|--|------|
| QY | 171 | GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe | 190 |
| Db | 540 | GGGCTTCGAACCCCTACGACTACACGGATACC | 599 |
| QY | 191 | LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGlyLysIleArg | 210 |
| Db | 600 | AAAGGCCAAATGGCGAGTTTCTGCTCTGAAATATATTACAGATGAGAGATCAGA | 659 |
| QY | 211 | GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGlyLysValMetAsp | 230 |
| Db | 660 | GGCGTCTGCAATTTATTCGGGCTCCCTCATTTGCCCTTCCAGGGGAGAAATATTGAT | 719 |
| QY | 231 | GluAlaGlyThrPheSerThrLysTyrLeuArgGlyAlaLeuGlnLysIleProAlaSer | 250 |
| Db | 720 | GAGGCTGAATCTTCTCTACCAATAATTTAAAGAAGCCCTGCAGAAAGATTCCGGTCTCC | 779 |
| QY | 251 | SerIleLeuSerLeuGlyLysIleArgAspValLeuGlyTyrGlyTyrPheIsthAsnLeuPro | 270 |
| Db | 780 | AGT---CTTTCGGAGAGATCGGGACGTTTGGAAATATGTTGGCACACATATTTCGG | 836 |
| QY | 271 | ArgLeuGlyAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsnLysAsnAla | 290 |
| Db | 837 | CGATTGGAAGCAAGAAATTACATCCAAAGTCTTTGGACAGACACTGAGAACACGAAGTCA | 896 |
| QY | 291 | -----AlaGlyLysLeuLeuGlyLeuValAlaLysLeuGlyPheAsnIlePheHisSer | 307 |
| Db | 897 | TATGTGAAGAGCAAAAACCTTTAGAACTCGCAAAATTGGAGTTCAACATCTTCAATCC | 956 |
| QY | 308 | LeuGlnGlyLysArgGlyLeuLysHisValSerArgTyrTrpLysAspSerGlySerProGly | 327 |
| Db | 957 | TTACAAAAGAGGAGTTAGAAAGTCTGGTCAGATGTTGGAAGAAGATCCGGTTTCCCTGAG | 1016 |
| QY | 328 | MetThrPheCysArgHisArgHisValGlyTyrTyrAlaLeuAlaSerCysIleAlaPhe | 347 |
| Db | 1017 | ATGACCTTCTGCCGACATCGTCACGTGAATACTACACTTTGGCTTCCCTGATTGCGTTTC | 1076 |
| QY | 348 | GlyProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal | 367 |
| Db | 1077 | GAGCCTCAACATTCTGATTCAGACTCGGCTTGGCCAAGCGTGTCACTTATCAGCGTT | 1136 |
| QY | 368 | LeuAspAspMetTyrAspValPheGlyThrValAspGlyLeuGlyLeuPheThrAlaThr | 387 |
| Db | 1137 | CTTGACGATATGTAGACACACCTTCGGCACAGTAGACGAGCTGGAACCTTCACAGCGACA | 1196 |
| QY | 388 | IleLysArgTyrAspProSerAlaMetGlyCysLeuProGlyTyrMetLysGlyValTyr | 407 |
| Db | 1197 | ATGAAGAGATGGATCCGTCCTCGATAGATTGCTCCAGATATATGAAGAAGAGTGTAC | 1256 |
| QY | 408 | MetMetValTyrHisIsthValAsnGluMetAlaArgValAlaGlyLysAlaGlnIleArg | 427 |
| Db | 1257 | ATAGCGGTTTACGACACCCGTAAATGAGCTCGAGAGGACAGAGGCGCTCAAGGCCGA | 1316 |
| QY | 428 | AspThrLeuAsnTyrAlaArgGlnAlaTyrGlyAlaCysPheAspSerTyrMetGlnIle | 447 |
| Db | 1317 | GATACGCTCACATATGCTCGGGAAGCTTGGAGGCTTATATGATTGCTATATGCAAGAA | 1376 |
| QY | 448 | AlaLysTyrIleAlaThrGlyTyrLeuProThrPheGlyGlyTyrLeuGlyAsnGlyLys | 467 |
| Db | 1377 | GCAAGGTGATCGCCACTGGTTACTGCCCTCTTGATGAGTACTACAGAAATGGGAAA | 1436 |
| QY | 468 | ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe | 487 |
| Db | 1437 | GTTAGCTGTGTCATCGCATATCCGCATTTGCAACCCCATTTGACAAATGACATCCCTTT | 1496 |
| QY | 488 | ProAspHisIleLeuLysGlyValAspPheProSerLysLeuAsnAspLeuIleCysIle | 507 |
| Db | 1497 | CCTGATCATATCTCAAGGAAGTTGACTTCCCATCAAAAGCTTAAAGACTTGGCATGTGCC | 1556 |
| QY | 508 | IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGlyLys | 527 |
| Db | 1557 | ATCCTTCGATTACGAGGTGATACGCGGTGCTACAAAGCGGACAGGGCTCGTGGAAGAA | 1616 |
| QY | 528 | AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGlyLysAspAlaLeu | 547 |

[illegible]

```

RESULT 6
US-10-041-007-21
; Sequence 21, Application US/10041007
; Publication No. US20020164736A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seiichi P.T.
; APPLICANT: Schepmann, Håla G
; TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase
; FILE REFERENCE: P02081US1
; CURRENT APPLICATION NUMBER: US/10/041,007
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259,881
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 2018
; TYPE: DNA
; ORGANISM: Abies grandis
US-10-041-007-21

```

| | | | |
|------------------------|-----------|---------------|------|
| Alignment Scores: | 8.17e-279 | Length: | 2018 |
| Pred. No.: | 2453.00 | Matches: | 475 |
| Score: | 84.63% | Conservative: | 59 |
| Percent Similarity: | 75.28% | Mismatches: | 81 |
| Best Local Similarity: | 75.45% | Indels: | 16 |
| Query Match: | 14 | Gaps: | 6 |
| DB: | | | |

US-10-025-145A-65 (1-618) x US-10-041-007-21 (1-2018)

QY 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
|||||:::|||||:::|||||
Db 6 ATGAGCTTAGTTCTACACCGCACCGTTGGCTTCCAATCATGCTGCACAAATCGTTGATC 65
QY 16 SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGluIleCysArg 35
|||||:::|||||:::|||||:::|||||
Db 66 AGTTCTACCCATGAGCTTAAGGCTCTCTCTAGAACAAATTCAGCTCTAGGAATGAGTAGG 125
QY 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
|||||:::|||||:::|||||:::|||||
Db 126 CGAGGGAATCTATCATCTCCTTCATCAGCATGAGCTCTACCACCGCTGTGAACCGATGAT 185
QY 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75
|||||:::|||||:::|||||:::|||||
Db 186 GGTGTACGAAGACGCATGGGCGCATTTCCATTCCAACCTCTGGAGCATGATGTACATACAG 245
QY 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
|||||:::|||||:::|||||:::|||||
Db 246 TCTTTA---CCAACGGCTTATGAGAAAATAATCGTACCTGAGCGCTGTGAGAAACTGATC 302
QY 96 GlyGluValLysAspIleMetCysAsnPheLysSerLeuGluAspGlyCyl----- 112
|||||:::|||||:::|||||
Db 303 GGGGAAGTAAAGAAC---ATGTTCAATTGCATGTCTATTGAGAAGATGAGAGCTTAATGAGT 359


```
QY 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
Db 360 CCGCTCAATGATCTCATTCACGCGCTTTGGATTGTGCACAGCCTTGAACGTTGGGGATC 419
QY 131 AspArgHisPheIleGlySerGluIleValSerThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
Db 420 CATAGACATTTTCAAGATGAGATAAATCCGCGCTGATTATGTTTACAGTTATTGGGGC 479
QY 151 GluIleGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170
Db 480 GAAATGGCATCGGATCGGGAGGAGAGTGTGTACTGATCTGAACCTCAACTGCGCTTG 539
QY 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
Db 540 GGGCTTCGAACCCCTACGACTACAGGATACCCTGGTGTCTTCAGATGTTTCAAGCTTTC 599
QY 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyIleArg 210
Db 600 AAGGCCAAATGGGAGTTCCTGCTCTGAAAATATTCAGACAGATGAAGAGATCAGA 659
QY 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGluGluLysValMetAsp 230
Db 660 GGGCTTCTGAATTTATTCGGGCGCTCCCTCATTCGCTTCCAGGGAGAAATATGAT 719
QY 231 GluAlaGluThrPheSerThrIleTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250
Db 720 GAGGCTGAATCTTCTCTACCAATATTTAAAGAGCCCTGCAAAAGATTCCGGTCTCC 779
QY 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrPheIleThrAsnLeuPro 270
Db 780 AGT---CTTTCGCGAGAGATCGGGACGTTTGGAAATATGTTGGACACATATTGCGG 836
QY 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsnLysAsnAla 290
Db 837 CGATTGCAAGCAAGGAATTACATCCAAAGTCTTTGGACAGACACTGAGAAACAGAACTCA 896
QY 291 -----AlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307
Db 897 TATGTGAAGAGCAAAAACCTTTTGAAGACTCGCAAAATTTGAGTTCAACATCTTCAATCC 956
QY 308 LeuGlnGluArgGluLeuLysHisValSerArgTyrTyrAlaLeuAlaSerCysIleAlaPhe 327
Db 957 TTACAAAGAAGGAGTTAGAAAGTCTGTCAGATGTTGGAAGAAATCCGGTTCCTGAG 1016
QY 328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347
Db 1017 ATGACCTTCTGCGACATCGTACGTGAATACTACACTTTGGCTTCTTCATTCGCTTC 1076
QY 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367
Db 1077 GAGCTCAACATTTCTGATTCACTCGGCTTTGCCAAGACGTGTCTATCACCAGTT 1136
QY 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluPheThrAlaThr 387
Db 1137 CTTGACGATATGTACGACACCTTCGACACAGTAGACAGCTGGAACCTTCACACAGCACA 1196
QY 388 IleLysArgTyrAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407
Db 1197 ATGAAGAGATGGGATCCGCTCGATAGATTGCCCTCCAGATATATGAAGAAGAGTGTAC 1256
QY 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg 427
Db 1257 ATAGCGGTTTACGACACCGTAATGAATGGCTCGAGAGGCGAGAGAGGCTCAAGGCCGA 1316
QY 428 AspThrLeuAsnTyrAlaArgGlnAlaTyrGluAlaCysPheAspSerTyrMetGlnGlu 447
Db 1317 GATACGCTCACATATGTCTCGGAAGCTTGGAGGCTTATATTGATTCTATATGCAAGAA 1376
QY 448 AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467
Db 1377 GCAAGGTGGATCGCACTGTACTCGCTCTTGTATGAGTACTACGAGAATGGGAAA 1436
```

```
QY 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
Db 1437 GTTAGCTGTGTGTCATCCGATATCCGATTCGAACCCCATTTCTGACAAATGACATCCCTTT 1496
QY 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507
Db 1497 CTTGATCATATCTCAAGGAAGTTGACTTCCCATCAAAAGCTTAAAGACTTGGCATGTGCC 1556
QY 508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGlu 527
Db 1557 ATCTTCGATTACGAGGTGATACGCGGTGTACAAAGCGGACAGGCGCTGTGAGAGAA 1616
QY 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547
Db 1617 GCTTCCTCTATATCATGTATATGAAGACAATCCTGGAGTATCAGAGAGATGCTTTC 1676
QY 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567
Db 1677 GATCATATCAACGCCATGATCAGTACGTACGTATCAAAAGATTAATGGAACTTCTCAA 1736
QY 568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp 587
Db 1737 CCAGACATCAATGTTCCCATCTCGCGCAAGAAACATGCTTTTGACATCGCCAGAGCTTTC 1796
QY 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607
Db 1797 CATTAAGGCTACAAATATACGAGACGCGCTACAGCGTTGCCAACGTTGAAGAGAGTTTG 1856
QY 608 ValMetArgThrValIleGluProValProLeu 618
Db 1857 GTCAAGAGAACCCCTCTTGAATCTGTGCTTGG 1889

RESULT 7
US-10-025-145A-3
; Sequence 3, Application US/10025145A
; Publication No. US20030175861A1
; GENERAL INFORMATION:
; APPLICANT: Croceau, Rodney B.
; APPLICANT: Bohlmann, Joerg
; APPLICANT: Steele, Christopher L.
; APPLICANT: Phillips, Michael A.
; TITLE OF INVENTION: Monoterpene Synthases from Grand Fir (Abies Grandis)
; FILE REFERENCE: WSUR18414
; CURRENT APPLICATION NUMBER: US/10/025,145A
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 09/360,545
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: PCT/US98/14528
; PRIOR APPLICATION NUMBER: US 60/052,249
; PRIOR FILING DATE: 1997-07-11
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2018
; TYPE: DNA
; ORGANISM: Abies Grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)..(1892)
; OTHER INFORMATION:
US-10-025-145A-3

Alignment Scores:
Pred. No.: 8.17e-279 Length: 2018
Score: 2453.00 Matches: 475
Percent Similarity: 84.63% Conservative: 59
Best Local Similarity: 75.28% Mismatches: 81
Query Match: 75.45% Indels: 16
DB: 15 Gaps: 6

US-10-025-145A-65 (1-618) x US-10-025-145A-3 (1-2018)
```

```
QY      1 MetAlaLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
DB      6 ATGGCTCTGATTCTACCGCACCCTGGCTTCCAATCATGCTGCACAAATCGTTGATC 65
QY      16 SerSerHisGluIleLysAlaLeuArgThrIleProThrLeuGlyIleCysArg 35
DB      66 AGTTCACCATGAGCTTAAGGCTCTCTCTAGAACAAATTCACGCTCTAGGAATGAGTAGG 125
QY      36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
DB      126 CGAGGAAATCTATCACTCCTTCATCAGCATGAGCTCTACACCGTGTAAACGATGAT 185
QY      56 SerValGlnArgArgValGlyAsnTyxHisSerAsnLeuTrpAspAspPheIleGln 75
DB      186 GGTGTACGAGACGCGATGGCGATTCCATTCCAACCTCTGGAGCAGATGTCATACAG 245
QY      76 SerLeuIleSerThrProTyrglyAlaProAspTyrrArgGluArgAlaAspArgLeuIle 95
DB      246 TCTTTA---CCACGGCTTATGAGGAAATACTGTAACCTGAGCGTGTGAGAAACTGATC 302
QY      96 GlyGluValLysAspIleMetPheAsnPhelySerLeuGluAspGlyGly----- 112
DB      303 GGGGAAGTAAGAAC--ATGTTCAATTCCAGTGTATTAGAAGATGAGAGTTAATGAGT 359
QY      113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
DB      360 CCGCTCAATGATCTCATTCACACGCTTGGATGTGACACAGCCTTGAACTTTGGGATC 419
QY      131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrrValAsnSerTyrrAsn 150
DB      420 CATAGACATTCAAAAGATGAGATAAATCGCGCTTGATTATGTACAGTTATTGGGCG 479
QY      151 GluLysGlyIleGlyCysGlyArgGluSerValIleThrAspLeuAsnSerThrAlaLeu 170
DB      480 GAAATATGGCATCGGATGCGGAGGAGAGTGTGTTACTGATCTGAATCAACTGCGTTG 539
QY      171 GlyLeuArgThrLeuArgLeuHisGlyTyrrThrValSerSerAspValLeuAsnValPhe 190
DB      540 GGGCTTCGAACCTACGACTACACGAGATACCCGCTGCTTCAGATGTTTCAAAGCTTTC 599
QY      191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluIleArg 210
DB      600 AAAGGCCAAATGGGCAGTTTCTCTGCTGTAATAATATTCAAGACAGATGAAGATCAGA 659
QY      211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230
DB      660 GCGCTTCGAATTATTATCCGGGCTCCTTCATGCTCTTCCAGGGGAGAAATTATGAT 719
QY      231 GluAlaGluThrPheSerThrLysTyrrLeuArgGluAlaLeuGlnLysIleProAlaSer 250
DB      720 GAGGCTGAATCTTCTCTACCAATATTAAAGAACCCCTGCAAAAGATTCCGGTCTCC 779
QY      251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrrGlyTyrrHisThrAsnLeuPro 270
DB      780 AGT---CTTCGCGAGAGATCGGGGACGTTTGGAAATATGTTGGCACACATATTGCCG 836
QY      271 ArgLeuGluAlaArgAsnTyrrMetAspValPheGlyGlnHisThrLysAsnLysAsnAla 290
DB      837 CGATTGGAAGCAAGGAATTACATCCAAAGTCTTTGGACAGACACTGAGAACACGAAGTCA 896
QY      291 -----AlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307
DB      897 TATGTGAAGACAAAAAATTTAGAACTTCGCAAAATTGGAATTGCAATCTTTCAATCC 956
QY      308 LeuGlnGluArgGluLeuLysHisValSerArgTyrrTrpLysAspSerGlySerProGlu 327
DB      957 TTACAAAAGAGGAGTTAGAAAGTCTGTGATGATGTTGAAAGAAATCGGTTTCTCGAG 1016
QY      328 MetThrPheCysArgHisArgHisValGluTyrrTyrrAlaLeuAlaSerCysIleAlaPhe 347
DB      1017 ATGACCTTCTGCGACATCGTCACGTCGAATACACTTGTGCTTCCGCAATTCGCGTTC 1076
QY      348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367
```

```
DB      1077 GAGCCTCAACATTCYGATTACAGACTCGGCTTTGCCAAGACGTCGTCACTTATCACGGTT 1136
QY      368 LeuAspAspMetTyrrAspValPheGlyThrValAspGluLeuGluPheThrAlaThr 387
DB      1137 CTTGACGATATGTACGACACCTTCGACAGTAGACAGAGCTGGAATCTTCACAGCGACA 1196
QY      388 IleLysArgTyrrAspProSerAlaMetGluCysLeuProGluTyrrMetLysGlyValTyrr 407
DB      1197 ATGAAGAGATGGGATCCGCTCGATAGATTGCTTCAGAAATATGAAAGAGTGTAC 1256
QY      408 MetMetValTyrrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg 427
DB      1257 ATAGCGGTTTACGACACCGTAATGAATGGCTCGAGAGGCAAGAGGCTCAAGCCGA 1316
QY      428 AspThrLeuAsnTyrrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrrMetGlnGlu 447
DB      1317 GATACGCTCACATATGTCTCGGGAAGCTTGGGAGGCTTATATTGATTCTGATATGCAAGAA 1376
QY      448 AlaLysTrpIleAlaThrGlyTyrrLeuProThrPheGluGluTyrrLeuGluAsnGlyLys 467
DB      1377 GCAAGGTGATCGCCACTGTTACTGCTCCCTCTTGATGAGTACTTACGAGAATGGGAAA 1436
QY      468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
DB      1437 GTTAGCTGTGTCATCGCATATCCGCAATGCAACCATTCGACAAATGACATCCCTTT 1496
QY      488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507
DB      1497 CCTGATCATATCTCAAGAGAGTGAATCTCCCATCAAGCTTAACGACTTGGCATGTGCC 1556
QY      508 IleLeuArgLeuArgGlyAspThrArgCysTyrrLysAlaAspArgAlaArgGlyGluGlu 527
DB      1557 ATCCTTCGATTACGAGGTGATACCGGCTGCTCAAGCGGACAGGCTCGTGAGAGAA 1616
QY      528 AlaSerSerIleSerCysTyrrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547
DB      1617 GCTTCCTATATATCATGTTATATGAAGAACAATCTGAGATATCAGAGAGATGCTCTC 1676
QY      548 AsnHisIleAsnPhemMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567
DB      1677 GATCATATCAACGCCATGATCAGTGAAGTAATCAAGATTAATGGGAATCTCTCAA 1736
QY      568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp 587
DB      1737 CCAGACATCAATGTTCCCATCTCGGGAAGAAACATGCTTTGACATCGCCAGAGCTTTC 1796
QY      588 HisHisGlyTyrrArgTyrrArgAspGlyTyrrSerPheAlaAsnValGluThrLysSerLeu 607
DB      1797 CATTACGGCTCAAAATACCGAGACGGCTACAGCGTTGCCAACGTTGAAGAAGATTGG 1856
QY      608 ValMetArgThrValIleGluProValProLeu 618
DB      1857 GTCACGAGAACCTCCTTGAAATCTGTGCTTTG 1889

RESULT 8
US-10-025-145A-66
; Sequence 66, Application US/10025145A
; Publication No. US20030175861A1
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B.
; APPLICANT: Bohlmann, Joerg
; APPLICANT: Steele, Christopher L.
; APPLICANT: Phillips, Michael A.
; TITLE OF INVENTION: Monoterpene Synthases from Grand Fir (Abies Grandis)
; FILE REFERENCE: WSIU113414
; CURRENT APPLICATION NUMBER: US/10/025,145A
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 09/360,545
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: PCT/US98/14528
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: US 60/052,249
```

; PRIOR FILING DATE: 1997-07-11
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 2186
; TYPE: DNA
; ORGANISM: Abies Grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (34)..(1923)
; OTHER INFORMATION:
; US-10-025-145A-66

Alignment Scores:
Pred. No.: 1.99e-256 Length: 2186
Score: 2264.00 Matches: 435
Percent Similarity: 80.53% Conservative: 78
Best Local Similarity: 68.29% Mismatches: 98
Query Match: 69.64% Indels: 26
DB: 15 Gaps: 9

US-10-025-145A-65 (1-618) x US-10-025-145A-66 (1-2186)

QY 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
DB ATGGCTTGCTTCTTCCGCAACC-----AAATCCTGCTGCACAAATCGTTGATC 84
QY 16 ---SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCys 34
DB AGGTCTTCACTCATGAGCTCAAGCCTCTGCGCAGAACCATCCCACTCTTGAATGTGT 144
QY 35 ArgProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThr 54
DB AGGCGAGGAAATCTTTCACACCTTCTGTGAGCATGAGTTTGACCACCGCTGTATCTGAT 204
QY 55 AspSerValGlnArgArgValGlyAsnTyrrHisSerAsnLeuTrpAspAspPheIle 74
DB GATGGTCTACAAAGACGCATAGGTGACATCATCTCAATCTCTGGACGACGATTTCATA 264
QY 75 GlnSerIleIleSerThrProTyrrGlyAlaProAspTyrrArgGluArgAlaAspArgLeu 94
DB CAGTCTCTA---TCAACGCCCTTATGGGAGCCTTCTTACCAGAACGTGCTGAGAACTG 321
QY 95 IleGlyGluValLysAspIleMetPheAsnPhelySerLeuGluAspGlyGly----- 112
DB ATTGCGGGAAGTGAAGAG--ATGTTCAATTCAATGCCATCGAAGATGGAATCAATG 378
QY 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGly 129
DB AGTCCCTCAATGATCTTATTGAACGACTTTGGATGTCGATAGCGTTGAACGTTGGGG 438
QY 130 IleAspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrrValAsnSerTyrrTrp 149
DB ATTGATGACATTTCAAAAAAGAGATAAATCAGCCCTTGATTTATGTTTACAGTTATTGG 498
QY 150 AsnGluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAla 169
DB AACGAAAAAGTATGTGATGCGGTAGAGATAGTGTCTTCTGATGTCAACTCGACTGCC 558
QY 170 LeuGlyLeuArgThrLeuArgLeuHisGlyTyrrThrValSerSerAspValLeuAsnVal 189
DB TCGGGGTTTCGAACCTCTTCGCTACACGATACAGTGTCTCTTCAGAGTTTGAAGTA 618
QY 190 PheLysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyIle 209
DB TTTCAAGACCAAAATGGGCAAGTTTGCATTCTCTCTAGTACAAAA--GAGAGACATC 675
QY 210 ArgGlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMet 229
DB AGAACCGTTCTGAATTATATCGGGCTTCTTTCATTGCTTCTGCGGAGAGAAAGTTATG 735
QY 230 AspGluAlaGluThrPheSerThrLysTyrrLeuArgGluAlaLeuGlnLysIleProAla 249
DB ::

DB 736 GAAGAGGCTGAAATTTTCTTCAAGATATTGAAAGAGCCGTGCAAAAGATTCCGGTC 795
QY 250 SerSerIleLeuSerLeuGluIleArgAspValLeuGluTyrrGlyTyrrHisThrAsnLeu 269
DB TCCAGT---CTTCAACAAGAAATAGACTACACTTGGAAATATGGTTGGCACACAAATATG 852
QY 270 ProArgLeuGluAlaArgAsnTyrrMetAspValPheGlyGlnHisThr----- 285
DB CCAGATTGGAAACAAGAAATTATAGATGATTTGGACATCTTACAGTCCATGGCTC 912
QY 286 LysAsnLysAsnAla-----AlaGluLysLeuLeuGluLeuAlaLysLeuGlu 301
DB AAGAAAGAAAAGACGCAATATCTGACAGCGAAAAGCTTTTAGAACTCGCAAAATTGAG 972
QY 302 PheAsnIlePheHisSerLeuGlnGluArgGluLeuLysHisValSerArgTyrrTrpLys 321
DB TTCAACATCTTTCACCTCCCTTCAACAGAGAGTTACAGTATCTCTCCAGATGGTGATA 1032
QY 322 AspSerGlySerProGluMetThrPheCysArgHisArgHisValGluTyrrTyrrAlaLeu 341
DB CATTCGGGTTTGCCCTGAACCTGACCTTTGGTCGGCATCGTCACGTGAATACTACACCTG 1092
QY 342 AlaSerCysIleAlaPheGluProGlnHisSerGlyPheArgLeuGlyPheThrLysMet 361
DB AGCTCTTGACATTGCGACTGAGCCAAACATTCTGCATTGCAATGGGCTTGGCCAAACG 1152
QY 362 SerHisLeuIleThrValLeuAspAspMetTyrrAspValPheGlyThrValAspGluLeu 381
DB TGTCATCTTATCACGGTTCTGGACGATATCTACGACACTTTTGGAAACGATGAGAAATC 1212
QY 382 GluLeuPheThrAlaThrIleLysArgTrpAspProSerAlaMetGluCysLeuProGlu 401
DB GAACCTTTCACAGAGCAGTATGAGATGGAATCCGTGCGAGAAAGACGCTCCACAGA 1272
QY 402 TyrMetLysGlyValTyrMetMetValTyrHisThrValAsnGluMetAlaArgValAla 421
DB TATATGAAGAAGAAATCTACATGCGACTCTACGAGCCCTTACTGACATGGCGGAGAGCA 1332
QY 422 GluLysAlaGlnGlyArgAspThrLeuAsnTyrrAlaArgGlnAlaTrpGluAlaCysPhe 441
DB GAGAAAGACACAAGGCCGAGACGCTCAATTATGCTAGAAAGCTTGGGAAGTTTATCTT 1392
QY 442 AspSerTyrrMetGlnGluAlaLysTrpIleAlaThrGlyTyrrLeuProThrPheGluGlu 461
DB GATTCTGATACACAAGAGCAAGTGAATGCGCAGCGGTATCTGCCAATTTCGAGAG 1452
QY 462 TyrLeuGluAsnGlyLysValSerSerAlaHisArgProCysAlaLeuGlnProIleLeu 481
DB TACTTAGAGAAACGGAAGTTAGCTCTGTATCGTCAGCGGCATTGACACCCCTCTG 1512
QY 482 ThrLeuAspIleProPheProAspHisIleLeuLysGluValAspPheProSerLysLeu 501
DB ACATTGGACGTACCGCTCTGATGACGCTTGAAGGAAATAGATTTTCCATCGAGATT 1572
QY 502 AspAspLeuIleCysIleIleLeuArgLeuArgGlyAspThrArgCysTyrrLysAlaAsp 521
DB AATGATTTGGCATCTTCTCTTGAAGTAAAGAGTGACACAGATGCTACAGGCAAGC 1632
QY 522 ArgAlaArgGlyGluGluAlaSerSerIleSerCysTyrrMetLysAspAsnProGlyLeu 541
DB AGGGACCGAGAGAGAGCGCTCAAGCATATCGTGTACATGAAAAGCAATCCCGGATTA 1692
QY 542 ThrGluGluAspAlaLeuAsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeu 561
DB ACAGAGAAAGATGCTCTCAATCATATCAATGCCATGATCAACGACATATCAAAAGATT 1752
QY 562 AsnTrpGluLeuLeuLysProAspAsnSerValProIleThrSerLysLysHisAlaPhe 581
DB AATTGGAACTTCTCAAAACCCGATAGCAATATTCCAATGACTGCACGGAACATGCTTAT 1812
QY 582 AspIleSerArgValTrpHisHisGlyTyrrArgTyrrArgAspGlyTyrrSerPheAlaAsn 601
DB GAGATTAACAGAGCTTTCACCAACTTACAAATATATAGATGGCTTCAGCGTTGCCACT 1872

Qy 602 ValGluThrIysSerLeuValMetArgThrValIleGluProValProLeu 618
Db 1873 CAAGAAACGAAAGTTTGGTGAGAGAACGGTCTTGAACCACTGCTCTT 1923

RESULT 9

US-09-887-586A-29
; Sequence 29, Application US/09887586A
; Patent No. US20020094556A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20020094556A1, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/887,586A
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (69)...(1949)
; OTHER INFORMATION: myrcene synthase
US-09-887-586A-29

Alignment Scores:
Pred. No.: 6.37e-249 Length: 2196
Score: 2200.50 Matches: 427
Percent Similarity: 80.38% Conservative: 77
Best Local Similarity: 68.10% Mismatches: 106
Query Match: 67.69% Indels: 17
DB: 9 Gaps: 7

US-10-025-145A-65 (1-618) x US-09-887-586A-29 (1-2196)

Qy 1 MetAlaLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
Db 69 ATGGCTCTGTTTCTATCTCACCCTGGCTTGAATCTGCTGCCGAAGTCGTGATC 128
Qy 16 SerSerSerHisGluIleLeuValAlaLeuArgThrIleProThrLeuGlyIleCysArg 35
Db 129 AGTTCAATTCAATGAACATTAAGCCCTCCCTATGAACAATCCCAATCTTGAATGCGTAGG 188
Qy 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
Db 189 CGAGGAAATCTGTACAGCCCTTCCATGAGCATCAGTTGGCCACCGCTGCACCTGATGAT 248
Qy 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75
Db 249 GGTGTACAAGACGACATAGTGACTACCATTCATATCTGGGACGATGATTCTATACAG 308
Qy 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
Db 309 TCTCTA--TCAACGCCCTTATGGGGAACCTCTTACCAGGAACGTGCTGAGAGATTAAIT 365
Qy 96 GlyGluValIysAspIleMetPheAsnPhelysSerLeuGluAspGlyGly----- 112
Db 366 GTGAGAGTAAAGAGATA--TTCAATTCAATGTAACCTGATGATGAGAGATTAAAGAT 422
Qy 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
Db 423 TCCTTTAATGATCTCATGCAACGCCCTTGGATGATGATAGCGTTGAACGTTGGGGATA 482

Qy 131 AsparGHisPheLeuValGluIleLeuThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
Db 483 GCTAGACATTTTCAAGAACGAGATTAACATCAGCTCTGATTATGTTTCCGTTACTGGGAG 542
Qy 151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170
Db 543 GAAACCGCATTCGATGTGGAGAGACAGATATTGTTACTGATCTCACTCAACGCGTGG 602
Qy 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
Db 603 GGGTTTCAACTCTTCGATTACACGGGTACAGTATCTCCAGAGGTTTAAAGCTTTT 662
Qy 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyIleArg 210
Db 663 CAAGATCAAAATGACAGACTTGTATGCTCCCGCGT--CAGACAGAGGTGAGATCAGA 719
Qy 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230
Db 720 AGCGTCTTAATTATATCGGGCTTCCCTCATTTGCCCTTCCGTGAGAGAAATTATGAA 779
Qy 231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250
Db 780 GAAGCTGAATCTTCTCCACAGATATTGAAAGAAAGCTTCAAAAGATTCCAGTCTCC 839
Qy 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrPheIleThrAsnLeuPro 270
Db 840 GCT--CTTCAACAAGAGATAAGTTTGTATGGAATATAGCTGGCACAAATTGGCCA 896
Qy 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLys-----Asn 287
Db 897 AGATTGGAAGCAAGAATTATACATAGACACACTTGAGAAAGACACACGTCATGCTCAAT 956
Qy 288 LysAsnAlaAlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307
Db 957 AAAAATGCTGGGAAGAAGCTTTAGAACTTGCAGAAATTGGAAGTTCAATATTTAACTCC 1016
Qy 308 LeuGlnGluArgGluLeuLysHisValSerArgTyrTrpLysAspSerGlySerProGlu 327
Db 1017 TTACACAAAGAAATTAACAATATCTTTGAGATGTGGAAAGAGTGGATTGGCTTAA 1076
Qy 328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347
Db 1077 TTGACATTTGCTGGCATCGTCATGTGAATTCTACACTTGGCTCTTGTATTGCCATT 1136
Qy 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367
Db 1137 GACCAAAACATTCCTGCATTCAGACTGAGCTTGCAGAAATGTGTACTTGTACAGATT 1196
Qy 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluLeuPheThrAlaThr 387
Db 1197 TTGACGATATTATACGACACTTTTGAACGATTGACGAGCTTGAACCTTTCACATCTGCA 1256
Qy 388 IleLysArgTyrAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407
Db 1257 ATTAAGAGATGGAATTTCATCAGAGATGAACACCTTCCAGAAATATGAATGTGTATC 1316
Qy 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnIleArg 427
Db 1317 ATGTCGTGTTGAACCTGTAATGAATGACACAGAGAGCGGAGAGACTCAAGGGAGA 1376
Qy 428 AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu 447
Db 1377 AACACTCTCAACTATGTTGGAAGGCTTGGAGGCTTATTTGATCATATATGGAAGAA 1436
Qy 448 AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467
Db 1437 GCAAAATGATCTCTAATGTTATCTGCAATGTTTGAAGAGTACATGAGATGGGAAA 1496
Qy 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
Db 1497 GTGAGCTCTGCATATCGCGTAGCAACATTGCAACCCATCCTCACTTGAATGCATGCGCTT 1556

Qy 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db 1557 CcTGAATACATCTTGAAAGGAATGATTTTCCATCCAGGTTCAATGATTTGGCATCGTCC 1616
Qy 508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu 527
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db 1617 TTCCCTCGGCTACGAGGTGACACACGCTGCTACAAAGCCGATGCGATCGTGAAGAA 1676
Qy 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db 1677 GCTTCGTATATCATGTATATGAAAGACAATCCTGATCAACCGAAGAAGATGCCCTC 1736
Qy 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db 1737 AATCATATCAATGCCATGGTCAATGACATAATCAAGAATTAAATTGGGAACCTCTAAGA 1796
Qy 568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp 587
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db 1797 TCCAACGACAATATTCCAATGCTGGCCAAGAACATGCTTTGACATAACAGAGCTCTC 1856
Qy 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db 1857 CACCACTCTCATATATCGAGATGGCTTTAGTGTGCCAACAAAGAAACAAAAAATTG 1916
Qy 608 ValMetArgThrValIleGlu 614
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db 1917 GTTATGGAACAACACTCCTTGAA 1937

RESULT 10
US-09-903-012-29
; Sequence 29, Application US/09903012
; Patent No. US20020094557A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20020094557A1, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903,012
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for windows Version 3.0
; SEQ ID NO 29
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (69)...(1949)
; OTHER INFORMATION: myrcene synthase
US-09-903-012-29

Alignment Scores:
Pred. No.: 6.37e-249 Length: 2196
Score: 2200.50 Matches: 427
Percent Similarity: 80.38% Conservative: 77
Best Local Similarity: 68.10% Mismatches: 106
Query Match: 67.69% Indels: 17
DB: 9 Gaps: 7

US-10-025-145A-65 (1-618) x US-09-903-012-29 (1-2196)
Qy 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |

Db 69 ATGGCTCTGCTTCTATCTCAACCGTTGGCTTGGAAATCTTGCCGCGCAAGTCGTTGATC 128
Qy 16 SerSerSerHisGluIleLysAlaLeuArgThrIleProThrLeuGlyIleCysArg 35
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db 129 AGTTCAATTCATGAACATAGCCTCCCTATAGAACAAATCCAAATCTTGGAATGCGTAGG 188
Qy 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db 189 CGAGGGAATCTGTACGCCCTTCCATGAGCATCAGTTGGCCACCCTGCACCTGATGAT 248
Qy 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db 249 GGTGTACAAAGACGACATAGTGACTACCATATCTGGGACGATGATTCTATACAG 308
Qy 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db 309 TCTCTA--TCAACGCCCTTATGGGGAACCCCTTACCAGGAACGTGCTGAGAGATTATT 365
Qy 96 GlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly----- 112
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db 366 GTGGAGGTAAAGAGATA--TTCAATTCAATGTACTGATGATGGAAGATTAAATGACT 422
Qy 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db 423 TCCTTTAATGATCTCATGCAACGCTTTGGATAGTCGATGCGTTGAACGTTGGGATA 482
Qy 131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db 483 GCTAGACATTTCAAGAACGAGATAACATCAGCTCTGATATATGTTTCCGTACTGGAG 542
Qy 151 GluLysGlyIleGlyCysGlyArgGluSerValThrAspLeuAsnSerThrAlaLeu 170
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db 543 GAAACGGCATTTGATGTGGAGAGACAGATATTGTACTGATCTCAACTCAACTGCGTTG 602
Qy 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db 603 GGGTTTGAACCTCTTCGATTACACGGGTACACTGTATCTCCAGAGGTTTAAAGCTTTT 662
Qy 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyIleArg 210
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db 663 CAAGATCAAAATGGACAGTTTGTATGCTCCCGCGGT--CAGACAGAGGTTGAGATCAGA 719
Qy 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db 720 AGCGTTCTTAATTATATCGGCTTCCCTCATTTGCCCTGGTGAAGAAAGTTATGGA 779
Qy 231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db 780 GAAGCTGAATCTTCTCCACAGATATTGGAAGAAGCTGTACAAAGATTCAGTCTCC 839
Qy 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTrpHisThrAsnLeuPro 270
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db 840 GCT---CTTTCACAGAGATTAAGTTGTTATGGAATATGGCTGGCACACAATTTGCCA 896
Qy 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLys-----Asn 287
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db 897 AGATTGGAAGCAAGAAATTACATGACACACTTGAGAAAGACACCAGTGCATGGCTCAAT 956
Qy 288 LysAsnAlaAlaGlyLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db 957 AAAAATGCTGGGAAGAGCTTTTGAACCTTGCAAAATGGAGTTCAATATATTAACTCC 1016
Qy 308 LeuGlnGluArgGluLeuLysHisValSerArgTrpTrpLysAspSerGlySerProGlu 327
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db 1017 TTACACAACAAAGAAATTACATATCTTTGAGATGGTGAAGAGCTCGATTGCTTAAD 1076
Qy 328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db 1077 TTGACATTTGCTCGCATCGTCAATGGAATTTACACTTGCGCTCTGTATTGCCATT 1136
Qy 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367
| | | | | : : : | | | | | : : : | | | | | : : : | | | | |
Db 1137 GACCCAAACATTTCTGCATTCAGACTAGGCTTGCCCAAAATGTGTCACTCTGTCAAGATT 1196

Qy 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluLeuPheThrAlaThr 387
Db 1197 TTGGACGATATTACGACACTTTTGAACGATTGACGAGCTTGAACCTTCAACATCTGCA 1256
Qy 388 IleLysArgTTrpAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407
Db 1257 ATTAAGAGATGGAATTTCATCAGAGATGAAACACTTCAGAAATATGAAATGTGTGTAC 1316
Qy 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg 427
Db 1317 ATGGTCGCTTTGAAACTGTAATGAAGTCAACAGAGCGGAGAACTCAAGGAGA 1376
Qy 428 AspThrLeuAsnTyrAlaArgGlnAlaTPrGluAlaCysPheAspSerTyrMetGlnGlu 447
Db 1377 AACACTCTCACTATGTTCGAAAGGCTTGGAGGCTTATTTGATTGATATATGGAAGA 1436
Qy 448 AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluLys 467
Db 1437 GCATAATGATCTCTAATGTTATCTGCCAATGTTGAAGAGTACCATGAGAAATGGAAA 1496
Qy 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
Db 1497 GTGAGCTTCGATTCGCGTAGCAACATTCGAACCCATCTCACTTGAATGCATGGCTT 1556
Qy 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507
Db 1557 CCTGATTACATCTTGAAGGGAATGATTTCCATCCAGGTTCAATGATTGGCATCGTCC 1616
Qy 508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGlu 527
Db 1617 TTCCTTCGCGTACGAGGTGACACACGCTGCTACAGCGCATAGGATCGTGGAAGA 1676
Qy 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluLysAlaLeu 547
Db 1677 GCTTCGTGTATATCATGTTATATGAAGCAATCCTGGATCAACCCGAAGAATGCCCTC 1736
Qy 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567
Db 1737 AATCATATCAATGCCATGCTCAATGACATTAACAAGAAATTAATGGCACTTCTAAGA 1796
Qy 568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp 587
Db 1797 TCCACGACAAATATTCCAATGCTGGCCAAAGAACATGCTTTGACATTAACAAGCTCTC 1856
Qy 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607
Db 1857 CACCATCTCTACATATATCGAGATGGCTTAAAGTGTGCCAACAGAAACAAAATTCG 1916
Qy 608 ValMetArgThrValIleGlu 614
Db 1917 GTTATGGAACACTCCTTGAA 1937
RESULT 11
US-09-900-797-29
; Sequence 29, Application US/09900797
; Publication No. US20030087406A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20030087406A11, Joseph P.
; APPLICANT: Stark, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/900,797
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (69)...(1949)
; OTHER INFORMATION: myrcene synthase
US-09-900-797-29
Alignment Scores:
Pred. No.: 6.37e-249 Length: 2196
Score: 2200.50 Matches: 427
Percent Similarity: 80.38% Conservative: 77
Best Local Similarity: 68.10% Mismatches: 106
Query Match: 67.69% Indels: 17
DB: 10 Gaps: 7

US-10-025-145a-65 (1-618) x US-09-900-797-29 (1-2196)

Qy 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
Db 69 ATGGCTCTGCTTCTATCTCACCGTTGGCTTGAATCTTGCTGGCAAGTCGTGATC 128
Qy 16 SerSerHisGluIleLysAlaLeuArgGThrIleProThrLeuGlyIleCysArg 35
Db 129 AGTTCAATTCATGACATGAAGCCCTCCATAGAACAAATCCCAATCTTGAATGCGTAGG 188
Qy 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
Db 189 CGAGGGAATCTGTACAGCGCTTCATGAGCATCAGTTTGGCCACCGCTGCACCTGATGAT 248
Qy 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75
Db 249 GGTGTACAAAGACGCATAGGTGACTTCAATTCATATCTGGGACGATGATTTCATACAG 308
Qy 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
Db 309 TCTCTA---TCAACGCTTATGGGGAACCTCTTACCAGGAACGTGCTGAGATTAATT 365
Qy 96 GlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly----- 112
Db 366 GTGAGGTAAAGTAGATA---TTCAATTCATGTACCTGGATGATGGAAGATTAATGAGT 422
Qy 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
Db 423 TCCTTTAATGATCTCATGCAACGCTTTGGATAGTGCATAGCCGTTGAACGTTGGGAGTA 482
Qy 131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
Db 483 GCTAGACATTTCAAGACGAGATACATCAGCTCTGATTAATGTTTCCGTTACTGGGAG 542
Qy 151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170
Db 543 GAAACCGCATTTGATGTGGAGAGACAGATATTGTTACTGATCTCAACTCACTGCGGTG 602
Qy 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
Db 603 GGGTTTCGAACCTTCGATTACAGGGGTACACTGTATCTCCAGAGGTTTAAAGCTTTT 662
Qy 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyLysIleArg 210
Db 663 CAAGATCAAAATGAGACAGTTGTATGCTCCCGGT--CAGACAGAGGGTGAGATCAGA 719
Qy 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230
Db 720 AGCGTCTTAATTATATCGGGCTCCCTCATGCTCCCTGCTGAGAAAGTTATGAA 779
Qy 231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250
Db 780 GAAGCTGAATCTTCTCCACAGATATTGGAAGAAGCTCTACAAAGATTCCAGTCTCC 839

QY 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrPheIsthrAsnLeuPro 270
Db 840 GCT---CTTCAACAAGATAAAGTTTGTATGGAATATGGCTGGCACACAATTTGCCA 896
QY 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnIsthrLys-----Asn 287
Db 897 AGATTGGAAGCAAGAAATTACATGACACACTTGAGAAAGACACAGTCATGGCTCAAT 956
QY 288 LysAsnAlaIleGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307
Db 957 AAAAATCTGGGAAGAAGCTTTAGAACTTGCAAAATTGAGTTCAATATATTAACCTCC 1016
QY 308 LeuGlnGluArgGluLeuLysHisValSerArgTyrTrpLysAspSergLysSerProGlu 327
Db 1017 TTACAACAAAAGGAATTACATATCTTTGAGATGCTGGAAGAGTCGGATTTCCTAA 1076
QY 328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347
Db 1077 TTGACATTTGGCTCGGCATCGTCATGTGGAATTCTACACTTTGGCCTCTTGATTCGCAT 1136
QY 348 GluProGlnHisSergLysPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367
Db 1137 GACCCAAAACATTCTGCATTGACAGTAGGCTTCGCCAAAATGTGCATCTGTGCACAGTT 1196
QY 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluPheThrAlaThr 387
Db 1197 TTGAGCATATTTACGACACTTTTGGAACGATTGACGAGCTTGAACTCTTCACATCTGCA 1256
QY 388 IleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407
Db 1257 ATTAAGATGGAATTCATCATGAGATGAGAACACCTTCAGAAATATGAATGTGTGTAC 1316
QY 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg 427
Db 1317 ATGGTCGTGTTGAAACTGTAAATGAAGTGAACACGAGAGCGGAGAACACTCAAGGGAGA 1376
QY 428 AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSergTyrMetGlnGlu 447
Db 1377 AACACTCTCAACTATGTTGAAAGGCTTGGAGGCTTATTTGATTCATATATGGAAGAA 1436
QY 448 AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467
Db 1437 GCAAAATGATCTCTAATGTTATCGCAATGTTGAAGAGTACATGAGAATGGGAAA 1496
QY 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
Db 1497 GTGAGCTCGCATATCGCGTAGCAACATTGCAACCCTCTCACTTGAATGCATGGCTT 1556
QY 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507
Db 1557 CCTGATATCATCTTGAAGGGAATGATTTTCCATCCAGGTTCAATGATTTGGCATCGTCC 1616
QY 508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu 527
Db 1617 TTCCTTCGGCTACGAGGTGACACACGCTCTTACAAGGCCGATAGGGAATCGTGTGAAGAA 1676
QY 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547
Db 1677 GCTTCGTATATCATGTTATATGAAGACAATCTCGATCAACCGAAGAAAGATGCCCTC 1736
QY 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567
Db 1737 AATCATATCAATGCCATGTCATGACATAATCAAGAATTAATTGGGAATCTTCTAAGA 1796
QY 568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTyr 587
Db 1797 TCCAACGACAATATTCGAATGCTGGCCAAAGAAACATGCTTTGACATAACAAGAGCTCTC 1856
QY 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607
Db 1857 CACCATCTCTACATATATCGAGATGGCTTTAGTGTGCCAACAGGAACAATAAATTG 1916
QY 608 ValMetArgThrValIleGlu 614

Db 1917 GTTATGGAACAACACTCCTTGAA 1937
RESULT 12
US-09-893-820-29
; Sequence 29, Application US/09893820
; Publication No. US20040053386A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20040053386A1, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/893, 820
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US/09/398, 395A
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100, 993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130, 628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150, 262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Abies grandis
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (69)...(1949)
; OTHER INFORMATION: myrcene synthase
US-09-893-820-29
Alignment Scores:
Pred. No.: 6.37e-249 Length: 2196
Score: 2200.50 Matches: 427
Percent Similarity: 80.38% Conservative: 77
Best Local Similarity: 68.10% Mismatches: 106
Query Match: 67.69% Indels: 17
DB: 13 Gaps: 7
US-10-025-145A-65 (1-618) x US-09-893-820-29 (1-2196)
QY 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
Db 69 ATGGCTCTGCTTCTATCTCAACGCTTGCGCTTGAATCTTGCGCAAGTCGTGATC 128
QY 16 SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArg 35
Db 129 AGTTCATTCATGACATTAAGCCTCCCTATAGAACAAATCCCAATCTTGAATGCGTAGG 188
QY 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
Db 189 CGAGGGAATCTGTCAAGCCTTCCATGAGCATCAAGTTGGCCACCGCTGCACCTGATGAT 248
QY 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75
Db 249 GGTTACAAAGACGACATAGGTGACTACCATTCCAATATCTGGGACGATGATTCATACAG 308
QY 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
Db 309 TCTCTA---TCAACGCCCTTATGGGAAACCTCTTACACGAAACGTGCTGAGAGATTAAT 365
QY 96 GlyIleValLysAspIleMetCysPheAsnPheLysSerLeuGluAspGlyGly----- 112
Db 366 GTGAGGTAAGAAGATA--TTCAATTCAATGTACCTGATGATGGAAGATTAAATGAGT 422
QY 113 -----AsnAspLeuLeuGlnArgLeuLeuLeuValAspAspValGluArgLeuGlyIle 130
Db 423 TCCTTTAATGATCTCATGCAACGCCCTTTGGATAGTCGATAGCGTTGAACGTTGGGGATA 482

Qy 131 AsparghisbhelysgluilelythrAlaleuAspTyrValaenSerrTyrTrasn 150
Db 483 GCTAGACATTTCAAGAACGAGATTAACATCACTCTGGATTATGTTTCCGTTACTGGAG 542
Qy 151 GlulysgluilegIyCysglYArgGluSerValValThrAspLeuAsnSerThrAlaleu 170
Db 543 GAAACCGCATGTGATGTGGAGACAGATGTAATGTACTGATCTCACTCAACTGCGTTG 602
Qy 171 GlYleuArgThrleuArgleuHISglYTYrThrValSerSerAspValleuAsnValPhe 190
Db 603 GGGTTTGCAGACTCTTCGATTACACGGGTACACTGTATCTCCAGAGGTTTAAAGCTTTT 662
Qy 191 LysAspLysaenGluGlnPheSerSerThrAlaAsnIleGlnIleGluGluileArg 210
Db 663 CAAGATCAAAATGACAGACTTGTATGCTCCCGCGT---CAGACAGGGGTGAGATCAGA 719
Qy 211 GlYValleuAsnleuPheArgAlaSerleuValAlaPheProGluYgluLysValmetAsp 230
Db 720 AGCGTTCTTAACCTTATATCGGGCTTCCCTTCATTTGCCCTTCCGTGAGAAAGTTATGGA 779
Qy 231 GluAlaGluThrPheSerThrLysTYrleuArgGluAlaLeuGlnLysIleProAlaSer 250
Db 780 GAAGCTGAAATCTTCTCCACAAGATATTTGAAGAAGCTCTACAAAGATTTCCAGTCTCC 839
Qy 251 SerIleuSerleuGluileArgAspValleuGluTYrGluTYrPheIsthAsnleuPro 270
Db 840 GCT---CTTTCACAAGAGATAAAGTTGTGTAATGGAATATGGCTGGCACAAATTTGCCA 896
Qy 271 ArgleuGluAlaArgAsnTYrmetAspValPheGluGlnIsthLys-----Asn 287
Db 897 AGATTGGAAGCAAGAATATACATAGACACACTTGAGAAGACACACAGTCATGGCTCAAT 956
Qy 288 LysAsnAlaAlaGluLysleuLeuGluLeuAlaLysleuGluPheAsnIlePheHISer 307
Db 957 AAAAATGCTGGGAAGAAGCTTTTGAACCTTGCAAAATTTGAGTTCAATATTTAACTCC 1016
Qy 308 LeuGlnGluArgGluLeuLysHISValSerArgTYrTrpLysAspSerGlySerProGlu 327
Db 1017 TTACAACAAGAAGGAATTACAATATCTTTGAGATGGTGGAAGAGTCGGATTTCCTAAA 1076
Qy 328 MetThrPheCysArgHISArgHISValGluTYrTYrAlaLeuAlaSerCysIleAlaPhe 347
Db 1077 TTGACATTTGCTCGGCATCGTCATGTGAATTTCTACACTTTGGCTCTGTATTGCCATT 1136
Qy 348 GluProGlnHISerGlyPheArgleuGluPheThrLysMetSerHISleuIleThrVal 367
Db 1137 GACCCAAACATTTCTGCATTCAGACTAGGCTTCGCCAAATGTGTCTCTGTACAGATT 1196
Qy 368 LeuAspAspMetTYrAspValPheGluThrValAspGluLeuGluPheThrAlaThr 387
Db 1197 TTGGACGATATTTAAGACACTTTTGAACGATTTGACGAGCTTGAACCTTTCACATCTGCA 1256
Qy 388 IleLysArgTYrAspProSerAlaMetGluCysleuProGluTYrMetLysGluValTYr 407
Db 1257 ATTAAAGATGGAATTCATCAGAGATGAACACCTTCCAGATATATGAATGTGTGTAC 1316
Qy 408 MetMetValTYrHISThrValAsnGluMetAlaArgValAlaGluLysAlaGlnIlyArg 427
Db 1317 ATGTCGTGTTTGAACCTGTAATGAAGTGAACGAGAGGCGGAGAAGACTCAAGGGAGA 1376
Qy 428 AspThrleuAsnTYrAlaArgGlnAlaTrpGluAlaCysPheAspSerTYrMetGlnIlu 447
Db 1377 AACACTCTCAACTATGTTCGAAGGCTTGGAGGCTTATTTGATTTCATATATGGAAGAA 1436
Qy 448 AlaLysTrpIleAlaThrGluTYrleuProThrPheGluGluTYrleuGluAsnGluLys 467
Db 1437 GCAAAATGCATCTTAATGTTATGTGCAATGTTTGAAGAGTACATGAGAATGGAAA 1496
Qy 468 ValSerSerAlaHISArgProCysAlaLeuGlnProIleleuThrleuAspIleProPhe 487
Db 1497 GTGAGCTCTGCATATCGCGTAGCAACATTGCAACCCATCTCTCACTTGAATGCATGGCTT 1556

Qy 488 ProAspHISleuLeuLysGluValAspPheProSerLysleuAsnAspIleCysIle 507
Db 1557 CCTGATTACATCTTGAAGGAATGATTTTCCATCCAGGTTCAATGATTTGGCATCGTCC 1616
Qy 508 IleLeuArgleuArgGluAspThrArgCysTYrLysAlaAspArgAlaArgGluGlu 527
Db 1617 TTCCTTCGGCTACGAGGTGACACACGCTCTACAAAGCCGATAGGATCGTGGAAGA 1676
Qy 528 AlaSerSerIleSerCysTYrMetLysAspAsnProGluTYrleuThrGluGluAspAlaLeu 547
Db 1677 GCTTCGTGATATCATGTTATATGAAGACAATCTCGGATCAACCGAAGAGATGCCCTC 1736
Qy 548 AsnHISleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567
Db 1737 AATCATATCAATGCCATGTGTCATGACATTAATCAAGAATTAATTTGGAACTTCAAGA 1796
Qy 568 ProAspAsnSerValProIleThrSerLysLysHISAlaPheAspIleSerArgValTrp 587
Db 1797 TCCAAAGCAATAATCCAAATGCTGGCCAGAAACATGCTTTTGACATTAACAAGACTCTC 1856
Qy 588 HISHISglYTYrArgTYrArgAspGluTYrSerPheAlaAsnValGluThrLysSerLeu 607
Db 1857 CACCATCTCTACATATATCGAGATGGCTTTAGTGTGCCAACAGAAACAAAAAATTG 1916
Qy 608 ValmetArgThrValIleGlu 614
Db 1917 GTTATGGAACACTCCTTGAA 1937

RESULT 13
US-10-041-007-25
; Sequence 25, Application US/10041007
; Publication No. US20020164736A1
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Seiichi P.T.
; APPLICANT: Schepmann, Hala G
; TITLE OF INVENTION: Ginkgo Biloba Levopimaradiene Synthase
; FILE REFERENCE: P02081U51
; CURRENT APPLICATION NUMBER: US/10/041, 007
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: US 60/259, 881
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Abies grandis
; US-10-041-007-25

Alignment Scores:
Pred. No.: 6,37e-249 Length: 2196
Score: 2200.50 Matches: 427
Percent Similarity: 80.38% Conservative: 77
Best Local Similarity: 68.10% Mismatches: 106
Query Match: 67.69% Indels: 17
DB: 14 Gaps: 7

US-10-025-145A-65 (1-618) x US-10-041-007-25 (1-2196)
Qy 1 MetaLaleuLeuSerIleThrProLeuValSerArgSerCysleu----- 15
Db 69 ATGCTCTGCTTCTATCTCACCGCTTGGCTTGCAAACTTGGCTGCGCAAGTCGTGATC 128
Qy 16 SerSerHISgluileLysAlaLeuArgTYrIleProThrleuGluIleCysArg 35
Db 129 AGTTCAATTCATGAACATAGCCTCCCTATAGAACAAATCCCAATCTTGAATGCGTAGG 188
Qy 36 ProGluLysSerValAlaHISerIleAsnMetCysleuThrSerValAlaSerThrAsp 55
Db 189 CGAGGAATCTGTACGCGCTTCATGAGCATCACTTGGCCACCGCTGCACCTGATGAT 248
Qy 56 SerValGlnArgArgValGluAsnTYrHISerAsnleuTrpAspAspPheIleGln 75

Db 249 GGTTACAAGACGCATAGGTGACTACCATTCATATCTGGGACGATGATTTCATACAG 308
QY 76 SerleuIleSerThrProTyrGlyAlaProaspTyrArgGluArgAlaaspArgLeuIle 95
Db 309 TCTCTA---TCAACGCTTATGGGAAACCTCTTACCAGAAAGTGGAGATTAATT 365
QY 96 GlyGluValIysAspIleMetPheAsnPhelysSerLeuGluAspGlyGly----- 112
Db 366 GTGGAGGTAAAGAAGATA---TTCATTTCAATGTACCTGGATGATGGAAGATTAAAGAT 422
QY 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
Db 423 TCCTTTAATGATCTCATGCCAACGCCCTTGGATAGTCGATAGCGTTGAACGTTGGGGATA 482
QY 131 AspArgHisPheIysIleGlyValIleThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
Db 483 GCTAGACATTTCAAGAACGAGATACATCAGCTCTGATTATGTTTCCGTTACTGGGAG 542
QY 151 GluIysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170
Db 543 GAAACGGCATTTGATGTGGAGAGACAGTATGTTACTGATCTCAACTCAACTGCGTTG 602
QY 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
Db 603 GGGTTTCGAACCTCTTCGATTACACGGGTACACTGTATCTCCAGAGCTTTTAAAGCTTTT 662
QY 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyIleArg 210
Db 663 CAAGATCAAAATGACAGATTGTATGCTCCCGCGT---CAGACAGAGGATGAGATCAGA 719
QY 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230
Db 720 AGCGTTCTTAATTATATCGGGCTTCCTCATTCGCTCCCTGCGAGAAAGTTATGGAA 779
QY 231 GluAlaGluThrPheSerThrIleGlyLeuArgGluAlaLeuGlnIleProAlaSer 250
Db 780 GAAGCTGAATCTTCTCCACAAGATATTGAAAGAAAGCTCTACAAAAGATTCCAGTCTCC 839
QY 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrPheIleThrAsnLeuPro 270
Db 840 GCT---CTTTCACAAGAGATAAAGTTTGTATGGAATATGGCTGGCACACAATTTGCCA 896
QY 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrIlys-----Asn 287
Db 897 AGATTGGAAGCAAGAAATTACATGACACACTTGAGAAAGACACAGTCATGCTCAAT 956
QY 288 LysAsnAlaAlaGlyLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307
Db 957 AAAAATGCTGGGAAGAGCTTTAGAACTTGCAAAATTGAGTTCAATATATTAACTCC 1016
QY 308 LeuGlnGluArgGluLeuLysHisValSerArgTyrTrpLysAspSerGlySerProGlu 327
Db 1017 TTACACAACAAAGGAATTACAATATCTTTGAGATGTTGGAAGAGTCGGATTTCCTAAA 1076
QY 328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347
Db 1077 TTGACATTTCCTCGGCATCGTCATGTGGAATTCTACACTTTGGCCTCTTGTAATGCCATT 1136
QY 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367
Db 1137 GACCCAAAACATTCTGCATTCAAGACTAGGCTTCGCCAAAATGTGTCACTTGTCAAGATT 1196
QY 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluLeuPheThrAlaThr 387
Db 1197 TTGAGCATATTTTACGACACTTTTGAACGATTGACGAGCTTGAACCTTTCACATCTGCA 1256
QY 388 IleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407
Db 1257 ATTAAGATGGAATTTCATCAGAGATGAGAACCCTTCAGAAATATATGAATGTGTGTAC 1316
QY 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg 427
Db 1317 ATGGTCGTGTTGAAACTGTAAATGAATGACACGAGAGGCGGAGAGAAGACTCAAGGGAGA 1376

QY 428 AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu 447
Db 1377 AACACTCTCAACTATGTTGCAAAAGCTTGGAGGCTTATTTTGAATCATATATGGAAGAA 1436
QY 448 AlaIysTrpIleAlaThrGlyTyrLeuProThrPheGlnGluTyrLeuGluAsnGlyLys 467
Db 1437 GCAAAATGATCTCTAATGTTATCTGCCAATGTTTGAAGATACCATGAGATGGGAAA 1496
QY 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
Db 1497 GTGAGCTCTGCATATCGCGTAGCAACATTGCAACCCTCACTTGAATGCATGGCTT 1556
QY 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507
Db 1557 CCTGATTACATCTTGAAGGGAATTGATTTTCCATCCAGGTTCAATGATTGGCATCGTCC 1616
QY 508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGlnGlu 527
Db 1617 TTCCTTCGGCTACGAGGTGACACACGCTGCTACAAAGCCGATAGGATCGTGTGAAGAA 1676
QY 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547
Db 1677 GCTTCGTATATCATGTTATATGAAGAACAATCCTGATCAACCGAAGAAGATGCCCTC 1736
QY 548 AsnHisIleAsnPhenMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLeuLys 567
Db 1737 AATCATATCAATGCCATGGTCAATGACATTAATCAAAAGAAATTAATTGGGAACCTCTAGA 1796
QY 568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp 587
Db 1797 TCCAACGACAAATATTCCAATGCTGGCCCAAGAAACATGCTTTTGACATACAAAGAGCTTC 1856
QY 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607
Db 1857 CACCATCTCTACATATATCGAGATGCTTTAGTGTGGCAACAGGAAACAAAAAATTG 1916
QY 608 ValMetArgThrValIleGlu 614
Db 1917 GTTATGGAACAACACTCCTTGAA 1937

RESULT 14
US-10-025-145A-1
; Sequence 1, Application US/10025145A
; Publication No. US20030175861A1
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney B.
; APPLICANT: Bohlmann, Joerg
; APPLICANT: Steele, Christopher L.
; APPLICANT: Phillips, Michael A.
; TITLE OF INVENTION: Monoterpene Synthases from Grand Fir (Abies Grandis)
; FILE REFERENCE: WSUR118414
; CURRENT APPLICATION NUMBER: US/10/025,145A
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 09/360,545
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: PCT/US98/14528
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: US 60/052,249
; PRIOR FILING DATE: 1997-07-11
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2196
; TYPE: DNA
; ORGANISM: Abies Grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (69)..(1952)
; OTHER INFORMATION:
; US-10-025-145A-1

Alignment Scores:

Pred. No.: 6.37e-249 Length: 2196
 Score: 2200.50 Matches: 427
 Percent Similarity: 80.38% Conservative: 77
 Best Local Similarity: 68.10% Mismatches: 106
 Query Match: 67.69% Indels: 17
 DB: 15 Gaps: 7

US-10-025-145A-65 (1-618) x US-10-025-145A-1 (1-2196)

```

QY      1 MetAlaLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
DB      69 ATGGCTGCTGTTCTATCTCACCGTGGCTCGAATCTTGCCTGCGCAAGTCGTTGATC 128
QY      16 SerSerSerHisGluIleLeuValalaLeuArgThrIleProThrLeuGluIleCysArg 35
DB      129 AGTTCATATCATGAACATTAAGCCTCCCTATAGAACAAATCCCAATCTTGAATGCGTAGG 188
QY      36 ProGluLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
DB      189 CGAGGGAATCTGTCAAGCCTTCCATGAGCATGTTGGCCACCGCTGCACCTGATGAT 248
QY      56 SerValGlnArgArgValGluAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75
DB      249 GGTGTACAAGACGCAATAGTGAATCCCAATATCTGGACGATGATTTTCATACAG 308
QY      76 SerLeuIleSerThrProTyrGluAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
DB      309 TCTCTA---TCAAGCCTTATGGGGAACCTCTTACCAGGAACGTGCTGAGAGATTATTT 365
QY      96 GluGluValLysAspIleMetCysPheAsnPheLysSerLeuGluAspGluGly----- 112
DB      366 GTGAGAGTAAAGAGATA--TTCAATTCAATGTAACCTGGATGATGGAAGATTATGAGT 422
QY      113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGluIle 130
DB      423 TCCTTTAATGATCTCATGCAACGCCCTTGGATAGTTCGATAGCGGTTGAACGTTTGGGATA 482
QY      131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
DB      483 GCTAGACATTTCAAGAACGAGATACATCACTCTGATTATGTTTCCGTTACTGGGAG 542
QY      151 GluLysGluIleGluCysGluArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170
DB      543 GAAACGCGCATTTGGATGTGGAGAGACAGATGTTACTGATCTCAACTCAACTGCGTTG 602
QY      171 GluLeuArgThrLeuArgLeuHisGluTyrThrValSerSerAspValLeuAsnValPhe 190
DB      603 GGGTTTCAACTCTTCGATTACACGGGTACACTGTATCTCCAGAGGTTTAAAGCTTTT 662
QY      191 LysAspLysAsnGluGlnPheSerSerThrAlaAsnIleGlnIleGluGluIleArg 210
DB      663 CAAGATCAAAATGACACAGTTGTATGCTCCCGCGT--CAGACAGAGGGTGAGATCAGA 719
QY      211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGluGluValMetAsp 230
DB      720 AGCGTTCTTAATCTATATCGGGCTTCCCTCATGTCCTTCCCTGGTGAGAAAGTTATGGA 779
QY      231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250
DB      780 GAAGCTGAATCTTCTCCACAGATATTGAAAGAAAGCTCTACAAAGATTCCAGTCTCC 839
QY      251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGluTyrPheIleThrAsnLeuPro 270
DB      840 GCT---CTTCAACAAGAGATTAAGTTGTATGGAATATGCTGGCACACAATTTGCCA 896
QY      271 ArgLeuGluAlaArgAsnTyrMetAspValPheGluGlnHisThrLys-----Asn 287
DB      897 AGATTGGAAGCAAGAAATTACATAGACACCTTGAGAAAGACACACGTCATGCTCAAT 956
QY      288 LysAsnAlaAlaGluLysLeuLeuGluValAlaLysLeuGluPheAsnIlePheHisSer 307
DB      957 AAAAATGCTGGGAAGAGCTTTTAGAAGCTTGCAAAATTTGAGGTTCAATATTTAACTCC 1016
  
```

```

QY      308 LeuGlnGluArgGluLeuLysHisValSerArgTrpTrpLysAspSerGlySerProGlu 327
DB      1017 TTACAACAAGAAAGAAATTACAAATATCTTTGAGATGGTGGAAGAGTCGATTGCTTAA 1076
QY      328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347
DB      1077 TTGACATTTGCTCGGCATCGTCATGTGGAATTCTACACTTTGGCCTCTGTATGCCATT 1136
QY      348 GluProGlnHisSerGluPheArgLeuGluPheThrLysMetSerHisLeuIleThrVal 367
DB      1137 GACCCAAGACATTTCTGCATTACAGACTAGGCTTCCCAAAATGTGTCACTTGTACAGATT 1196
QY      368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluPheThrAlaThr 387
DB      1197 TTGACGATATTTAACGACACTTTTGGAAAGATTGACGAGCTTGAATCTTCACATCTGCA 1256
QY      388 IleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyrMetLysGluValTyr 407
DB      1257 ATTAAGAGATGAATTCATCAGAGATGAAACACCTTCAGAAATATGAAATGTGTGTAC 1316
QY      408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGluArg 427
DB      1317 ATGCTCGTTTGAACCTGTAATGAACTGACACGAGAGCGCGAAGAACTCAAGGAGA 1376
QY      428 AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu 447
DB      1377 AACACTCTCAACTATGTTGAAAGGCTTGGGAGGCTTATTTGATTATATATGGAAGAA 1436
QY      448 AlaLysTrpIleAlaThrGluTyrLeuProThrPheGluGluTyrLeuGluAsnGluLys 467
DB      1437 GCMAATGATCTCTAATGTTATGTCGCCAATGTTGAAGAGTACATGAGAAATGGGAAA 1496
QY      468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
DB      1497 GTGAGCTGCAATTCGCGTAGCAACATGCAACCCATCTCACTTGAATGCATGCTT 1556
QY      488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507
DB      1557 CCTGATTACATCTTGAAGGAAATGATTTTCCATCCAGGTTCAATGATTTGGCATCGTCC 1616
QY      508 IleLeuArgLeuAlaArgGluAspThrArgCysTyrLysAlaAspArgAlaArgGluGlu 527
DB      1617 TTCCTTCGGCTTACGAGGTGACACACGCTGCTCAAGGCCGATAGGATCGTGAGAGA 1676
QY      528 AlaSerSerIleSerCysTyrMetLysAspAsnProGluLysLeuThrGluGluAspAlaLeu 547
DB      1677 GCTTCGTATATCATGATTATATGAAACAAATCTCGATCAACCGAAGAGATGCCCTC 1736
QY      548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567
DB      1737 AATCATATCAATGCCATGTGTCATGACATTAATCAAAAGAAATTAATGGAACTTCTAAGA 1796
QY      568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp 587
DB      1797 TTCAACGACAAATATTCCAATGCTGCGCAAGAAACATGCTTTGACATTAACAAGAGCTTC 1856
QY      588 HisHisGluTyrArgTyrArgAspGluTyrSerPheAlaAsnValGluThrLysSerLeu 607
DB      1857 CACCATCTCTACATATATCGAGATGCGTTTAGTGTGCCAACAAGAAACAAAAAATTG 1916
QY      608 ValMetArgThrValIleGlu 614
DB      1917 GTTATGGAACAACCTCCTTGA 1937
  
```

RESULT 15

US-10-025-145A-31

; Sequence 31, Application US/10025145A

; Publication No. US20030175861A1

; GENERAL INFORMATION:

; APPLICANT: Croteau, Rodney B.

; APPLICANT: Bohlmann, Joerg

; APPLICANT: Steele, Christopher L.

; APPLICANT: Phillips, Michael A.

; TITLE OF INVENTION: Monoterpene Synthases from Grand Fir (Abies Grandis)
; FILE REFERENCE: MSUR118414
; CURRENT APPLICATION NUMBER: US/10/025,145A
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 09/360,545
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: PCT/US98/14528
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: US 60/052,249
; PRIOR FILING DATE: 1997-07-11
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 2205
; TYPE: DNA
; ORGANISM: Abies Grandis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (57)..(1943)
; OTHER INFORMATION:
US-10-025-145A-31

Alignment Scores:
Pred. No.: 1.45e-248 Length: 2205
Score: 2197.50 Matches: 427
Percent Similarity: 80.38% Conservative: 77
Best Local Similarity: 68.10% Mismatches: 106
Query Match: 67.59% Indels: 17
DB: 15 Gaps: 7

US-10-025-145A-65 (1-618) x US-10-025-145A-31 (1-2205)

QY 1 MetAlaleuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
Db 57 ATGGCTGTGGTTTCTATCTCACCGTTGGCTTCGAATCTTGCCCTGCCAAGTCGTGATC 116
QY 16 SerSerSerHisGluIleLeuValalaLeuArgThrIleProThrLeuGlyIleCysArg 35
Db 117 AGTTCAATTCAATGACATTAAGCCCTCCCTATAGAACAAATCCCAAATCTTGGAAATGCCTAGG 176
QY 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
Db 177 CGAGGGAATCTGTACAGCCCTTCCATGACATCAGTTTGGCCACCCGCTGCACCTGATGAT 236
QY 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75
Db 237 GGTGTCAAAAGACGATAGGTGACTACCATTCATATCTGGGACGATGATTTCATACAG 296
QY 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
Db 297 TCTCTA---TCAACGCAATTATGGGGAACCTCTTACCAGGAACGTGTCGAGAGATTAAATT 353
QY 96 GlyGluValLysAspIleMetPheAsnPhelysSerLeuGluAspGlyGly----- 112
Db 354 GTGAGAGTAAAGAAGATA--TTCAATTCAATGTAACCTGGATGATGAGAATTAATGAGT 410
QY 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
Db 411 TCCTTTAATGATCTCATGCAACGCCCTTGGATAGTCGATAGCGTTGAACGTTGGGGATA 470
QY 131 AspArgHisPheLeuLysGluIleLeuThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
Db 471 GCTAGACATTTTCAAGAACGAGATTAACATCAGCTCTGATTAGTTTCCGTTACTGGGAG 530
QY 151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170
Db 531 GAAACCGCATGTGATGTGGAGAGACAGTATTGTTACTGATCTCAACTCAACTGCGTTG 590
QY 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
Db 591 GGGTTTGAACCTCTTCGATTACACGGGTACACTGTATCTCCAGAGGTTTAAAGCTTTT 650
QY 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGluIleArg 210

Db 651 CAAGATCAAAATGACAGCTTTGTATGCTCCCGCGT--CAGACAGAGGTGAGATCAGA 707
QY 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230
Db 708 AGCGTTCTTAACCTATATACGGGCTTCCCTCATTCGCTTCCCTGGTGAGAAAGTTATGAA 767
QY 231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250
Db 768 GAAGCTGAATCTTCTCCACAGATATTGAAAGAAAGCTCTACAAAGATTCCAGTCTCC 827
QY 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrPheIleThrAsnLeuPro 270
Db 828 GCT---CTTCCACAGAGATTAAGTTGTTATGGAATATGGCTGGCACACAAATTTGCCA 884
QY 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLys-----Asn 287
Db 885 AGATTGAAAGCAAGAAATTACATAGACACACTTGAGAAAGACACAGTCATGGCTCAAT 944
QY 288 LysAsnAlaAlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307
Db 945 AAAAATGCTGGGAAGAGCTTTTGAACCTTGCAAAATTTGAGTTCAATATATTAACTCC 1004
QY 308 LeuGlnGluArgGluLeuLysHisValSerArgTyrTrpLysAspSerGlySerProGlu 327
Db 1005 TTACACAAAGAGATTTACATATCTTTTGAGATGTGGAAGAGATCGATTGGCTTAA 1064
QY 328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347
Db 1065 TTGACATTTGCTCGGCATCGTCATGTGAATTCTACACTTTGCCCTTGATTTGCCATT 1124
QY 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367
Db 1125 GACCCAAACATTTCTGCATTCAGACTAGGCTTCGCCAAATGTGTCACTTGTCAACAGTT 1184
QY 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluPheThrAlaThr 387
Db 1185 TTGACGATATTTACGACACTTTTGGAAAGATTGACGAGCTTGAACCTTTCACATCTGCA 1244
QY 388 IleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407
Db 1245 ATTAAGAGATGGAATTCACTCAGAGATAGAACACCTTCCAGAAATATATGAATGTGTAC 1304
QY 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnIleArg 427
Db 1305 ATGGTCGTGTTGAACCTGTAATGAACCTGACACGAGAGCGGAGAAAGACTCAAGGAGA 1364
QY 428 AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu 447
Db 1365 AACACTCTCAACTATGTTCCAAAGCCTTGGGAGGCTTATTGATTATATATGAGAGA 1424
QY 448 AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467
Db 1425 GCAAAATGATCTTAAATGTTATCTGCCAACGTTTGAAGAGTACCATGAGAAATGGGAA 1484
QY 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
Db 1485 GTGAGCTCTGCATATCGCTAGCAACATTCGAACCCATCTTGAATGCATGGCTT 1544
QY 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507
Db 1545 CCGATTACATCTTGAAGGAATTGATTTCATCCAGGTTCAATGATTGGCATCGTCC 1604
QY 508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu 527
Db 1605 TTCTTCGGCTACGAGGTGACACGCTGTACAAAGCGGATAGGATCGTGTAAGAA 1664
QY 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547
Db 1665 GCTTCGTATATCATGTTATATGAAGAACAATCTTGATCAACCGAAGAGATGCCCTC 1724
QY 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567

| | | | |
|----|------|--|------|
| Db | 1725 | AATCATATCAATGCCATGTCATGACATTAATCAAGAATTAATGGAACTTCTAAGA | 1784 |
| Qy | 568 | ProAspAsnSerValProIleThrSerIleYsHisAlaPheAspIleSerArgValTyr | 587 |
| Db | 1785 | TCCAACGACATATATCCCAATGCTGGCCAGAAACATGCTTTGACATAACAAGAGCTTC | 1844 |
| Qy | 588 | HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu | 607 |
| Db | 1845 | CACCATCTCTACATATATCGAGATGGCTTTAGTGTGCCAACAGGAAACAAAAAATTG | 1904 |
| Qy | 608 | ValMetArgThrValIleGlu | 614 |
| Db | 1905 | GTATGGAACACTCCTTGAA | 1925 |

Search completed: July 26, 2004, 22:09:45
Job time : 737 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 26, 2004, 16:57:24 ; Search time 5644 Seconds
(without alignments)
4745.924 Million cell updates/sec

Title: US-10-025-145A-65
Perfect score: 3251
Sequence: 1 MALLSTPLVSRSCLSSE.....FANVETKSLVMRTVIEPVPL 618

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_{p2n}.model -DEV=xlp
-Q=/cgn2.1/USPTO.spool_p/US10025145/runat.23072004.092622.22889/app_query.fasta.1.775
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bites -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10025145 @CGN.1.1.5600 @runat.23072004.092622.22889 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl: *
1: gb_ba: *
2: gb_htg: *
3: gb_in: *
4: gb_cm: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vi: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *

29: em_vi: *
30: em_htg_hum: *
31: em_htg_inv: *
32: em_htg_other: *
33: em_htg_mus: *
34: em_htg_pln: *
35: em_htg_kod: *
36: em_htg_nam: *
37: em_htg_vrt: *
38: em_sy: *
39: em_htgo_hum: *
40: em_htgo_mus: *
41: em_htgo_other: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|------------|---------------------|
| 1 | 3251 | 100.0 | 2013 | 6 AR222136 | AR222136 Sequence |
| 2 | 3251 | 100.0 | 2013 | 8 AGU87910 | U87910 Abies grand |
| 3 | 2456.5 | 75.6 | 1958 | 8 AY237645 | AY237645 Picea sit |
| 4 | 2453 | 75.5 | 2018 | 6 BD227661 | BD227661 Synthesas |
| 5 | 2453 | 75.5 | 2018 | 6 AR222097 | AR222097 Sequence |
| 6 | 2453 | 75.5 | 2018 | 6 AR240696 | AR240696 Sequence |
| 7 | 2453 | 75.5 | 2018 | 6 AR266971 | AR266971 Sequence |
| 8 | 2453 | 75.5 | 2018 | 6 AR316320 | AR316320 Sequence |
| 9 | 2453 | 75.5 | 2018 | 6 AR338463 | AR338463 Sequence |
| 10 | 2453 | 75.5 | 2018 | 6 AR429869 | AR429869 Sequence |
| 11 | 2453 | 75.5 | 2018 | 8 AGU87909 | U87909 Abies grand |
| 12 | 2328.5 | 71.6 | 2032 | 8 AF543527 | AF543527 Pinus tae |
| 13 | 2266.5 | 69.7 | 2162 | 8 AF543529 | AF543529 Pinus tae |
| 14 | 2264 | 69.6 | 2186 | 6 AR222137 | AR222137 Sequence |
| 15 | 2264 | 69.6 | 2186 | 8 AF139205 | AF139205 Abies gra |
| 16 | 2237 | 68.8 | 2198 | 8 AF369918 | AF369918 Picea abi |
| 17 | 2205.5 | 67.8 | 2150 | 8 AF369919 | AF369919 Picea abi |
| 18 | 2200.5 | 67.7 | 2196 | 6 BD227666 | BD227666 Synthesas |
| 19 | 2200.5 | 67.7 | 2196 | 6 AR222096 | AR222096 Sequence |
| 20 | 2200.5 | 67.7 | 2196 | 6 AR240701 | AR240701 Sequence |
| 21 | 2200.5 | 67.7 | 2196 | 6 AR266976 | AR266976 Sequence |
| 22 | 2200.5 | 67.7 | 2196 | 6 AR316325 | AR316325 Sequence |
| 23 | 2200.5 | 67.7 | 2196 | 6 AR338468 | AR338468 Sequence |
| 24 | 2200.5 | 67.7 | 2196 | 6 AR429874 | AR429874 Sequence |
| 25 | 2200.5 | 67.7 | 2196 | 8 AGU87908 | U87908 Abies grand |
| 26 | 2197.5 | 67.6 | 2205 | 6 AR222116 | AR222116 Sequence |
| 27 | 2163.5 | 66.5 | 2186 | 8 AF461460 | AF461460 Picea abi |
| 28 | 2151 | 66.2 | 2100 | 8 AF543530 | AF543530 Pinus tae |
| 29 | 2137 | 65.7 | 1890 | 6 AR222146 | AR222146 Sequence |
| 30 | 2137 | 65.7 | 1893 | 6 AF139206 | AF139206 Abies gra |
| 31 | 2084.5 | 64.1 | 2429 | 6 AR222138 | AR222138 Sequence |
| 32 | 2084.5 | 64.1 | 2429 | 8 AF139207 | AF139207 Abies gra |
| 33 | 2046.5 | 62.9 | 3306 | 8 AF326517 | AF326517 Abies gra |
| 34 | 2031.5 | 62.5 | 3089 | 6 BD227677 | BD227677 Synthesas |
| 35 | 2031.5 | 62.5 | 3089 | 6 AR222098 | AR222098 Sequence |
| 36 | 2031.5 | 62.5 | 3089 | 6 AR240712 | AR240712 Sequence |
| 37 | 2031.5 | 62.5 | 3089 | 6 AR266987 | AR266987 Sequence |
| 38 | 2031.5 | 62.5 | 3089 | 6 AR316336 | AR316336 Sequence |
| 39 | 2031.5 | 62.5 | 3089 | 6 AR338479 | AR338479 Sequence |
| 40 | 2031.5 | 62.5 | 3089 | 6 AR429885 | AR429885 Sequence |
| 41 | 2031.5 | 62.5 | 3089 | 8 AF006193 | AF006193 Abies gra |
| 42 | 1985.5 | 61.1 | 1960 | 8 AF543531 | AF543531 Pinus tae |
| 43 | 1921.5 | 59.1 | 2084 | 8 AF543528 | AF543528 Pinus tae |
| 44 | 1699 | 52.3 | 3116 | 8 AF326518 | AF326518 Abies gra |
| 45 | 1617.5 | 49.8 | 1513 | 6 BD272958 | BD272958 Materialis |

RESULT 1

ALIGNMENTS

AR222136 AR222136 2013 bp DNA linear PAT 26-SEP-2002
LOCUS AR222136 Sequence 64 from patent US 6429014.
DEFINITION AR222136
ACCESSION AR222136
VERSION AR222136.1 GI:23329510
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 2013)
AUTHORS Steele,C.L., Bohlmann,J. and Croteau,R.B.
TITLE Monoterpene synthases from grand fir (Abies grandis)
JOURNAL Patent: US 6429014-A 64 06-AUG-2002;
FEATURES location/Qualifiers
source 1. 2013
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 2.03e-255 Length: 2013
Score: 3251.00 Matches: 618
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-025-145A-65 (1-618) x AR222136 (1-2013)

QY 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeuSerSerHisGlu 20
Db |||||||
36 ATGGCTCTCTTCTTACTACCGCTGGTTCCAGGTCGTGCTCAGTCTTCTCATGAG 95
QY 21 IleYsaAlaLeuArgArgThrIleProThrLeuGlyIleCysArgProGlyLysSerVal 40
Db |||||||
96 ATTAAGGCTCTCCGTAGAACAACTCCCACTTGGATCTGCAGCGCGGGAATCCGTC 155
QY 41 AlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAspSerValGlnArgArg 60
Db |||||||
156 GCGCATTCATAAATCATGTGTGACAAACGTCGCATCTAGATTCTGTACAGAGCGC 215
QY 61 ValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGlnSerLeuIleSerThr 80
Db |||||||
216 GTGGGCACTATCATTCCAACCTGTGGGACGATGATTTCATACAGTCTCTCAACG 275
QY 81 ProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIleGlyGluValLysAsp 100
Db |||||||
276 CTTATGAGCACCCTGATTACCGGAACTGTCTGACAGACTTATGGGGAAGTAAAGCAT 335
QY 101 IleMetPheAsnPheLysSerLeuGluAspGlyGlyAsnAspLeuLeuGlnArgLeuLeu 120
Db |||||||
336 ATTAATGTTCAATTTCAAGTCGTGGAAGATGAGGCAATGATCTCTTCAACGACTTTTG 395
QY 121 LeuValAspAspValGluArgLeuGlyIleAspArgHisPheLysGlyIleLysThr 140
Db |||||||
396 CTGGTCGATGACGTTGAACGTTGGGAATCGACAGGCATTTCAAAAAGAGATAAAACG 455
QY 141 AlaLeuAspTyrValAsnSerTyrTrpAsnGlyLysGlyIleGlyCysGlyArgGluSer 160
Db |||||||
456 GCACCTCGATTATGTTAACAGTTATGGAAAGAAAGGCAATTGATGTGGGAGGAGAGT 515
QY 161 ValValThrAspLeuAsnSerThrAlaLeuGlyLeuArgThrLeuArgLeuHisGlyTyr 180
Db |||||||
516 GTTGTCGATGACCTCAACTCAACCGCTTTGGGGCTTCGAACCTCTCCGACTACACGGATAC 575
QY 181 ThrValSerSerAspValLeuAsnValPheLysAspLysAsnGlyGlnPheSerSerThr 200
Db |||||||
576 ACTGTGCTTCAGATGTTTGAACGTTTAAAGACAAAATGGGCAATTTTCTCCACT 635
QY 201 AlaAsnIleGlnIleGlyGlyLysIleArgGlyValLeuAsnLeuPheArgAlaSerLeu 220
Db |||||||
636 GCCAATATTCAGATAGAGGAGAGATTAAGGCGTTCTCAATTTATTCAGGGCCTCCCTC 695

QY 221 ValAlaPheProGlyGlyLysValMetAspGluAlaGluThrPheSerThrLysTyrLeu 240
Db |||||||
696 GTGCGCTTCCCGCGAGAAAGTTATGGATGAAGCTGAACATTTCTACAAAATATTTA 755
QY 241 ArgGluAlaLeuGlnLysIleProAlaSerSerIleLeuSerLeuGluIleArgAspVal 260
Db |||||||
756 AGAGAAAGCCCTGCAAAAAGATCCGGCATCCAGTATACTTTCACCTAGAGATACGGAGCTT 815
QY 261 LeuGluTyrGlyTyrPheThrAsnLeuProArgLeuGluAlaArgAsnTyrMetAspVal 280
Db |||||||
816 CTGGAATATGTTGGCACAACCAATTTGCCACGCTTGAAGCAAGAAATTACATGACGCTC 875
QY 281 PheGlyGlnHisThrLysAsnLysAsnAlaAlaGlyLysLeuLeuGluLeuAlaLysLeu 300
Db |||||||
876 TTGGACACGACACTAAATAAGAAACGCCCGCGGAACCTTTTGAACCTTGCAAAATTG 935
QY 301 GluPheAsnIlePheHisSerLeuGlnGluArgGluLeuLysHisValSerArgTyrTrp 320
Db |||||||
936 GAATTCAATATATTTCACCTCTTACAAAGAGAGAGATTAAACATGTTCCCGATGGTGG 995
QY 321 LysAspSerGlySerProGluMetThrPheCysArgHisArgHisValGluTyrTyrAla 340
Db |||||||
996 AAAGACTCGGGTCTCCGTGAGATGACCTTCTGTGCACATCGTCAACGTAATACCTACGCT 1055
QY 341 LeuAlaSerCysIleAlaPheGluProGlnHisSerGlyPheArgLeuGlyPheThrLys 360
Db |||||||
1056 TTGGCTTCCGATTCGCTGCGTTCGACCTCAACATTCGTGATTCAAGCTCGGCTTACCAAG 1115
QY 361 MetSerHisLeuIleThrValLeuAspAspMetTyrAspValPheGlyThrValAspGlu 380
Db |||||||
1116 ATGTCTCATCTTATCACGGTCTTGACGACATGTACGACGCTTCGGCACAGTAGACGAG 1175
QY 381 LeuGluLeuPheThrAlaThrIleLysArgTrpAspProSerAlaMetGluCysLeuPro 400
Db |||||||
1176 CTGGAACCTTTCACAGCGCAATTAAGAGATGGGATCCGTCGCCGATGGAATGCCCTTCCA 1235
QY 401 GluTyrMetLysGlyValTyrMetMetValTyrHisThrValAsnGluMetAlaArgVal 420
Db |||||||
1236 GAATATATGAAGAGAGTGATGATGTTATCACACCGTAAATGAATGGCTCGAGTG 1295
QY 421 AlaGluLysAlaGlnGlyArgAspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCys 440
Db |||||||
1296 GCAGAGAAAGCTCAAGGCGCGAGACACGCTCAACTATGACAGACAGGCTGGAGGCGTGT 1355
QY 441 PheAspSerTyrMetGlnGluAlaLysTrpIleAlaThrGlyTyrLeuProThrPheGlu 460
Db |||||||
1356 TTGTATTGTTATATGACAGAAACAAAGTGATCGCCACTGTTATCTGCCACGTTTGAG 1415
QY 461 GluTyrLeuGluAsnGlyLysValSerSerAlaHisArgProCysAlaLeuGlnProIle 480
Db |||||||
1416 GAGTACTTGGAAGAACGGGAAGTTAGCTCTGCTCATCGCCCATGCGCAATCCCAATT 1475
QY 481 LeuThrLeuAspIleProPheProAspHisIleLeuLysGluValAspPheProSerLys 500
Db |||||||
1476 CTGACGTTGGACATCCCTTCTCTGATCACATCTCAAGGAAGTTGACTTCCCATCGAAG 1535
QY 501 LeuAsnAspLeuIleCysIleIleLeuArgLeuArgGlyAspThrArgCysTyrTyrAla 520
Db |||||||
1536 CTCAATGACTTGATATGATATATCTTTCGATTAAAGAGTGATACACGGTGCTACAAAGCA 1595
QY 521 AspArgAlaArgGlyGlyGluAlaSerSerIleSerCysTyrMetLysAspAsnProGly 540
Db |||||||
1596 GACAGGCGCCGTGGAAGAAAGCTTCGTCTATATCATATGTAATAAGAACAAATCCTGGA 1655
QY 541 LeuThrGluGluAspAlaLeuAsnHisIleAsnPheMetIleArgAspAlaIleArgGlu 560
Db |||||||
1656 TTAAAGGAAGAAGATGCTGTGAATCATATCAACTTCATGATCAAGGACGAATCAGAGAA 1715
QY 561 LeuAsnTrpGluLeuLeuLysProAspAsnSerValProIleThrSerLysLysHisAla 580
Db |||||||
1716 TTAAATTGGAGCTTCTAAAGCCACAGACAGTGTTCCTCATCTTCCAAGAAACACGCA 1775
QY 581 PheAspIleSerArgValTrpHisHisGlyTyrArgTyrArgAspGlyTyrSerPheAla 600

| | | | |
|---------------------|-----------|--|---|
| Db | 1776 | TTGACATAGCAGAGTTGGCATCACGGTTACAGATACCGAGATGGCTTACAGCTTGCC | 1835 |
| Qy | 601 | AsnValGluThrIysSerLeuValMetArgThrValIleGluProValProLeu | 618 |
| Db | 1836 | AACGTGAACAAGAGTTTGGTGAAGAACCGTCATTGAACCTGTGCTTTG | 1889 |
| RESULT 2 | | | |
| AGU87910 | | 2013 bp | mRNA |
| LOCUS | | | linear |
| DEFINITION | | Abies grandis (-)-camphene synthase (AG6.5) | mRNA, complete cds. |
| ACCESSION | | U87910 | |
| VERSION | | U87910.1 | GI:2411484 |
| KEYWORDS | | | |
| SOURCE | | Abies grandis | |
| ORGANISM | | Abies grandis | |
| REFERENCE | | | |
| AUTHORS | | Bohlmann, J., Steele, C.L. and Croteau, R. | |
| TITLE | | Monoterpene synthases from grand fir (Abies grandis). cDNA isolation, characterization, and functional expression of myrcene synthase, (-)-(4S)-limonene synthase, and (-)-(1S,5S)-pinene synthase | |
| JOURNAL | | J. Biol. Chem. | 272 (35), 21784-21792 (1997) |
| MEDLINE | | 97413772 | |
| PUBMED | | 9268308 | |
| REFERENCE | | | |
| AUTHORS | | Bohlmann, J., Phillips, M., Ramachandiran, V., Katoh, S. and Croteau, R. | |
| TITLE | | cDNA cloning, characterization, and functional expression of four new monoterpene synthase members of the Trpsd gene family from grand fir (Abies grandis) | |
| JOURNAL | | Arch. Biochem. Biophys. | 368 (2), 232-243 (1999) |
| MEDLINE | | 99373092 | |
| PUBMED | | 10441373 | |
| REFERENCE | | | |
| AUTHORS | | Bohlmann, J., Steele, C.L. and Croteau, R. | |
| TITLE | | Direct Submission | |
| JOURNAL | | Submitted (31-JAN-1997) | Institute of Biological Chemistry, Washington State University, Clark Hall, Pullman, WA 99164-6340, USA |
| FEATURES | | | |
| source | | 1. .2013 | location/Qualifiers |
| gene | | /organism="Abies grandis" | |
| CDS | | /mol_type="mRNA" | |
| | | /db_xref="taxon:46611" | |
| | | 1. .2013 | |
| | | /gene="AG6.5" | |
| | | 36. .1892 | |
| | | /gene="AG6.5" | |
| | | /note="terpene synthase; monoterpene synthase; terpene cyclase" | |
| | | /codon_start=1 | |
| | | /product="(-)-camphene synthase" | |
| | | /protein_id="AAB70707.1" | |
| | | /db_xref="GI:2411485" | |
| | | /translation="MALSLIRPLVSRSLSSSHEIKALRRTIPTLGICRPGKSVASHI | |
| | | NMCLTSTVSDVQRRVGNVSHNLMDDDFIQSLISTPYGADPYRERADRLIGEVKDIM | |
| | | FNPKSLDGGNDLQRLRLVDYVERLIGIDRHPKKEIKTALDYNSYMNKEGIGCGRES | |
| | | VVTDLNSTALGLRTRLHGTYVSSDVLVNPKDKNGQFSSTANIQIEGIRGVNLPRRA | |
| | | SLVAFPEKVMDEAETFTSKYLREALOKIPASSILSLERDVLLEYGMHTNLPRLERAN | |
| | | YMDVFGQHTKNKNAEKLLEAKLEFNI FHSLOERELKIVSRWMDSGSPEMTFCHRR | |
| | | HVEYVALASCI AFEPQSHGFRIGFTKMSHLITVLDMDYVFGTVDELELFTATIKRD | |
| | | PSAMECLPEYMKGVMMVYHTVEMARVAEKAQGRDTLVNARQAWACFDSYMGEAKV | |
| | | IATGYLPTFEYLENGKVSARPCALQPILTLDIPDPHILKEVDFPSKLDNLICII | |
| | | LRLRGDTRCYKADRRARGEASISICYMKDNPGLTEEDALNHINFMIRDAIRELNLWELL | |
| | | KPDNSVPITSKGHAFDISRVVHHGYRRYRDGYSFANVETKSLVMRTVIEPVPL" | |
| ORIGIN | | | |
| Alignment Scores: | | | |
| Pred. No.: | 2.03e-255 | Length: | 2013 |
| Score: | 3251.00 | Matches: | 618 |
| Percent Similarity: | 100.00% | Conservative: | 0 |

| | | | |
|---|---------|---|------|
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 8 | Gaps: | 0 |
| US-10-025-145A-65 (1-618) x AGU87910 (1-2013) | | | |
| Qy | 1 | MetaLaleuLeuSerIleThrProLeuValSerArgSerCysLeuSerSerSerHisGlu | 20 |
| Db | 36 | ATGGCTCTTCTTTCTATTACTCCGCTGGTTCAGGTCGTGCTCAGTTCTTCTCATGAG | 95 |
| Qy | 21 | IleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArgProGlyLysSerVal | 40 |
| Db | 96 | ATTAAGGCTCTCCGTAGACAATCCCACTCTTGGAACTTGACAGCCGGGGAATCCGTC | 155 |
| Qy | 41 | AlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAspSerValGlnArgArg | 60 |
| Db | 156 | GCGCATTCATTAACATGTGTTGACAGCGTCGCATCTACTGATTCGTACAGAGACGC | 215 |
| Qy | 61 | ValGlyAsnThrHisSerAsnLeuTrpAspAspPheIleGlnSerLeuIleSerThr | 80 |
| Db | 216 | GTGGGCACTATCATCTCCAACCTGTGGAGCATGATTTTCATACAGTCTCTGATCTCAACG | 275 |
| Qy | 81 | ProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIleGlyGluValLysAsp | 100 |
| Db | 276 | CCTTATGGAGCACTGATTACCGGGACGTCGTACAGACTTATTCGGGGAAGTAAGGAT | 335 |
| Qy | 101 | IleMetPheAsnPhelysSerLeuGluAspGlyGlyAsnAspLeuGlnArgLeuLeu | 120 |
| Db | 336 | ATAATGTTCAATTTCAAGTCGCTGGAAGATGAGCAATGATCTCTTCAACGACTTTTG | 395 |
| Qy | 121 | LeuValAspAspValGluArgLeuGlyIleAspArgHisPheLysGluIleLysThr | 140 |
| Db | 396 | CTGGTCGATGACGTTGAACGTTTGGGAATCGACAGGCATTTCAAAAAAGATAAAAAAG | 455 |
| Qy | 141 | AlaLeuAspTyrValAsnSerTyrTrpAsnGluLysGlyIleGlyCysGlyArgGluSer | 160 |
| Db | 456 | GCACCTGATATGTTAAACAGTTATGGAACGAAAAAGCATTTGATGGAGGAGAGAT | 515 |
| Qy | 161 | ValValThrAspLeuAsnSerThrAlaLeuGlyLeuArgThrLeuArgLeuHisGlyTyr | 180 |
| Db | 516 | GTTGTGACTGACCTCACTCAACCGCTTGGGCTTCGAACCTCTCGAAGCTACACGGATAC | 575 |
| Qy | 181 | ThrValSerSerAspValLeuAsnValPheLysAspLysAsnGlyGlnPheSerSerThr | 200 |
| Db | 576 | ACTGTGCTTCAATGTTTGAACGTTTAAAGACAAAAATGGCAATTTCTCTCCACT | 635 |
| Qy | 201 | AlaAsnIleGlnIleGluGlyGluIleArgGlyValLeuAsnLeuPheArgAlaSerLeu | 220 |
| Db | 636 | GCCAATATTCAGATAGAGGAGAGATTAGAGCGCTTCTCAATTTATTCAAGGCCCTCCCTC | 695 |
| Qy | 221 | ValAlaPheProGlyGlyLysValMetAspGluAlaGluThrPheSerThrLysTyrLeu | 240 |
| Db | 696 | GTCGCCCTTCCCGCGAGAAAGTTATGATGAAGCTGAACATTTCTCAAAAAATATTTA | 755 |
| Qy | 241 | ArgGluAlaLeuGlnLysIleProAlaSerSerIleLeuSerLeuGluIleArgAspVal | 260 |
| Db | 756 | AGAGAGCCCTGCAAAAGATCCGGCATCCAGTACTTTCACCTAGAGATACGGAGCTT | 815 |
| Qy | 261 | LeuGluTyrGlyTyrPheIleThrAsnLeuProArgLeuGluAlaArgAsnTyrMetAspVal | 280 |
| Db | 816 | CTGGAATATGCTTGGCACACCAATTTGCCACGCTTGAAGCAAGAAATTACATGACGTC | 875 |
| Qy | 281 | PheGlyGlnHisThrLysAsnLysAsnAlaAlaGluLysLeuLeuGluAlaLysLeu | 300 |
| Db | 876 | TTTGACAGCACTAAATAATAGAACGCCCGGAGAACTTTTGAACCTTGCACAAATTG | 935 |
| Qy | 301 | GluPheAsnIlePheHisSerLeuGlnGluArgGluLeuLysHisValSerArgTyrTrp | 320 |
| Db | 936 | GAATTCATATATTTCACTCTTCAACAAGAGAGAGATTAAACATGTTCCCGATGGTGG | 995 |
| Qy | 321 | LysAspSerGlySerProGluMetThrPheCysArgHisArgHisValGluTyrTyrAla | 340 |
| Db | 996 | AAAGACTCGGGTCTCTCTGAGATGACCTTCTGTGCACATCGTCACGTGAATACTACGCT | 1055 |

Qy 341 LeuAlaSerCysIleAlaPheGluProGlnHisSerGlyPheArgLeuGlyPheThrLys 360
Db 1056 TTGGCTTCCTGCATTCGCTTCGAGCCTCAACATTCGTGATTCAGACTCGGCTTACCAAG 1115
Qy 361 MetSerHisLeuIleThrValLeuAspMetTyrAspValPheGlyThrValAspGlu 380
Db 1116 ATGTCTCATCTTATCACGGTTCCTGACGACATGTACGACGCTTCGGCACAGTAGACGAG 1175
Qy 381 LeuGluLeuPheThrAlaThrIleLysArgTrpAspProSerAlaMetGluCysLeuPro 400
Db 1176 CTGGAATCTTTCACAGCGACAATTAAAGATGGGATCCGTCGCCGATGGAATGCCCTTCCA 1235
Qy 401 GluTyrMetLysGlyValTyrMetMetValTyrHisThrValAsnGluMetAlaArgVal 420
Db 1236 GAATATATGAAGAGAGTGTACATGATGTTTATCACACCGTAATGAATGGCTCGAGTG 1295
Qy 421 AlaGluLysAlaGlnGlyArgAspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCys 440
Db 1296 GCAGAGAGGCTCAAGGCCGAGACACGCTCAACTATGCAAGACAGGCTTGGAGGCGTGT 1355
Qy 441 PheAspSerTyrMetGlnGluAlaLysTrpIleAlaThrGlyTyrLeuProThrPheGlu 460
Db 1356 TTTGATTCGTATATGCAGAGCAAGTGATCGCCACTGTTATCTGCCCAAGTTTGAG 1415
Qy 461 GluTyrLeuGluAsnGlyLysValSerSerAlaHisArgProCysAlaLeuGlnProIle 480
Db 1416 GAGTACTTGGAGAACCGGAAAGTTAGCTCTGCTCATCGCCCATGCGCACTGCAACCCATT 1475
Qy 481 LeuThrLeuAspIleProPheProAspHisIleLeuLysGluValAspPheProSerLys 500
Db 1476 CTGACGTTGGACATCCCTTCTTGATCATCTCTCAAGGAAGTTGACTTCCCATCGAAG 1535
Qy 501 LeuAsnAspLeuIleCysIleIleLeuArgLeuArgGlyAspThrArgCysTyrLysAla 520
Db 1536 CTCATGACTTGATATGATGATCATCTTCGATTAAAGAGTGATACACGGTGCTTACAAAGCA 1595
Qy 521 AspArgAlaArgGlyGlnGluAlaSerSerIleSerCysTyrMetLysAspAsnProGly 540
Db 1596 GACAGGGCCCGTGAGAGAAGACTTCGTATATCATGTATATGAACAATCCTGGA 1655
Qy 541 LeuThrGluGluAspAlaLeuAsnHisIleAsnPheMetIleArgAspAlaIleArgGlu 560
Db 1656 TTTAACGGAAGAAGATGCTCTGAATCATATCACTTCATGATCAGGAGCGCAATCAGAGAA 1715
Qy 561 LeuAsnTrpGluLeuLeuLysProAspAsnSerValProIleThrSerLysLysHisAla 580
Db 1716 TTTAAATTGGAGCTTCTTAAAGCCAGACACAGTGTCCCATCATCTTCCAAAGAAACAGCA 1775
Qy 581 PheAspIleSerArgValTrpHisIleGlyTyrArgTyrArgAspGlyTyrSerPheAla 600
Db 1776 TTTGACATTAAGCAGAGTTTGGCATCACGGTTTACAGATACCAGAGATGGCTTACAGCTTGGC 1835
Qy 601 AsnValGluThrLysSerLeuValMetArgThrValIleGluProValProLeu 618
Db 1836 AACGTTGAAACAAAGAGTTTGGTGTGATGAAACCGTCATTGAACCTGTGCTTTG 1889
RESULT 3
AY237645 1958 bp mRNA linear PLN 13-SEP-2003
LOCUS Picea sitchensis pinene synthase mRNA, complete cds.
DEFINITION
AY237645
ACCESSION
AY237645.1 GI:34582666
VERSION
KEYWORDS
SOURCE
ORGANISM
Picea sitchensis (Sitka spruce)
REFERENCE
1 (bases 1 to 1958)
AUTHORS
Byun McKay,S.A., Hunter,W.L., Goddard,K.A., Wang,S.X., Martin,D.M.,
Bohlmann,J. and Plant,A.L.
TITLE
Insect Attack and Wounding Induce Traumatic Resin Duct Development
and Gene Expression of (-)-Pinene Synthase in Sitka Spruce

JOURNAL Plant Physiol. 133 (1), 368-378 (2003)
PUBMED 12970502
REFERENCE 2 (bases 1 to 1958)
AUTHORS Byun McKay,A.S., Hunter,W.L., Goddard,K.A., Wang,S.X., Martin,D.,
Bohlmann,J. and Plant,A.L.
TITLE Direct Submission
JOURNAL Submitted (17-FEB-2003) Biology, Simon Fraser University, 8888
University Drive, Burnaby, BC V5A 1S6, Canada
FEATURES
source
1. 1958
/organism="Picea sitchensis"
/mol_type="mRNA"
/db_xref="taxon:3332"
/clone="19-2-1/12-3"
75. 1958
/note="terpene synthase; monoterpene synthase; terpene
cyclase; (-)-pinene synthase"
/codon_start=1
/product="pinene synthase"
/protein_id="AAP72020.1"
/db_xref="GI:34582667"
/translation="MALVSVAPMASRSLHKSLSSSAHELKTCRTPTLGMGRGKS
ATPSMSMLTTTVSDGVORRMGDFHSNLWNPFIQSLSTSYGSPYRERAERLIGEY
KKMFNSMSEDEGLISPHNDLIQVMMVDSVERLGIERFKNEIKSALDYVYSWSEK
GICGRESVADLNTSLGFRTRLRHGYAVSADVLNLFKDQNGFACSPSQTBEEIRS
VLNLYRASLIAFPGEKMEAEISAKYLEESLQKISVSSLSQEIADVLEGYWHTYLP
RMEARNHIDVFGDTONSKSCINTEKLELAKLEFNIHSLQKRELYLVRWKDSGS
POMTFCHRHRHVEYTLASCIAPEPHSGFRIGFAKACHIITILDMDYDTFGTVDELEL
FTAMKRWDPSSAADCLPEYMGVLLILDVTNETSREAEKAQGRDLDYARAWDYL
DSYMQEAKMIATGYLPTPAEYENGKVS SGHRTSALQPILTMDI PFPHILKEVDFPS
KLNDLASAILRLGDRCYKADRARGEASISCYMKDNPGATEEDALDHINMISDV
IRGLNWELLNPNSSVVISKKHVFDISRAFHGYKYRDKGYSVANIEKSLVARTVIDP
VTL"
ORIGIN
Alignment Scores:
Pred. No.: 1.17e-190 Length: 1958
Score: 2456.50 Matches: 473
Percent Similarity: 84.79% Conservative: 62
Best Local Similarity: 74.96% Mismatches: 79
Query Match: 75.56% Indels: 17
Gaps: 7
US-10-025-145A-65 (1-618) x AY237645 (1-1958)
Qy 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
Db 75 ATGGCTCTGGTTTCTGTGTGCGCCTATAGGCTTCAGATCATGCCCTGCACAATACTGTTAGC 134
Qy 16 SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArg 35
Db 135 AGTTCTGCTCAGCAGCTTAAAGCATCTGTAGAACAAATCCCACTCTTGAATGTCTAGG 194
Qy 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
Db 195 CGAGGAAATCTGCGACGCCCTTCTATGAGCATGAGTTTGACCACTGATCTGATGAT 254
Qy 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75
Db 255 GGGTACAAAGACGAGTGGCGCATTCATTCCAACCTATGGAACGATGATTCATACAG 314
Qy 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
Db 315 TCTCTC---TCAACGCTTTATGGGGAACCTTCTTACCGGGAACGAGCTGAGAGACTGAT 371
Qy 96 GlyGluValLysAspIleMetPheAsnPhelysSerLeuGluAspGly----- 111
Db 372 GGGGAAGTAAAGAAG--ATGTTCAATTCAATGTCAATCGGAGACGAGAGTTAATCACT 428
Qy 112 --GlyAsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
Db 429 CCCACAAATGATCTCATTCACGCGTTTGGATGTTGATAGTGTGAACGTTTAGGATA 488

| | | | | |
|----|--|------|---|------|
| Oy | | 131 | AspArgHisPheLysGluIleLeuThrAlaLeuAspTyrValAsnSerTyrTrpAsn | 150 |
| Db | | 489 | GAGAGACATTTCAAAAATGAGATAAAATCAGCGCTGGATTATGTTCACAGTTATTGGAGC | 548 |
| Oy | | 151 | GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu | 170 |
| Db | | 549 | GA AAAAAGGCATTGGATGTGGAAGAAGAACGTTGTTGCTGATCTGAAC TCAACTGCCCTTG | 608 |
| Oy | | 171 | GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe | 190 |
| Db | | 609 | GGGTTTCGAAC TCTTCGACTACACGGATACGCTGTGTCTGCCGACGTTTGAATCTTTTC | 668 |
| Oy | | 191 | LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyIleArg | 210 |
| Db | | 669 | AAAGACC AAAATGGG CAGTTTGCA TGCTCTCCGAGT--CAGACAGAGGAAGAGATCACA | 725 |
| Oy | | 211 | GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGlyLysValMetAsp | 230 |
| Db | | 726 | AGCGTA CTCAATTATATCGGGCTTCCCTCATCGCTTTCCCCGGGAGAAAGTTATGGAA | 785 |
| Oy | | 231 | GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer | 250 |
| Db | | 786 | GAGGCTGA AATCTCTCTGCCAAATATTGGAGAAGATCCCTGCAAAAGATTTCAGTCTCC | 845 |
| Oy | | 251 | SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrPheIsthArAsnLeuPro | 270 |
| Db | | 846 | AGT---CTTTCACAGAGATACGGGACGTTCTGGAATATGGTTGGCACACATATTGGCCA | 902 |
| Oy | | 271 | ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsnLysAsnAla | 290 |
| Db | | 903 | CGAATGGA AGCAAGGAATCACATCGACGCTTTGGACAGGACACTCAGAATTCAAAGTCA | 962 |
| Oy | | 291 | -----AlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer | 307 |
| Db | | 963 | TGTATAAATACAAAACTTTGGAACTTGCAAAATTGGAGTTCAACATCTTCACTCC | 1022 |
| Oy | | 308 | LeuGlnGluArgGluLeuLysHisValSerArgTyrTrpLysAspSergLysSerProGlu | 327 |
| Db | | 1023 | TTACAAAAGAGAGAGTAGTAATATCTCGTAGATGGTGAAGATTCAAGTTCACTCAA | 1082 |
| Oy | | 328 | MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe | 347 |
| Db | | 1083 | ATGACCTTTTGTGCACATCGTCACGTGCAATACTACACTTTGGCCTCTTGCA TTGCGTTT | 1142 |
| Oy | | 348 | GluProGlnHisSergLypheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal | 367 |
| Db | | 1143 | GAGCCTCA ACATTTCTGGATTCAGACTCGGCTTTGCCAAAGCGTGCATATTATCAGCAT | 1202 |
| Oy | | 368 | LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluPheThrAlaThr | 387 |
| Db | | 1203 | CTCGACGATATGTACGACACCTTTGGAAACAGTTGACGAGCTCGAACTTTCACACGGGCA | 1262 |
| Oy | | 388 | IleLysArgTyrAspProSeralametGluCysLeuProGluTyrMetLysGlyValTyr | 407 |
| Db | | 1263 | ATGAAGAGATGGGATCCGTCGGCGCTGATTGCTTCCAGAAATATATGAAGAAGATGTAC | 1322 |
| Oy | | 408 | MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg | 427 |
| Db | | 1323 | CTGATACCTTTACGACACCGTAATGA AACGTCTCGAGAGCGAGAAAGGCTCAAGGAAGA | 1382 |
| Oy | | 428 | AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu | 447 |
| Db | | 1383 | GACACGCTCGACTATGCTCGACGGGCTTGGGACGATTA TCTTGATTCGTATATGCAAGAA | 1442 |
| Oy | | 448 | AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys | 467 |
| Db | | 1443 | GC AAAGTGATCGCCACTGGTTATCTGCCAACGTTTGGCGGAGTACTACGAGAACGGAAA | 1502 |
| Oy | | 468 | ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe | 487 |
| Db | | 1503 | GTTAGCTCTG GTCATTCGACATCGGCATTGCCAACCACTTCTGACGATGGA CATCCCCTTT | 1562 |
| Oy | | 488 | ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle | 507 |

Db 1563 CCTCCTCACATCCTCAAGGAAGTTGACTTTCATCGAAGCTCAATGACTTGGCATCTGCC 1622

QY 508 ILeuArgIleuArgGlyAspThrArgCysTyrIleuAlaAspArgAlaArgGlyGlu 527

Db 1623 ATCCTTCGACTACGAGGTGATACGCCGTGCTACAGCGGACAGAGCCCGTGAGAGA 1682

QY 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547

Db 1683 GCTTCTAGTATATCTGTGTATATGAAAGCAATCTTGAGCAACAGAGGAAGATGCTTC 1742

QY 548 AsnHisIleAsnPhenMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLeuLys 567

Db 1743 GACCATATCAAGCCATGATCAGTACGCTAATCAGAGATTAAATTGGAGCTTCTCAAC 1802

QY 568 ProAspAsnSerValProIleThrSerLysIleHisAlaPheAspIleSerArgValTrp 587

Db 1803 CCAACAGCAGTGTTCCTCATATCTTCCAAGAAACATGTTTGTGACATTAAGCAGAGCTTTC 1862

QY 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607

Db 1863 CATTACGGGTACAAATATCGAGATGGCTACAGCGTTGCCAACATTGAACAAGAGTTTG 1922

QY 608 ValMetArgThrValIleGluProValProLeu 618

Db 1923 GTGAGAGAACCGTATGATCTGTGACTTTG 1955

[illegible]

Query Match: 75.45% Indels: 16
DB: 6 Gaps: 6
US-10-025-145A-65 (1-618) x BD227661 (1-2018)

QY 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
DB 6 ATGGCTCTAGTTTCTACCCGACCGCTTGCGCTTCCAATCATGCCTGCACAAATCGTTGATC 65
QY 16 SerSerSerHisGluIleLysAlaLeuArgThrIleProThrLeuGlyIleCysArg 35
DB 66 AGTTCTACCCATGAGCTTAAGGCTCTCTAGAACAAATTCAGACTCTAGGAATGAGTAGG 125
QY 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
DB 126 CGAGGAAATCTATCACTCCTTCCATCAGCATGAGCTCTACCACTGTAACCGATGAT 185
QY 56 SerValGlnArgArgValGlyAsnTyrrHisSerAsnLeuTrpAspAspPheIleGln 75
DB 186 GGTGTACGAAGACGCATGGCGAATTCCATTCCAACCTCTGGAGCATGATGTCATACAG 245
QY 76 SerLeuIleSerThrProTyrrGlyAlaProAspTyrrArgGluArgAlaAspArgLeuIle 95
DB 246 TCTTTA---CCAACGGCTTATGAGGAAAAATCGTACCCTGGAGCGTCTGAGAAACTGATC 302
QY 96 GlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly----- 112
DB 303 GGGGAAGTAAGAAC--ATGTTCAATTCCGATGTCATTAGAAAGATGGAAGCTTAATGACT 359
QY 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
DB 360 CCGCTCAATGATCTCATTCAACGCGCTTGGAATTGTCGACAGCGTTGAACGTTTGGGATC 419
QY 131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrrValAsnSerTyrrTrpAsn 150
DB 420 CATAGCATTTCAAAGATGAGATTAATACTGGCGCTTGATTATGTTTACAGTTATTGGGCG 479
QY 151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170
DB 480 GAAATGGCATCGGATGCGGAGGAGAGTGTGTACTGATCTGAACCTCAACTCGCTTG 539
QY 171 GlyLeuArgThrLeuArgLeuHisGlyTyrrThrValSerSerAspValLeuAsnValPhe 190
DB 540 GGGCTTCGAACCCCTACGACTACAGGATACCCGGTGCTTCAGATGTTTCCAAGCTTTC 599
QY 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyIleArg 210
DB 600 AAAGGCCAAAATGGGCAAGTTTCTGCTCTGAAAATATTCAAGACAGATGAAGAGATCAGA 659
QY 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230
DB 660 GGCCTCTGAATTTATTCGGGCGCTCCCTCATTCGCTTCCAGGGAGAAAATTATGAT 719
QY 231 GluAlaGluThrPheSerThrLysTyrrLeuArgGluAlaLeuGlnLysIleProAlaSer 250
DB 720 GAGGCTGAATCTCTCTACCAATAATTAAAGAGAGCCCTGCAAAAGATTCGCGTCTCC 779
QY 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrrGlyTyrrHisThrAsnLeuPro 270
DB 780 AGT---CTTCGCGAGAGATCGGGAGCGTTTGGATATGCTGGGACACATATTTCGCCG 836
QY 271 ArgLeuGluAlaArgAsnTyrrMetAspValPheGlyGlnHisThrLysAsnLysAsnAla 290
DB 837 CGATTGGAGCAAGGAATTACATCCAGTCTTTGGACAGGACACTGAGAAACAGAGAGTCA 896
QY 291 -----AlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307
DB 897 TATGTGAAGAGCAAAAACTTTAGAACTCGCAAAATTGAGTTCAACATCTTCAATCC 956
QY 308 LeuGlnGluArgGluLeuLysHisValSerArgTrpTrpLysAspSerGlySerProGlu 327
DB 957 TTACAAGAGAGGAGTTAGAAAGTGTGTGATGATGTTGGAAGAAATCGGGTTTTCCTGAG 1016

QY 328 MetThrPheCysArgHisArgHisValGluTyrrTyrrAlaLeuAlaSerCysIleAlaPhe 347
DB 1017 ATGACCTTCTGCCGACATCGTCACTGGAATACTACACTTTGGCTTCTGCAATTGCCGTTTC 1076
QY 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367
DB 1077 GAGCTCAACATCTTGATTCAAGCTCGGCTTGGCCAAGACGTGTCACTTATCACCGGTT 1136
QY 368 LeuAspAspMetTyrrAspValPheGlyThrValAspGluLeuGluLeuPheThrAlaThr 387
DB 1137 CTTGACGATATGTACGACACCTTCGGACAGTAGACGAGCTGGAACCTTCCACAGCGACA 1196
QY 388 IleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyrrMetLysGlyValTyrr 407
DB 1197 ATGAAGAGATGGGATCCGCTCCGATAGATTGCTTCCAGAAATATAGAAAGAGTGTAC 1256
QY 408 MetMetValTyrrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg 427
DB 1257 ATAGCGGTTTACGACACCGTAATGAATGGCTCGAGAGGACAGAGGCTCAAGGCCGA 1316
QY 428 AspThrLeuAsnTyrrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrrMetGlnGlu 447
DB 1317 GATACGCTCACATATGCTCGGGAAGCTTGGAGGCTTATATGTAATTCGTATATGCAAGAA 1376
QY 448 AlaLysTrpIleAlaThrGlyTyrrLeuProThrPheGluGluTyrrLeuGluLysGlyLys 467
DB 1377 GCAAGGTGATCGCCACTGGTTAAGCTGCGCTTGTGATGAGTACTACGAGAATGGGAAA 1436
QY 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
DB 1437 GTTAGCTGTGTCATCGCATATCCGCATTTGCAACCCATCTGACAATGACATCCCTTTT 1496
QY 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507
DB 1497 CCTGATCATATCTCAAGGAAGTTGACTTCCCATCAAGCTTAACGACTTGGCATGTGCC 1556
QY 508 IleLeuArgLeuArgGlyAspThrArgCysTyrrLysAlaAspArgAlaArgGlyGluGln 527
DB 1557 ATCTTCGATTACGAGGTGATACGGGTGCTACAAAGGCGGACAGGCTCGTGAGAGAA 1616
QY 528 AlaSerSerIleSerCysTyrrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547
DB 1617 GCTTCCTCTATATCATGTTATATGAAGAACAATCCTGAGATATCAGAGGAAGATGCTTTC 1676
QY 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567
DB 1677 GATCATATCAACGCCATGATGATGACGTAAATCAAAAGATTAATGGGAATCTTCAAA 1736
QY 568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp 587
DB 1737 CCAGACATCAATGTTCCCATCTCGGCGAAGAAACATGCTTTGACATCGCAGAGCTTTC 1796
QY 588 HisHisGlyTyrrArgTyrrArgAspGlyTyrrSerPheAlaAsnValGluThrLysSerLeu 607
DB 1797 CATTAACGCTACAATAACCGAGACGGCTACAGCGTTGCCCAAGTTGAACGAGAGATTG 1856
QY 608 ValMetArgThrValIleGluProValProLeu 618
DB 1857 GTACGAGAAACCTCCTTGAAATCTGTGCTTTG 1889

RESULT 5
AR222097 2018 bp DNA linear PAT 26-SEP-2002
LOCUS AR222097
DEFINITION Sequence 3 from patent US 6429014.
ACCESSION AR222097
VERSION AR222097.1 GI:23329471
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2018)
AUTHORS Steele,C.L., Bohlmann,J. and Croteau,R.B.
TITLE Monoterpene synthases from grand fir (*Abies grandis*)

JOURNAL Patent: US 6429014-A 3 06-AUG-2002;
FEATURES Location/Qualifiers
source 1. 2018
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:

| | | | |
|------------------------|-----------|---------------|------|
| Pred. No.: | 2.34e-190 | Length: | 2018 |
| Score: | 2453.00 | Matches: | 475 |
| Percent Similarity: | 84.63% | Conservative: | 59 |
| Best Local Similarity: | 75.28% | Mismatches: | 81 |
| Query Match: | 75.45% | Indels: | 16 |
| DB: | 6 | Gaps: | 6 |

US-10-025-145A-65 (1-618) x AR222097 (1-2018)

QY 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
DB 6 ATGGCTCTAGTTTCTACCGCACCGCTGGCTTCCAAATCATGCTGCACAAATCGTTGATC 65
QY 16 SerSerHisGluIleLeuValArgGlyThrIleProThrLeuGlyIleCysArg 35
DB 66 AGTTCTACCCATGAGCTTAAGGCTCTCTGTAACAATTCCAGCTCTGAGAAATGAGTAGG 125
QY 36 ProGlySerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
DB 126 CGAGGGAATCTATCACTCCTTCATCAGCATGAGCTCTACCAACCGTTGTAACCGATGAT 185
QY 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75
DB 186 GGTGTACGAAGACGCATGGCGATTTCCTCAACCTCTGGAGACGATGATCATACAG 245
QY 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
DB 246 TCTTTA---CCAA CGGCTTATGAGAAAAATCGTACCTGAGCGTGTGAGAAACTGATC 302
QY 96 GlyGluValIleAspIleMetPheAsnLeuSerLeuGluAspGlyGly----- 112
DB 303 GGGGAGTAAAGAAC--ATGTTCAATTGATGTCTATTAGAGATGAGAGTTAATGAGT 359
QY 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
DB 360 CCGCTCATATGATCTCATTCACGCGCTTGGATGTGACAGACCTTGAACGTTGGGATC 419
QY 131 AspArgHisPheLeuSylsGluIleLeuThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
DB 420 CATAGACATTTCAAAGATGAGATTAATCGCGCTTGATTATGTTTACAGTTATTGGGGC 479
QY 151 GlyLeuGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170
DB 480 GAAATGCGATCGGATCGGAGGAGAGTGTTGTTACTGATCTGAATCAACTCGCGTTG 539
QY 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
DB 540 GGGCTTCGAACCTTACGACTACACGGAATACCGGTGCTTCAGATGTTTCAAAGCTTTC 599
QY 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyIleArg 210
DB 600 AAAGGCCAAATGGGAGTTTCTGCTGTAATAATATTACAGACAGATGAAGAGATCAGA 659
QY 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230
DB 660 GGGCTTCTGAATTTATTCGGGCTCCTTCATTCGCTTCCAGGGGAGAAATATGATGAT 719
QY 231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250
DB 720 GAGGCTGAATCTTCTCTACCAATATTTAAAGAAGCCCTGCAAAAGATTCGGTCTCC 779
QY 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrHisThrAsnLeuPro 270
DB 780 AGT---CTTTCGCGAGAGATCGGGGACGTTTGGAAATATGTTGGCACACATATTGCCG 836

QY 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnIleThrLysAsnLysAsnAla 290
DB 837 CGATTGGAAGCAAGGAATTACATCCAGTCTTTGGACAGACACTGACGAACAGAGTCA 896
QY 291 -----AlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307
DB 897 TATGTGAAGACCAATAAATCTTTAGAACTCGCAAAATTTGAGTTCAATCTTCATCC 956
QY 308 LeuGlnGluArgGluLeuLysHisValSerArgTyrTrpLysAspSerGlySerProGlu 327
DB 957 TTACAAAGAGGAGGAGTTAGAAAGTCTGCTCAGATGTTGGAAGAATCGGCTTTCCTGAG 1016
QY 328 MetThrPheCysArgHisValGlnIleGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347
DB 1017 ATGACCTTCTGCCGACATCGTACGTAATTACTACACTTGGCTTCTGCAATTGCGTTC 1076
QY 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367
DB 1077 GAGCCTCAACATTCCTGATTCAGACTCGGCTTGGCCAAAGACGTGATCTTATCACGGTT 1136
QY 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluPheThrAlaThr 387
DB 1137 CTGACGATATGTACGACACCTTCGGCAGTAGACGAGCTGAACTCTTACACGACGA 1196
QY 388 IleLysArgTyrAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407
DB 1197 ATGAAGAGATGGGATCCGCTCCTCGATGATGCTCCTCCAGAAATATATGAAGAAGTGTAC 1256
QY 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnIleArg 427
DB 1257 ATAGCGGTTTACGACACCGTAATGAATGGCTCGAGAGGACAGAGGAGCTCAAGGCCGA 1316
QY 428 AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnIle 447
DB 1317 GATACGCTCATATATGCTCGGGAAGCTTGGGAGCTTATATGATGATTCGATATGCAAGAA 1376
QY 448 AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467
DB 1377 GCAAGGTGATCGCCACTGCTGATCCGCCCTCTTGTGATGAGTACTACGAGAATGGGAA 1436
QY 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
DB 1437 GTTAGCTGTGCTATCGCATATCCGCATTCGAACCATCTTGACAAATGACATCCCTTT 1496
QY 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507
DB 1497 CCTGATCATATCTCAAGGAAGTTGACTTCCATCAAAAGCTTAAAGCACTTGGCATGTGCC 1556
QY 508 IleLeuArgLeuLysGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu 527
DB 1557 ATCCTTCGATTACGAGGTGATACGGGTGCTTACAGGCGGACAGGCTCGTGAGAAAGAA 1616
QY 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547
DB 1617 GCTTCCTATATATCATGTTATATGAAGAACAATCCTGAGTATCAGAGAAGATGCTCTC 1676
QY 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLeuLys 567
DB 1677 GATCATATCAACGCCATGATCAGTACGTAATCAAAAGATTAATGGGAATCTCTCAA 1736
QY 568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp 587
DB 1737 CCAGACATCAATGTTCCCATCTCGGCGAAGAAACATGCTTTTGACATCGCCAGAGCTTTC 1796
QY 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607
DB 1797 CATTAAGCTACAAATACCGAGAGCGCTACAGCGTTGCCAACGTTGAACGAAAGATTG 1856
QY 608 ValMetArgThrValIleGluProValProLeu 618
DB 1857 GTACAGGAACCTCCTGGAATCTGTGCTTTG 1889

RESULT 6

AR240696 AR240696 2018 bp DNA linear PAT 20-DEC-2002
LOCUS AR240696
DEFINITION Sequence 19 from patent US 6468772.
ACCESSION AR240696
VERSION AR240696.1 GI:27285845
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 2018)
AUTHORS Chappell,J., Manna,K.R., Noel,J.P. and Starks,C.M.
TITLE Methods of making modified polypeptides
JOURNAL Patent: US 6468772-A 19 22-OCT-2002;
FEATURES Location/Qualifiers
source 1. 2018
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 2.34e-190 length: 2018
Score: 2453.00 Matches: 475
Percent Similarity: 84.63% Conservative: 59
Best Local Similarity: 75.28% Mismatches: 81
Query Match: 75.45% Indels: 16
DB: 6 Gaps: 6
US-10-025-145A-65 (1-618) x AR240696 (1-2018)

QY 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
DB 6 ATGGCTCTAGTTTCTACCGCACCGCTTGCTTCCAATCATGCTGCACAAATCGTTGATC 65
QY 16 SerSerSerHisGluIleLysAlaLeuArgThrIleProThrLeuGlyIleCysArg 35
DB 66 AGTTCTACCCATGAGCTTAAGGCTCTCTAGAACAATCCAGCTTGAAGATGAGTAGG 125
QY 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
DB 126 CGAGGGAATCTATCACTCCCTCCATCAGCATGAGCTTACCACCGTTGTAAACCGATGAT 185
QY 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75
DB 186 GGTGTACGAAGACGATGGGCGATTTCATCCAACTCTGGAGCATGATGCATACAG 245
QY 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
DB 246 TCTTTA--CCAACGGCTTATGAGAAAAATCGTACCCTGGAGCGTGTGAGAAACTGATC 302
QY 96 GlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly----- 112
DB 303 GGGGAAGTAAAGAAC--ATGTTCAATTGCGATGTCATTAGAAGATGGAAGAGTTAATGAGT 359
QY 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
DB 360 CCGCTCAATGATCTCATTTCAACGCGCTTGGATTGTCAGACAGCCTTGAACGTTTGGGATC 419
QY 131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
DB 420 CATAGACATTTCAAGAATGAGATGAATAATCGCGCTTGATTAATGTTTAAAGTTATGGGCG 479
QY 151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170
DB 480 GAAATGCGATCGGATGCGGAGGAGGAGGTGTTGTTACTGATCTGAACCTCACTCGCTTG 539
QY 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
DB 540 GGGCTTCGAACCTTACGACTACCGGATACCCGGTGTCTTCAGATGTTTCAAAAGCTTTC 599
QY 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyLysIleArg 210
DB 600 AAAGGCCAAATGGGCGAGTTTCTCTGCTGAAATATTTCAGACAGATGAAGAGATCAGA 659

QY 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGlyLysValMetAsp 230
DB 660 GGGCTTCTGAATTATTCCGGGCGCTCCCTCATTTGCCCTTCCAGGGGAGAAAAATTATGAT 719
QY 231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250
DB 720 GAGCTGAAATCTTCTTACCAATATTATAAAGAAGCCCTGCAAAAGATTCCGGTCTCC 779
QY 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrHisThrAsnLeuPro 270
DB 780 AGT---CTTTCGAGAGATCGGGGACGTTTGGAAATGTGTTGGCACACATATTGGCCG 836
QY 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsnLysAsnAla 290
DB 837 CGATTGGAAGCAAGGAATTACATCCAAAGTCTTTGACAGACACTGAGAACAGAGTCA 896
QY 291 -----AlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307
DB 897 TATGTGAAGAGCAAAAACTTTTGAACCTCGCAAAATTGAGATTCAACATCTTCAATCC 956
QY 308 LeuGlnGluArgGluLeuLysHisValSerArgTyrTrpLysAspSerGlySerProGlu 327
DB 957 TTACAAAGAGGAGGAGTTAGAAAGTCTGTGTCAGATGTGTGAAGAATCGGTTTCTCTAG 1016
QY 328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347
DB 1017 ATGACCTTCTGCCGACATCGTCACTGAATACACTTGTGCTTCCCTGATTCGCTTC 1076
QY 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367
DB 1077 GAGCTCAACATTTCTGATTCAGACTCGGCTTGGCCAAGCGTGCATCTTATCACGGTT 1136
QY 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluPheThrAlaThr 387
DB 1137 CTTCAGATATGTACGACACCTTCGGCACAGTAGACGAGCTGGAACCTTCACAGCGACA 1196
QY 388 IleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407
DB 1197 ATGAAGAGATGGGATCCGCTCTCGATAGATTGCCCTCCGAATATATGAAGAAGTGTAC 1256
QY 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg 427
DB 1257 ATAGCGGTTTACGACACCGTAAATGAATGGCTCGAGAGCGAGAGGAGCTCAAGGCCGA 1316
QY 428 AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu 447
DB 1317 GATACGCTCACATATGCTCGGGAAGCTTGGAGGCTTATATGATTGCTATATGCAAGAA 1376
QY 448 AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467
DB 1377 GCAAGTGGATCGCCACTGGTTAACTGCCCTCTTGATGAGTACTACGAGAATGGGAAA 1436
QY 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
DB 1437 GTTAGCTGTGTCATCGCATATCCGCATTCGAACCCATCTGACAATGACATCCCTTT 1496
QY 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507
DB 1497 CCTGATCATATCTCAAGGAAGTTGACTTCCCATCAAGCTTAAAGCACTTGGCATGTGCC 1556
QY 508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu 527
DB 1557 ATCTTCGATTACGAGGTGATACGGGTGTACAAAGCGGACAGGCGTGTGAGAGAA 1616
QY 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluLysAspAlaLeu 547
DB 1617 GCTTCCTCTATATCATGTATTATGAAGAACAATCCTGGAGTATCAGAGAAAGATGCTTC 1676
QY 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLeuLys 567
DB 1677 GATCATATCAACGCCATGATCACTGACGTAATCAAAAGATTAAATTGGGAACCTTCAAA 1736
QY 568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp 587

Db 1737 CCAGACATCATGTTCCTCCATCTCGCGGAGAAACATGCTTTTGACATCGCCAGAGCTTTC 1796
Qy 588 HishiegIyTyArgTyArgAspGlyTySerPheAlaAsnValGluThrLysSerLeu 607
Db 1797 CATTAAGGCTACAATATACCGAGACGGCTTACAGCGTTGCCAACGTTGAACGAAGAGTTTG 1856
Qy 608 ValMetArgThrValIleGluProValProLeu 618
Db 1857 GTCACGAGAACCTCCTTGAATCTGTGCTTGG 1889

RESULT 7
AR266971 AR266971 2018 bp DNA linear PAT 10-APR-2003
LOCUS Sequence 19 from patent US 6495354.
DEFINITION AR266971
ACCESSION AR266971
VERSION AR266971.1 GI:29696426
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 2018)
AUTHORS Chappell,J., Manna,K.R., Noel,J.P. and Starks,C.M.
TITLE Synchases
JOURNAL Patent: US 6495354-A 19 17-DEC-2002;
FEATURES Location/Qualifiers
SOURCE 1. 2018
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 2.34e-190 Length: 2018
Score: 2453.00 Matches: 475
Percent Similarity: 84.63% Conservative: 59
Best Local Similarity: 75.28% Mismatches: 81
Query Match: 75.45% Indels: 16
DB: Gaps: 6

US-10-025-145A-65 (1-618) x AR266971 (1-2018)

Qy 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
Db 6 ATGGCTCTAGTTTCTTACCGCACCGTGGCTTCCAAATCATGCTGCACAAATCGTTGATC 65
Qy 16 SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArg 35
Db 66 AGTTCTACCCATGAGCTTAAGGCTCTCTAGAACAATTCCAGCTCTAGGAATGAGTAGG 125
Qy 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
Db 126 CGAGGGAATCTATCACTCCCTTCCATCAGCATGAGCTCTACCACTGTTGAACCGATGAT 185
Qy 56 SerValGlnArgArgValGlyAsnTyHisSerAsnLeuThrAspAspAspPheIleGln 75
Db 186 GGTGTACGAAGACGCGATGGCGATTTCATTCCAACTTGGGACGATGATCATACAG 245
Qy 76 SerLeuIleSerThrProTyrgIyAlaProAspTyArgGluArgAlaAspArgLeuIle 95
Db 246 TCTTTA---CCAACGGCTTATGAGGAAAAATCGTACCTGAGCGTGTGAGAAAAGTATC 302
Qy 96 GlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly----- 112
Db 303 GGGGAAGTAAGAAC--ATGTTCAATTTCGATGTAGAGATGAGAGAGTAAATGAGT 359
Qy 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
Db 360 CCGCTCAATGATCTCATTCACGCTTTGGATTGTGACAGCGCTTGAAGTTGGGATC 419
Qy 131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyValAsnSerTyTrpAsn 150
Db 420 CATAGACATTTCAAAGATGAGATAAATCGGCGCTGTATATGTTTACAAGTTATGGGCG 479

Qy 151 GluLysGlyIleGlyCysGlyArgGluSerValIleThrAspLeuAsnSerThrAlaLeu 170
Db 480 GAAATGGCATCGGATGCGGAGGAGAGTGTGTACTGATCTGAACCTCAACTCGCTTG 539
Qy 171 GlyLeuArgThrLeuArgLeuHisGlyTyThrValSerSerAspValLeuAsnValPhe 190
Db 540 GGGCTTCAACCTTACGACTACACGGATACCCGGTGTCTTCAGATGTTTCAAAGCTTTC 599
Qy 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyIleArg 210
Db 600 AAAGGCCAAATGGCGAGTTTCTGCTCTGAAAATATTTCAGACAGATGAAGAGATCAGA 659
Qy 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230
Db 660 GCGCTTCTGAATTTATTCGGGCGCTCCCTCATTTGCCCTTCCAGGGGAGAAAATATGAT 719
Qy 231 GluAlaGluThrPheSerThrLysTyThrLeuArgGluAlaLeuGlnLysIleProAlaSer 250
Db 720 GAGGCTGAATCTTCTCTACCAATATTTAAAGAAGCCCTGCAAAGAATTCGGTCTCC 779
Qy 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrgIyTrpHisThrAsnLeuPro 270
Db 780 AGT---CTTCCGCGAGAGATCGGGGACGTTTGGATATGTTGGCACACATATTGGCCG 836
Qy 271 ArgLeuGluAlaArgAsnTyMetAspValPheGlyGlnHisThrLysAsnLysAsnAla 290
Db 837 CGATTGGAAGCAACGAATTACATCCAGTCTTTGGACAGGACACTGAGAACACGAAGTCA 896
Qy 291 -----AlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307
Db 897 TATGTGAGAGCAAAAACTTTAGACTCGCAAAATTGGAGTTCAACATCTTCAATCC 956
Qy 308 LeuGlnGluArgGluLeuLysHisValSerArgTrpTrpLysAspSerGlySerProGlu 327
Db 957 TTACAAGAAGAGGAGATTAGAAAGTGGTCAGATGGTGAAGAAGATCGGTTTCTCTGAG 1016
Qy 328 MetThrPheCysArgHisArgHisValGluTyrrTyrrAlaLeuAlaSerCysIleAlaPhe 347
Db 1017 ATGACCTTGTGCCGACATCGTACGCGAATACTACACTTGGCTTCCCTGATTCGCTTC 1076
Qy 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367
Db 1077 GAGCCTCAACATYCTGATTCAAGCTCGGCTTGGCCAGACGTCATCTTATCACGGTT 1136
Qy 368 LeuAspAspMetTyrrAspValPheGlyThrValAspGluLeuGluPheThrAlaThr 387
Db 1137 CTTGACATATGTAGACACACTTGGCACAGTAGACGAGCTGGAACCTTTCACAGCGACA 1196
Qy 388 IleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyrrMetLysGlyValTyrr 407
Db 1197 ATGAAGAGATGGGATCCGCTCGATGATGCTTCCAGAAATATGAAAAGAGTGTAC 1256
Qy 408 MetMetValTyrrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnIyArg 427
Db 1257 ATAGCGGTTTACGACACCGTAATGAATGGCTCGAGAGGACGAGAGGCTCAAGCGCA 1316
Qy 428 AspThrLeuAsnTyrrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrrMetGlnGlu 447
Db 1317 GATACGCTCACATATGCTCGGGAAGCTTGGAGGCTTATATGATTCGTATATGACAAGA 1376
Qy 448 AlaLysTrpIleAlaThrGlyTyrrLeuProThrPheGluGluTyrrLeuGluAsnGlyLys 467
Db 1377 GCAAGGTGATCGCCACTGCTTACCTGCCCTCTTGTATGAGTACTACGAGAATGGGAAA 1436
Qy 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProphe 487
Db 1437 GTTAGCTGTGTCATCGCATATCGCATTTGCAACCCATTTGACAAATGACATCCCTTT 1496
Qy 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507
Db 1497 CCTGATCATATCTCAAGGAAGTGACTTCCCATCAAGCTTAAAGCACTTGGCATGTGCC 1556
Qy 508 IleLeuArgLeuArgGlyAspThrArgCysTyrrLysAlaAspArgAlaArgGlyGluGlu 527

Db 1557 ATCCTTCGATTACGAGGTGATACGGCGGTCTACAGAGCGGACGGGCTCGTGAGAAAGA 1616
QY 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547
Db 1617 GCTTCCTATATCATGTATATGAAGAACAATCCTGGAGTATCAGAAGAAGATGCTCTC 1676
QY 548 AsnHisIleAsnPhenMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLeuLys 567
Db 1677 GATCATATCAACGCCCATGATCAGTACGTAATCAAAAGGATTAAATTGGGAACCTCTCAA 1736
QY 568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp 587
Db 1737 CAGACATCAATGTTCCTCATCTCGCGGAAGAAACATGCTTTGACATCGCCAGAGCTTTC 1796
QY 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607
Db 1797 CATTAACGGCTACAATAACCGAGCGGCTACAGCGTTGCCAACGTTGAAACGAAAGATTTC 1856
QY 608 ValMetArgThrValIleGluProValProLeu 618
Db 1857 GTCAAGAGAACCCTCCTTGAATCTGTGCCTTTG 1889

RESULT 8
AR316320 2018 bp DNA linear PAT 12-JUN-2003
LOCUS AR316320
DEFINITION Sequence 19 from patent US 6559297.
ACCESSION AR316320
VERSION AR316320.1 GI:31711055
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2018)
AUTHORS Chappell,J., Manna,K.R., Noel,J.P. and Starke,C.M.
TITLE Syntheses
JOURNAL Patent: US 6559297-A 19 06-MAY-2003;
FEATURES location/Qualifiers
source 1. 2018
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 2.34e-190 length: 2018
Score: 2453.00 Matches: 475
Percent Similarity: 84.63% Conservative: 59
Best Local Similarity: 75.28% Mismatches: 81
Query Match: 75.45% Indels: 16
DB: 6 Gaps: 6

US-10-025-145A-65 (1-618) x AR316320 (1-2018)
QY 1 MetaIaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
Db 6 ATGGCTCTAGTTTCTACCGCACCGTTGGCTTCCAATCATGCTGCACAAATCGTTGATC 65
QY 16 SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArg 35
Db 66 AGTTCTAACCATGAGCTTAAGGCTCTCTAGAACAAATCCAGCTTAGAATGAGTAGG 125
QY 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
Db 126 CGAGGAAATCTATCACTCCTTCATCAGCATGAGCTCTACCAACCGTTGTAAACGATGAT 185
QY 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75
Db 186 GGTGTACGAAGACGCATGGCGATTTCATTCCAACCTCTGGGAGCATGATGCATACAG 245
QY 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
Db 246 TCTTTA---CCAAACGGCTTATGAGAAATAATCGTACCTGAGCGTGTGAGAAAAGTATC 302

QY 96 GlyGluValLysAspIleMetPheAsnPhelySerLeuGluAspGlyGly----- 112
Db 303 GGGGAAGTAAAGAAC--ATGTTCAATTTCGATGTCAATTAGAAGATGGAGAGTTAATGAGT 359
QY 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
Db 360 CCGCTCAATGATCTCATTTCAACGCCCTTTGGATTGTTCGACAGCCTTGAAACGTTTGGGGATC 419
QY 131 AspArgHisPheLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
Db 420 CATGACATTTCAAAAGATGAGTAAATCGGCGCTTGATTATGTTTACAGTTATGGGCG 479
QY 151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170
Db 480 GAAATGGCATCGGATGCGGAGGAGAGAGTGTGTACTGATCTGAACTCAACTGCGTTG 539
QY 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
Db 540 GGGCTTCGAACCCCTACGACTACACGAGTACCCGCTGTCTCAGATGTTTCAAGCTTTC 599
QY 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyIleArg 210
Db 600 AAAGGCCAAATGGGACGTTTCTCCTCTGAAAATATTTCAGACACAGATGAAGAGATCAGA 659
QY 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230
Db 660 GCGCTTGAATTATTCTCGGGCTCCTCATTTGCCAGGGGAGAAAATTATGAT 719
QY 231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250
Db 720 GAGGCTGAATCTTCTCTACCAATAATTAAAGAACCCCTGCAAAAGATTCCGCTCC 779
QY 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrHisThrAsnLeuPro 270
Db 780 AGT---CTTTCGAGAGAGATCGGGAGCGTTTGAATATGGTTGGCACACATATTGGCCG 836
QY 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsnLysAsnAla 290
Db 837 CGATTGGAAGCAAGGAATTACATCCAAAGTCTTTGACAGACAGACTGAGAACACGAAAGTCA 896
QY 291 -----AlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307
Db 897 TATGTGAAGAGCAAAAACTTTGAACCTCGCAAAATTGGAGTTCAACATCTTTCAATCC 956
QY 308 LeuGlnGluArgGluLeuLysHisValSerArgTyrTrpLysAspSerGlySerProGlu 327
Db 957 TTACAAAGAGGAGGAGTTAGAAAGTCTGTCAGATGTGGAAGAAATCGGGTTTCTCTGAG 1016
QY 328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347
Db 1017 ATGACCTTCTCGCCGACATCGTCAGTGAATACTACACTTTGGCTTCCTGATTCGCTTC 1076
QY 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367
Db 1077 GAGCCTCAACATTTCTGATTCAGACTCGGCTTTGCCAAGACGTGTCACTTATCAGGTT 1136
QY 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluLeuPheThrAlaThr 387
Db 1137 CTTGACGATATGTACGACACCTTCGCGACAGTAGACGAGCTGGAACCTTCACAGCGACA 1196
QY 388 IleLysArgTyrAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407
Db 1197 ATGAAGAGATGGATCCGTCCTCATGATGATTCCTTCAGAAATATGAAAAGAGTGATC 1256
QY 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg 427
Db 1257 ATAGCGGTTTACGACACCGTTAAATGAATGGCTCGAGAGCGAGAGGCTCAAGGCCGA 1316
QY 428 AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu 447
Db 1317 GATACGCTCACATATGCTCGGGAAGCTTGGAGGCTTATATGATTCGTATATGCAAGAA 1376
QY 448 AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467

Db 1377 GCAAGGTGATCGCCACTGGTTACTGCGCTCTTGATGAGTACTGAGAAATGGAAA 1436
Qy 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
Db 1437 GTTAGCTGTGTGTCATCGCATATCCGCAATTGCAACCATTCTGACAAATGCAATCCCTTT 1496
Qy 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507
Db 1497 CCTGATCATATCCTCAAGGAAGTGTACTTCCCATCAAGCTTAACGACTTGCGATGTGCC 1556
Qy 508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGlu 527
Db 1557 ATCTTCGATTACGAGGTGATACCGGCTCTACAAAGCGGACAGGGCTCGTGAGAAGAA 1616
Qy 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547
Db 1617 GCTTCTCTATATCATGTTATATGAAGCAATCCTGAGTATCAGAGGAAGATGCTCTC 1676
Qy 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567
Db 1677 GATCATATCAACGCCATGATCAGTACGTAATCAAAAGATTAAATGGGAACTTCTCAA 1736
Qy 568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp 587
Db 1737 CCAGACATCAATGTTCCTCATCTCGCGAAGAACAATGCTTTGACATCGCCAGAGCTTTC 1796
Qy 588 HisIleGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607
Db 1797 CATTACGCTACAATATACGAGACGGCTACAGCGTGCACACGTTGAACGAAGAGTTTG 1856
Qy 608 ValMetArgThrValIleGluProValProLeu 618
Db 1857 GTCACGAGAACCTCTCTGAAATCTGTGCTTTG 1889

RESULT 9
AR338463
LOCUS AR338463 2018 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 19 from patent US 6569656.
ACCESSION AR338463
VERSION AR338463.1 GI:33725240
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2018)
AUTHORS Chappell,J., Manna,K.R., Noel,J.P. and Starks,C.M.
TITLE Synthesizes
JOURNAL Patent: US 6569656-A 19 27-MAY-2003;
FEATURES location/Qualifiers
source 1..2018
/organisms="unknown"
/mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 2.34e-190 Length: 2018
Score: 2453.00 Matches: 475
Percent Similarity: 84.63% Conservative: 59
Best Local Similarity: 75.28% Mismatches: 81
Query Match: 75.45% Indels: 16
DB: Gaps: 6
US-10-025-145A-65 (1-618) x AR338463 (1-2018)

Qy 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
Db 6 ATGGCTCTAGTTTCTACCGCACCGTTGGCTTCCAATCATGCTGCACAATCGTTGATC 65
Qy 16 SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArg 35
Db 66 AGTTCTACCCATGAGCTTAAGGCTCTCTCTAGAACAAATTCACAGCTCTAGGAATGAGTAGG 125

Qy 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
Db 126 CGAGGGAATCTATCACTCCTTCCATCAGCATGAGCTCTACCAACCGTTGTAAACGATGAT 185
Qy 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75
Db 186 GGTGTACGAAACGATGGCGGATTTCCATTCCAACCTCTGGGACGATGATGCATACAG 245
Qy 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95.
Db 246 TCTTTA---CCAACGGCTTATGAGGAAAAATCGTACCTGGAGCGTGCTGAGAAACTGATC 302
Qy 96 GlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly----- 112
Db 303 GGGGAAGTAAAGAAC--ATGTTCAATTGATGTCATTAGAAAGATGAGAGTTAATGAGT 359
Qy 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
Db 360 CCGCTCAATGATCTCATCAACGCCCTTGATGTGCACAGCCTTGAACTTGCGGGATC 419
Qy 131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
Db 420 CATAGACATTTCAAGATGAGATAAATCGCGCTGATTATGTTACAGTTATTGGGCGC 479
Qy 151 GlyLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170
Db 480 GAAATGGCATCGCATGCGGAGGAGAGTGTGTTACTGATCTGAATCAACTGCGGTTG 539
Qy 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
Db 540 GGGCTTGAACCTTACGACTACACGGATACCCGGTGTCTTCAGATGTTTCAAGCTTTC 599
Qy 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyIleArg 210
Db 600 AAAGGCCAAATGAGCAGTTTCTGCTGCTGAATATTACAGACAGATGAAGAGATCAGA 659
Qy 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGlyLysValMetAsp 230
Db 660 GCGCTCTGAATTTATTCGGGCTCCTCATGCTTCCAGGGGAGAAAATTTATGAT 719
Qy 231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250
Db 720 GAGGCTGAATCTTCTCTACCAATATTTAAAGAAGCCCTGCAAAAGATTCCGGTCTCC 779
Qy 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrHisThrAsnLeuPro 270
Db 780 AGT---CTTTCGAGAGATCGGGGACGTTTGGAAATATGTTGGCACACATATTGGCCG 836
Qy 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsnLysAsnAla 290
Db 837 CGATTGGAAGCAAGAAATTACATCCAGTCTTTGGACAGACACTGAGAACACGAAAGTCA 896
Qy 291 -----AlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307
Db 897 TATGTGAAGAGCAAAAACTTTTAGAACTCGCAAAATTTGAGTTCAACATCTTCAATCC 956
Qy 308 LeuGlnGluArgGluLeuLysHisValSerArgTrpTrpLysAspSerGlySerProGlu 327
Db 957 TTACAAAGAAGAGGAGTTAGAAAGTCTGTCAGATGTGGAAGAATCGGGTTTCTCAGAG 1016
Qy 328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347
Db 1017 ATGACCTTCTGCCGACATCGTCACGTGAATACTACACTTTGGCTTCTGCATTGGCTTC 1076
Qy 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367
Db 1077 GAGCCTCAACATTTCTGATTACAGACTCGGCTTTGCCAAGACGTGTCACTTATCACGGTT 1136
Qy 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluPheThrAlaThr 387
Db 1137 CTTGACGATATGTACGACACCTTGGCAGAGTAGACGAGCTGGAATCTTTCACAGCGACA 1196
Qy 388 IleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407

Db 1197 ATGAAGATGGATCCGTCCTCGATAGATTGCCTCCAGAAATATATGAAGAAGTGTAC 1256
QY 408 MeMetValTyrHisThrValaengluMetAlaArgValAlaGlulysAlaGlnGlyArg 427
Db 1257 ATAGCGGTTTACGACACCGTAATGAATGGCTCGAGAGCGACGAGAGGCTCAAGCCGA 1316
QY 428 AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu 447
Db 1317 GATACGCTCACATATATGCTCGGGAAGCTTGGAGGCTTATATGATTGCTATATGCAAGAA 1376
QY 448 AlaIysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467
Db 1377 GCAAGGTGGATCGCCACTGGTATCTGCCCTCTTGATGAGTACTACGAAGATGGGAAA 1436
QY 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
Db 1437 GTTAGCTGTGTCATCGCATATCCGCATTGCAACCCATTCTGACAAATGGAACATCCCCTTT 1496
QY 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspIleCysIle 507
Db 1497 CCTGATCATATCTCAAGGAAGTGACTTCCCATCAAGCTTAACGACTTGCGATGTGCC 1556
QY 508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu 527
Db 1557 ATCCTTCGATTACGAGGTGATACGGGTGCTTACAAGCGGACAGGGCTCGTGAGAGAA 1616
QY 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547
Db 1617 GCTTCTCTATATCATGTTATATGAACAATCCTGAGTATCAGAGGAAGATGCTCTC 1676
QY 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567
Db 1677 GATCATATCAACGCCCATGATCAGTGAAGTAAATCAAGGATTAATGGCAACTTCTCAAA 1736
QY 568 ProAspAsnSerValProIleThrSerLysHisAlaPheAspIleSerArgValTrp 587
Db 1737 CCAGACATCAATGTTCCTCATCTCGGCGAAGAAACATGCTTTGACATCGCCAGAGCTTTC 1796
QY 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607
Db 1797 CATACGGCTACAATAACGAGACGGCTACAGCGTGGCCAAAGTTGAAGAAAGAGATTG 1856
QY 608 ValMetArgThrValIleGluProValProLeu 618
Db 1857 GTCACGAGAACCTCCTTGAAATCTGTGCTTTG 1889

RESULT 10
AR429869
LOCUS AR429869 2018 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 19 from patent US 6645762.
ACCESSION AR429869
VERSION AR429869.1 GI:40190267
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2018)
AUTHORS Chappell,J., Manna,K.R., Noel,J.P. and Starks,C.M.
TITLE Synchases
JOURNAL Patent: US 6645762-A 19 11-NOV-2003;
FEATURES location/Qualifiers
source 1..2018
/organism="unknown"
/mol_type="genomic DNA"

Alignment Scores:
Pred. No.: 2,34e-190 Length: 2018
Score: 2453.00 Matches: 475
Percent Similarity: 84.63% Conservative: 59
Best Local Similarity: 75.28% Mismatches: 81
Query Match: 75.45% Indels: 16

DB: 6 Gaps: 6
US-10-025-145A-65 (1-618) x AR429869 (1-2018)
QY 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
Db 6 ATGGCTCTAGTTCTTACCGCACCGTTGGCTTCCAATATGCTTGCACAAAATCGTTGATC 65
QY 16 SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArg 35
Db 66 AGTTCTAACCATGAGCTTAAGGCTCTCTAGAACAAATTCAGCTTAGGAATGAGTAGG 125
QY 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
Db 126 CGAGGGAATCTATCACTCCCTCCATCAGCATGAGCTGTACCAACCGTTGTAACCGATGAT 185
QY 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75
Db 186 GGTGTACGAAGACGATGGGCGATTTCATTCCAACCTCTGGAGACGATGATCATACAG 245
QY 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
Db 246 TCTTTA---CCAACGGCTTATGAGGAAAAATCGTACCTGGAGCGGTGCTGAGAAACTGATC 302
QY 96 GlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly----- 112
Db 303 GGGGAAGTAAAGAAC--ATGTTCAATTGATGTCATTAGAGATGAGAGTTAATGAGT 359
QY 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
Db 360 CCGCTCAATGATCTCATTCACGCCCTTTCGATTGTCCAGACGCTTGAAACGTTGGGATC 419
QY 131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
Db 420 CATAGACATTTCAAGATGAGATAAATCGCGCTTGATATGTTTACAGTTATGGGCG 479
QY 151 GluLysGlyIleGlyCysGlyArgGluSerValThrAspLeuAsnSerThrAlaLeu 170
Db 480 GAAATGGCATCGGATCGGGAGGAGAGAGTGTGTACTGATCTGAACCTCACTGCGGTTG 539
QY 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
Db 540 GGGCTTCGAACCTACGACTACACGGATACCCGGTGTCTTCAGATGTTTCAAAGCTTTC 599
QY 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyIleArg 210
Db 600 AAAGGCCAAATGGGCGAGTTTCTCTGCTGAAAATATTCAGACAGATGAAGAGATCAGA 659
QY 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230
Db 660 GCGCTTGAATTTATTCGGGCTCCCTCATTCCTTCAGGGGAGAAAATTATGAT 719
QY 231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250
Db 720 GAGGCTGAATCTTCTCTACCAATATTTAAAGAAGCCCTGCAAAAAGATTCCGTCCTCC 779
QY 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrHisThrAsnLeuPro 270
Db 780 AGT---CTTTCGAGAGATCGGGGACGTTTGGAAATATGTTGGCACACATATTTGCCG 836
QY 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsnLysAsnAla 290
Db 837 CGATTGGAAGCAAGGAATTACATCCAAAGTCTTGACAGAGACACTGAGAAACAGAACTCA 896
QY 291 -----AlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307
Db 897 TATGTGAAGAGCAAAAACTTTAGAATCGCAAAATTTGAGTTCAACATCTTCAATCC 956
QY 308 LeuGlnGluArgGluLeuLysHisValSerArgTrpTrpLysAspSerGlySerProGlu 327
Db 957 TTACAAAGAAGGAGGTAGAAAGCTGTCAGATGTTGGAAGAAGATCGGGTTTCTCTGAG 1016
QY 328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347

Db 1017 ATGACCTTCTGCCGACATCGTCACGTGGAATACTACACTTGGCTTCGATTCGCTTC 1076

Qy 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367

Db 1077 GAGCCTCAACATTCTGATTCAAGACTCGGCTTGCCAAAGACGTGCATCTTATCAGCGTT 1136

Qy 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluLeuPheThrAlaThr 387

Db 1137 CTTGACGATATGTACGACACCTTCGGACAGTAGACGAGCTGAACTCTTACAGCGACA 1196

Qy 388 IleYsArgTrpAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407

Db 1197 ATGAAGAGATGGGATCCGCTCCGATGATGCTTCGAGAATATGAAAGAGGTGAC 1256

Qy 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg 427

Db 1257 ATAGCGGTTTACGACACCGTAATGAATGGCTCGAGAGGCGAGAGGCTCAAGGCCGA 1316

Qy 428 AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu 447

Db 1317 GATACGCTCACATATGCTCGGGAAGCTTGGAGGCTTATATTGATTGTAATATGCAAGAA 1376

Qy 448 AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467

Db 1377 GCACGTGATCGCCACTGCTTACCTGCCCTCTTGATGAGTACTACGAGAATGGGAAA 1436

Qy 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487

Db 1437 GTTAGCTGTGTCATCGCATATCCGCATTCGCAACCATCTTGACATGACATCCCTTT 1496

Qy 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507

Db 1497 CCTGATCATATCTCTCAAGGAAGTGACTTCCCATCAAGCTTAAACGACTTGGCATGTGCC 1556

Qy 508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu 527

Db 1557 ATCCTTCGATTACGAGGTGATACGGGTGCTTACAAAGCGGACAGGCTCGTGAGAGAA 1616

Qy 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547

Db 1617 GCTTCCTCTATATCATGTTATATGAACAATCCTGAGTATCAGAGGAAGATGCTTC 1676

Qy 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567

Db 1677 GATCATATCAACGCCATGATGATGACGTAATCAAAAGATTAATTGGGAACCTTCAAA 1736

Qy 568 ProAspAsnSerValProIleThrSerLysHisAlaPheAspIleSerArgValTrp 587

Db 1737 CCAGACATCAATGTTCCTCCATCTCGGCGAAGAACAATGCTTTGACATCGCCAGAGCTTTC 1796

Qy 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607

Db 1797 CATTAAGGCTACAAATACCGAGACGGCTACAGCGTTGCCAAGCTTGAAACGAAGAGTTTG 1856

Qy 608 ValMetArgThrValIleGluProValProLeu 618

Db 1857 GTCAAGAGAACCTCCTTGAATCTGTGCTTTG 1889

RESULT 11

AGU87909 2018 bp mRNA linear PLN 24-SEP-1997

LOCUS AGU87909 2018 bp mRNA, complete cds.

DEFINITION Abies grandis pinene synthase (AG3.18) mRNA, complete cds.

ACCESSION U87909

VERSION U87909.1 GI:2411482

KEYWORDS

SOURCE Abies grandis

ORGANISM Abies grandis

REFERENCE 1 (bases 1 to 2018)

AUTHORS Bohlmann,J., Steele,C.L. and Croteau,R.

TITLE Monoterpene synthases from grand fir (Abies grandis). cDNA

isolation, characterization, and functional expression of myrcene synthase, (-)-(4S)-limonene synthase, and (-)-(1S,5S)-pinene synthase

JOURNAL J. Biol. Chem. 272 (35), 21784-21792 (1997)

MEDLINE 97413772

PUBMED 9268308

REFERENCE 2 (bases 1 to 2018)

AUTHORS Bohlmann,J., Steele,C.L. and Croteau,R.

TITLE Direct Submission

JOURNAL Submitted (31-JAN-1997) Institute of Biological Chemistry, Washington State University, Clark Hall, Pullman, WA 99164-6340, USA

FEATURES

source location/Qualifiers

1..2018

/organism="Abies grandis"

/mol_type="mRNA"

/db_xref="taxon:46611"

1..2018

/gene="AG3.18"

6..1892

/gene="AG3.18"

/note="monoterpene synthase; terpene synthase; monoterpene synthase; terpene cyclase"

/codon_start=1

/product="pinene synthase"

/protein_id="AAB71085.1"

/db_xref="GI:2411483"

/translation="MALVSTAPLASKSLHKSLSSTHELKALSRTPALGMSRGRKSLTPSISMSSTTVTDGVRRRMGDFHSLNMDVDVIOSLPTAYEKSYLERAEKLIGEYKNMENSMSLEDGELMSPLNDLIQRLMIVDSLRLGIRHFKDEIKSALDYVSYWGENGICGRISVTDLNSITLGLRTLRLHGYPVSSDVFKAFKQNGQFSSENIQTDEIRGLNLFISLAFPEGEKIMDEAEIFSTKYLKEALOKIPVSSLRSREIGDVLGYCMHTYLPRLRNRYIOVFGQDTEHTSKSVKSKLLELAKLEFNIFQSLQRELSLVRWWSGFPMTFCRHRHVEYITLASCIAFEPQHSFRLGFAKTHLITLVDMDYDTFTVDELELFTATMRMDPSSIDCLPEYMKGVYIAYDTVNEMARBAEAOGRDTLTVARAEWAYIDSYMQEARMIATGYLPSFDEYENGKVSCHGRISALQPIITMDIPFPDHILKEVDFPSKINDLACAILRLRGDTRCYKADRARGEASSISCYMKDNPVSEBDALDHINAMISDVIKGLNWECLKPDINVPISAKKHAFDIARAFHYGYKRRDGYSVANVETKSLVTRITLESVPL"

ORIGIN

Alignment Scores:

Pred. No.: 2.34e-190 Length: 2018

Score: 2453.00 Matches: 475

Percent Similarity: 84.63% Conservative: 59

Best Local Similarity: 75.28% Mismatches: 81

Query Match: 75.45% Indels: 16

DB: 8 Gaps: 6

US-10-025-145A-65 (1-618) X AGU87909 (1-2018)

Qy 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15

Db 6 ATGGCTTAGTTCTTACCGCACCGTTGGCTTCCAATCATGCGCTGCACAAATCGTTGATC 65

Qy 16 SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArg 35

Db 66 AGTTCTAACCATGAGCTTAAGGCTCTCTAGAACAAATTCAGACTCTAGGAATGAGTAGG 125

Qy 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55

Db 126 CGAGGAAATCTATCACTCCTTCATCAGCATGAGCTCTACCAACCGTTGTAACCGATGAT 185

Qy 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75

Db 186 GGTTACGAAGCGCATGGCGCATTTCCATTCCAACCTTCGGAGCAGATGATGATACAG 245

Qy 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95

Db 246 TCTTTA---CCAACGCGTTATGAGGAAATAATCGTACCTGAGCGCTGTGAGAACTGATC 302

Qy 96 GlyGluValLysAspIleMetPheAsnPhelySerLeuGluAspGlyGly----- 112

Db 303 GGGGAAGTAAAGAAC--ATGTTCAATTCGATGTCAATAGAGATGAGAGTTAATGAGT 359
Qy 113 -----AsnAspLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
Db 360 CCGCTCAATGATCTCATTCACAGACTTTGGATTGTGCACAGCCTTGAAAGTTTGGGATC 419
Qy 131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
Db 420 CATAGACATTTCAAAGATGAGATAAATCGCGCTTGATTACTTTACAGTTATTTGGGCG 479
Qy 151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170
Db 480 GAAATGCGCATCGGATCGGGAGGAGAGTGTGTACTGATCTGAACCTCACTCGCGTTC 539
Qy 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
Db 540 GGGCTTCGAACCCCTACGACTACCGGATACCCGGTGTCTTCAGATGTTTCAAAGCTTTC 599
Qy 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyIleArg 210
Db 600 AAAGGCCAAAATGGCGAGTTTCTGCTCTGAAATATATTCAGACAGATGAAGAGATCAGA 659
Qy 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230
Db 660 GGGCTTCTGAATTTATTCGGGCGCTCCCTCATTCGCTTCCAGGGGAGAAATATATGAT 719
Qy 231 GluAlaGluThrPheSerThrIleTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250
Db 720 GAGGCTGAAATCTTCTCTACCAATAATTTAAAGAAGCCCTGCAAAAGATTCGGGTCTCC 779
Qy 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrHisThrAsnLeuPro 270
Db 780 AGT---CTTTCGCGAGAGATCGGGGACGTTTGGAAATATGTTGGCACACATATTTGCCG 836
Qy 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsnLysAsnAla 290
Db 837 CGATTGGAAGCAAGAAATTACATCCAACTTTTGACAGAGACACTGAGAAACAGAACTCA 896
Qy 291 -----AlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307
Db 897 TATGTGAAGAGCAAAAACTTTTGAACCTCGCAAAATTGAGTTCAACATCTTCAATGCC 956
Qy 308 LeuGlnGluArgGluLeuLysHisValSerArgTyrTrpLysAspSerGlySerProGlu 327
Db 957 TTACAAAGAAGGAGGTAGAAAGTCTGCTCAGATGTTGGAAGAAGATCGGGTTTCCCTGAG 1016
Qy 328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347
Db 1017 ATGACCTTCTGCGGACATCGTCAGCGGAATACTACACTTTGGCTTCCATTCGCTTC 1076
Qy 348 GluProGlnHisSerGlyPheArgLeuGluPheThrLysMetSerHisIleuIleThrVal 367
Db 1077 GAGCCTCAACATTTCTGATTCAACTCGGCTTTGCCAAGACGTGTCACTTATCACGGTTC 1136
Qy 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluPheThrAlaThr 387
Db 1137 CTTGACGATATGTAACGACACCTTCGGCAGAGTAGACGAGCTGGAACCTTTCACAGCGACA 1196
Qy 388 IleLysArgTyrAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407
Db 1197 ATGAAGAGATGGGATCCGCTCTCGATAGATTGCTTCCAGAAATATGAAAGGAGTGTAC 1256
Qy 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg 427
Db 1257 ATAGCGGTTTACGACACCGTAATGGAATGGCTCGAGAGGAGAGAGGCTCAAGCGCGA 1316
Qy 428 AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu 447
Db 1317 GATACGCTCACATATATGCTCGGGAAGCTTGGGAGGCTTATATGATTCGATATGCAAGAA 1376
Qy 448 AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGlyTyrLeuGluAsnGlyLys 467
Db 1377 GCAAGGTGATCGCCACTGGTTACTCTCCCTCTTGATGAGTACTACGAGAATGGGAAA 1436

Qy 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
Db 1437 GTTAGCTGTGTCATCGCATATCCGCATTGGCAACCCATTCTGACAATGACATCCCTTT 1496
Qy 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507
Db 1497 CCTGATCATATCCTCAAGGAAGTTGACTTCCCATCAAGCTTAACGACTTGGCATGTGCC 1556
Qy 508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGlnGlu 527
Db 1557 ATCTTCGATTACGAGGTGATACCGGCTGCTACAGGCGGACAGGCTCGTGAGAGAGAA 1616
Qy 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluLysAlaLeu 547
Db 1617 GCTTCCTCTATATCATGTATATGAAAGACAATCCTGGAGTATCAGAGGAAGATGCTTC 1676
Qy 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567
Db 1677 GATCATATCAACGCCATGATCAGTACGTAATCAAGAGATTAAATTGGGAACCTTCAAA 1736
Qy 568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp 587
Db 1737 CCAGACATCAATGTTCCCATCTCGCGGAAGAAACATGCTTTGACATCGCCAGAGCTTTC 1796
Qy 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607
Db 1797 CATTAAGGCTACAATATCCAGACGCGCTACAGCGTTGCCAACGTTGAACGAGAGTTTG 1856
Qy 608 ValMetArgThrValIleGluProValProLeu 618
Db 1857 GTACAGAGAACCTCTTGAAATCTGTGCTTGG 1889
RESULT 12
AF543527 2082 bp mRNA linear PLN 10-MAR-2003
LOCUS
DEFINITION Pinus taeda (-)-alpha-pinene synthase mRNA, complete cds.
ACCESSION AF543527
VERSION AF543527.1 GI:28894481
KEYWORDS
SOURCE Pinus taeda (loblolly pine)
ORGANISM Pinus taeda
TITILE cDNA isolation, functional expression, and characterization of (+)-alpha-pinene synthase and (-)-alpha-pinene synthase from loblolly pine (Pinus taeda): Stereoccontrol in pinene biosynthesis
REFERENCE
AUTHORS Phillips,M.A., Wildung,M.R., Williams,D.C., Hyatt,D.C. and Croteau,R.
JOURNAL Arch. Biochem. Biophys. 411 (2), 267-276 (2003)
MEDLINE 22510022
PUBMED 12623076
REFERENCE
AUTHORS Phillips,M.A., Wildung,M.R., Williams,D.C. and Croteau,R.B.
TITLE Direct Submission
JOURNAL Submitted (09-SEP-2002) Institute of Biological Chemistry, Washington State University, PO Box 646340, Pullman, WA 99164-6340, USA
FEATURES
source location/Qualifiers
1..2082
/organism="Pinus taeda"
/mol_type="mRNA"
/db_xref="taxon:3352"
32..1921
/note="monoterpene synthase"
/codon_start=1
/product="(-)-alpha-pinene synthase"
/protein_id="AA061225.1"
/db_xref="GI:28894482"
/translation="MSPVSVISLPSDLCLPTSFIDRSGRELIPLHITIPNVAMRRQCK LMTASMSMNLRTAVSDDAVIRRGDFHSNLWDDLIQSLSPYGEPSYRERAERLTG EVKNSFNSMSNEDGESITPLDDLQRLMWVDSVERLIGIDRHFKKEIKSALDHVRYWS


```
Db      1880 AGTTTCGTGAAGAACCGTCATTCCTGCTCACTTTA 1918
RESULT 13
AF543529      2162 bp      mRNA      linear      PLN 10-MAR-2003
LOCUS      AF543529
DEFINITION  Pinus taeda alpha-terpineol synthase mRNA, complete cds.
ACCESSION  AF543529
VERSION    AF543529.1      GI:28894485
KEYWORDS
SOURCE
ORGANISM   Pinus taeda (loblolly pine)
            Pinus taeda
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
REFERENCE  1 (bases 1 to 2162)
            Phillips,M.A., Wildung,M.R., Williams,D.C., Hyatt,D.C. and
            Croteau,R.
            CDNA isolation, functional expression, and characterization of
            (+)-alpha-pinene synthase and (-)-alpha-pinene synthase from
            loblolly pine (Pinus taeda): Stereocontrol in pinene biosynthesis
            Arch. Biochem. Biophys. 411 (2), 267-276 (2003)
JOURNAL    22510022
MEDLINE    12623076
PUBMED
REFERENCE  2 (bases 1 to 2162)
            Phillips,M.A., Wildung,M.R., Williams,D.C. and Croteau,R.B.
            Direct Submission
            Submitted (09-SEP-2002) Institute of Biological Chemistry,
            Washington State University, PO Box 646340, Pullman, WA 99164-6340,
            USA
FEATURES
source     location/Qualifiers
            1..2162
              /organism="Pinus taeda"
              /mol_type="mRNA"
              /db_xref="taxon:3352"
              59..1942
                /note="monoterpene synthase; Pti10"
                /codon_start=1
                /product="alpha-terpineol synthase"
                /protein_id="AA061227.1"
                /db_xref="GI:28894486"
                /translation="MDLISVLPASAKSCVCLHKPLSSSTHTLKPCKTIRILVPRRW
                EFARPSMSLSTVASEDDIQRTGGLYNLMNDVIOFLSPYGLAYRERAERLIDEV
                RDIFFSMSLEDGEFSDLIQRLMVNVERLGIDRFKNEIKSALDIVSYWSEKIGC
                GTRKSITNLNSTALGFRTLRHGYPSADVLKHFNRQIGFVSCPSETEEDIRIMVNL
                YRASLIAFPVAFPEKVMEESESEKYLKETLOKIPDSLSREIGDVLHGWHTNLP
                RLEARNYIDVFGODTKNMEPRKTEKLELAKLEFNIPOSIQTELESLLRMNDSGS
                FOITFRHRHVEYVTLASCLAFEPQSGFRLGFAKACHILVLDMDYDLFGTVDELKL
                FTAAIKRWDPSATDCLPQYKMGIMYMNVTNVNEMSAEQAKGDRTLNVARQAMEDCL
                DSHQEAQMIATGFLPTPEEYLENGKVSSAHRVSLQPMITMDIPEPHILKEVDPS
                NUNDLIACAMRLRGDTRCYQADRARGEETSCISYMKNDGATEEDALNHLNVMISGV
                IKELNWECLKPNSVPISSKINFDITRAFYGYKVRDGSVSSVETKSLVMRTLEP
                VPL"
ORIGIN
Alignment Scores:
Pred. No.:      4.1e-175      Length:      2162
Score:          2266.50      Matches:      443
Percent Similarity: 82.31%      Conservative: 78
Best Local Similarity: 69.98%      Mismatches: 91
Query Match:    69.72%      Indels:      21
DB:            8      Gaps:      9
US-10-025-145A-65 (1-618) x AF543529 (1-2162)
QY      1 MetAlaLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
Db      59 ATGATTTAATATCTGCTTACCGCTGCTTCCAAATCGTGTGTGCTGCACAAACCC 118
QY      16 -----SerSerSerHisGluIleValAlaLeuArgArgThrIleProThrLeuGlyIle 33
Db      119 TTGAGTAGTCTACTCATAACTTAAGCCTTTCTGCACAAACAATCCGGAATCTTGTATG 178
QY      34 CysArgProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSer 53
```

```
Db      179 CCGAGGCGATGGGAATTTGCCAGGCCGCTCC-----ATGAGTCTGAGTACCGTTGCATCT 232
QY      54 ThrAspSerValGlnArgArgValGlyAsnTyrrHisSerAsnLeuTrpAspAspPhe 73
Db      233 GAAGATGATATACAAAGACGACGCGCGGTATCTTTCCAACTCTGGAAACGATGATGTG 292
QY      74 IleGlnSerLeuIleSerThrProTyrrGlyAlaProAspTyrrArgGluArgAlaAspArg 93
Db      293 ATACAG---TTTCTGTCAACGCCCTTATGGGGAACCTCGCTTACCGTGAACGTGTGAGCGA 349
QY      94 LeuIleGlyGluValLysAspIleMetPheAsnPhelySerLeuGluAspGlyGly--- 112
Db      350 CTGATTGATGAAGTAAGGACATA--TTCAGTTCGATGTCATTGGAAGATGGAGAATTC 406
QY      113 AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIleAspArg 132
Db      407 AGTATCTCATTCAACGCCCTTGGATGTCGATTAACGTTGAACGTTGGGATCGATAGG 466
QY      133 HisPheLysLysGluIleLysThrAlaLeuAspTyrrValAsnSerTyrrTrpAsnGlyLys 152
Db      467 CATTTCAAAATAGATCAATTCAGCGCTTGATTAATGTTTACAGTTACTGAGCGAATAA 526
QY      153 GlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeuGlyLeu 172
Db      527 GGCATTGGATGTGGACAAAGATATATTACTAATCTCAATCTCACTGCCCTTGGGCTTT 586
QY      173 ArgThrLeuArgLeuHisGlyTyrrThrValSerSerAspValLeuAsnValPheLysAsp 192
Db      587 CGAAGCTTTCGATTACACGGGATACCTGTTCTGCAGACGCTTTGAACATTTCAAGAAC 646
QY      193 LysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyIleArgGlyVal 212
Db      647 CAAATTGGGCAGTTTGTATCATGTCTTAAGT--GAGACAGAGGAAGACATAAGATCATG 703
QY      213 LeuAsnLeuPheArgAlaSerLeu-----ValAlaPheProGlyGluLysVal 228
Db      704 GTCAATTTATATCGGGCTTCCTCATTTGCCCTTCCCGTTCCTTCCGGTGAGAAAGTT 763
QY      229 MetAspGluAlaGluThrPheSerThrLysTyrrLeuArgGluAlaLeuGlnLysIlePro 248
Db      764 ATGGAAGAGGACAGAAAGCTTTCAGAGAAATATTAAAGAAACTCTGCACAAAGATTCG 823
QY      249 AlaSerSerIleLeuSerLeuGluIleArgAspValLeuGluTyrrGlyTrpHisThrAsn 268
Db      824 GACTGCAGT---CTTCAAGAGAGATAGGGGACGTTTGGAAACATGTTGGCACACAAAT 880
QY      269 LeuProArgLeuGluAlaArgAsnTyrrMetAspValPheGlyGlnHisThrLysAsn--- 287
Db      881 TTGCCCGCATTTAGAACCAAGGAATTAATCATGCAGCTCTTCGACACAAGACATAAGATATG 940
QY      288 -----LysAsnAlaAlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePhe 305
Db      941 GAGCCAAATAGGAAGACGAGAAACTGTTAGAACTTGCMAACTGGAATTCACACATCTTT 1000
QY      306 HisSerLeuGlnGluArgGluLeuLysHisValSerArgTrpTrpLysAspSerGlySer 325
Db      1001 CAATCATACAGAAAGACAGAGTTAGAGTCCCTCTTGAGATGTTGAATGATTCAAGTTG 1060
QY      326 ProGluMetThrPheCysArgHisArgHisValGluTyrrTyrrAlaLeuAlaSerCysIle 345
Db      1061 CCTCAGATTACCTTCACTCGACATCGCCACGCTGAGTACTACACTTTGGCTTCTGCATC 1120
QY      346 AlaPheGluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIle 365
Db      1121 GCGTTGAGCCTCAACATTTCTGATTCAGACTCGGCTTGGCAAGCTTGTCAATATCTC 1180
QY      366 ThrValLeuAspAspMetTyrrAspValPheGlyThrValAspGluLeuLeuPheThr 385
Db      1181 ACTGTTCTCGACGATATGTACGACCTCTTCGGAACAGTTGACGAGCTCAAACTTTCACA 1240
QY      386 AlaThrIleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyrrMetLysGly 405
```

Db 1241 GCCGCAATTAGAGATGGATCCGTCGCCACAGATTGCTTCCACAATATATGAAGA 1300
Qy 406 ValTyrMetMetValTyrHisThrValaenGluMetAlaArgValAlaGluValaGln 425
Db 1301 ATTTACATGATGTTTACACACACCGTAATGAATGTCTGCGAGGACAGAAAGCTCAA 1360
Qy 426 GlyArgAspThrLeuAsnTyrAlaArgGlnAlaTyrGluAlaCysPheAspSerTyrMet 445
Db 1361 GGCCGAGACACTCTCAACTATGCTCGACAGCGTTGGAGGATTGTCTTGATTTCACATATG 1420
Qy 446 GlnGluAlaIysTyrPheAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsn 465
Db 1421 CAAGAAGCAAGTGGATCGCCACTGGTTTCTGCCAACATTGAGAGAAATCTTGAGAAC 1480
Qy 466 GlyLeuValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIle 485
Db 1481 GCGAAGTAGCTCTGCTCATCGCGTATCGGCATTGCAACCCATGCTGACGATGACATC 1540
Qy 486 ProPheProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIle 505
Db 1541 CCCTTCCTCTCTCATCTCTCAAGGAAGTTGACTTTCATCCAACTCAATGACTTGGA 1600
Qy 506 CysIleIleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGly 525
Db 1601 TGTGCCATGCTTCGATTACGAGGTGATACCGATGTTATCAGGCGGACAGGGCTCGTGA 1660
Qy 526 GluGluAlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAsp 545
Db 1661 GAAGAACCTCTCTATATCTGTATATGAAGAACATCTCTGAGCAACAGAGAAAGAT 1720
Qy 546 AlaLeuAsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTyrGluLeu 565
Db 1721 GCTCTTAATCATCTCAACGTCATGATCAGTGGCGTAATTAAAGAAATTAATTGGAGCTT 1780
Qy 566 LeuLysProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArg 585
Db 1781 CTCAACCCCAACAGCAGTGTGCCCATTTCTTCCAAGAAATTAATTGACATTACAGAGA 1840
Qy 586 ValTyrPheHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLys 605
Db 1841 GCTTCCATTACGGTTACAAATACCGAGATGCTTACAGCGTTTCCAGCGTTGAACAAG 1900
Qy 606 SerLeuValMetArgThrValIleGluProValProLeu 618
Db 1901 AGTTGTGATGAGAACCTCTTGAACTGTGCTTTA 1939
RESULT 14
AR222137
LOCUS AR222137 2186 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 66 from patent US 6429014.
ACCESSION AR222137
VERSION AR222137.1 GI:23329511
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2186)
AUTHORS Steele,C.L., Bohlmann,J. and Croteau,R.B.
TITLE Monoterpene synthases from grand fir (Abies grandis)
JOURNAL Patent: US 6429014-A 66 06-AUG-2002;
FEATURES
source 1. 2186
/organism="Unknown"
/mol_type="genomic DNA"

Alignment Scores:
Pred. No.: 6.65e-175 Length: 2186
Score: 2264.00 Matches: 435
Percent Similarity: 80.53% Conservative: 78
Best Local Similarity: 68.29% Mismatches: 98
Query Match: 69.64% Indels: 26
DB: 6 Gaps: 9

US-10-025-145A-65 (1-618) x AR222137 (1-2186)
Qy 1 MetalaleuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
Db 34 ATGGCTGTGTTCTTCCGCAACC-----AAATCCTGCCTGCACAAATCGTTGATC 84
Qy 16 ---SerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCys 34
Db 85 AGTCTACTCATCATGAGCTCAAGCCTTGGCCAGAACCATCCCACTCTTGAATGTT 144
Qy 35 ArgProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThr 54
Db 145 AGCGAGGGAATCTTTCACACCTTCTGTGAGCATGAGTTGACCAACCGCTGATCTGAT 204
Qy 55 AspSerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTyrAspAspPheIle 74
Db 205 GATGGTCTACAAAGACGATAGGTGACTATTCATTCATCTCTGGAGCAGCATTTTCATA 264
Qy 75 GlnSerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeu 94
Db 265 CAGTCTCTA---TCAACGCTTATGGGAGCCTTCTTACCGAGAACGTGCTGAGAAACTG 321
Qy 95 IleGlyGluValLysAspIleMetPheAsnPhelysSerLeuGluAspGlyGly----- 112
Db 322 ATTGGGAGAGTGAAGAG--ATGTTCAATTCAATGCCATCGGAGATGAGAAATCAATG 378
Qy 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGly 129
Db 379 AGTCCCTCATGATCTTATGACGACTTTGGATGTCGATAGCGTTGAACGTTTGGGG 438
Qy 130 IleAspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrp 149
Db 439 ATTGATAGACATTTCAAAAAGAGATAAATCAGCCCTTGATTATGTTTACAGTATTGG 498
Qy 150 AsnGluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAla 169
Db 499 AACGAAAGGTATTTGATGCGGTAGAGATAGTGTTTTCTGATGTCAACTCGACTGCC 558
Qy 170 LeuGlyLeuArgThrLeuArgLysGlyTyrThrValSerSerAspValLeuAsnVal 189
Db 559 TCGGGTTTCGAACCTCTTCCCTACAGCATACAGTGTCTCTTCAAGAGTTTGAAAGTA 618
Qy 190 PheLysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGlyGluIle 209
Db 619 TTTCAGACCAAAATGCGCAGTTTGCATTTCTCTCCTAGTACAANA---GAGAGAGACATC 675
Qy 210 ArgGlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMet 229
Db 676 AGAACCGTTCTGAATTTATATCGGGCTTCTTTCATTGCTTCCCTGGGAGAAAGTTATG 735
Qy 230 AspGluAlaGlyThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAla 249
Db 736 GAAGAGGCTGAATTTCTCTTCAAGATATTGAAAGAACCGCTGCACAAAGATTCCGGTC 795
Qy 250 SerSerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrPheThrAsnLeu 269
Db 796 TCCAGT---CTTTCACAGAAATAGACTACACTTGGAAATATGTTGGCACACAAATATG 852
Qy 270 ProArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThr----- 285
Db 853 CCAGAGATTGAAACAAAGAAATTACTTGAATGATTTGGACATCCTACCAAGTCATGGCTC 912
Qy 286 LysAsnLysAsnAla-----AlaGluLysLeuLeuGluLeuAlaLysLeuGlu 301
Db 913 AAGAAGAAAGAGACGCAATATCTGACAGCGAAAGCTTTAGAACTCGCAAAATTGAGAG 972
Qy 302 PheAsnIlePheHisSerLeuGlnGluArgGluLeuLysHisValSerArgTyrTrpLys 321
Db 973 TTCAACATCTTCACTCCCTTCAACAGAGAGATTACAGATATCTCCAGATGCTGATA 1032
Qy 322 AspSerGlySerProGluMetThrPheCysArgHisArgHisValGluTyrTyrAlaLeu 341

Db 1033 CATTGGGTTTGCCCTGAACCTGACCTTTGGTCGGCATCGTCACCGTGGAATACTACACCCCTG 1092
Qy 342 AlasecysileAlaPhegluProGlnHisserglyPheargleuglyPheThrlysmet 361
Db 1093 AGCTCTTGCACTGCGACTGAGCCCAACATCTCGATTGAGATTGGCTTGGCCAAACG 1152
Qy 362 SerHisleuileThrValleuAspAspMetTyrAspValPheglyThrValAspGluLeu 381
Db 1153 TGTCACTCTTATCACGGTCTTGACGATATCTACGACACTTCCGAAAGATGATGAATC 1212
Qy 382 GluleuPheThrAlaThrilelysergTrpAspProserAlametGluCysleuProGlu 401
Db 1213 GAACCTCTTCAACGAGCGAGTTAGAGATGGAATCCGTCGAGAAAGAACGCCCTCCAGAA 1272
Qy 402 TyrMetlysglyValTyrMetMetValTyrHisThrValAsnGluMetAlaArgValAla 421
Db 1273 TATATGAAGAATCTACATGGCACTCTACGAAGCCTTAACTGACATGGCGGAGAGGCA 1332
Qy 422 GlulyAlaGlnGlyArgAspThrleuAsnTyrAlaargGlnAlaTrpGluAlaCysPhe 441
Db 1333 GAGAAACAACAAGCCGAGACACGCTCAATTATGCTAGAAAGCCTTGGGAAGTTTATCTT 1392
Qy 442 AspSerTyrMetGlnGluAlaTyrTrpIleAlaThrGlyTyrleuProThrPheGluGlu 461
Db 1393 GATTCTGTATACACAAGAAGCAAGTGAATGCCAGCGGTATCTGCCCAACTTTCAGAGAG 1452
Qy 462 TyrleuGluAsnGlylyValSerSerAlaHisArgProCysAlaLeuGlnProIleLeu 481
Db 1453 TACTTAGAGAACCGGAAGGTAGCTCTGTCATCGTCAGCGGCATTTGACACCCCTCCTG 1512
Qy 482 ThrleuAspIleProPheProAspHisIleleuLysgluValAspPheProserLyseu 501
Db 1513 ACATTGACGTAACCGCTCTCGATGACGCTTGAAGGGAATAGATTTCATCGAGATT 1572
Qy 502 AsnAspIleuileCysileileleuArgleuArgGlyAspThrArgCysTyrLyAlaAsp 521
Db 1573 AATGATTGGCATCTCTCTCTTACGTAAGAGGTGACACACGATGCTTCAAGGACAGAC 1632
Qy 522 ArgAlaargGlyGluAlaSerSerIleSerCysTyrMetLyAspAsnProGlyLeu 541
Db 1633 AGGACCGAGAGAGAAAGCGTCAAGCATATCGTTACATGAAGAACAATCCCGATT 1692
Qy 542 ThrGluGluAspAlaLeuAsnHisIleAsnPhemetIleArgAspAlaIleargGluLeu 561
Db 1693 ACAGAGAGAGATGCTCTCAATCATATGCATGATCAACGACATAATCAAGAATT 1752
Qy 562 AsnTrpGluLeuLeuLyAspAsnSerValProIleThrSerLyshisAlaPhe 581
Db 1753 AATTGGAACTTCTCAAAACCGATAGCAATATTCATGACTGCAACGAAACATGCTTAT 1812
Qy 582 AspIleSerArgValTrpHisIleGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsn 601
Db 1813 GAGATTAACGAGACTTTCACCACTTCAAAATATAGAGATGGCTTCAGCGTGCACCT 1872
Qy 602 ValGluThrLySerleuValMetArgThrValIleGluProValProleu 618
Db 1873 CAAGAAACGAAAGTTGGTGAGAGACGGTCTTGAACCAAGTGCCTT 1923

RESULT 15
AF139205 2186 bp mRNA linear PLN 24-JUL-2001
LOCUS Abies grandis beta-phenylalanine synthase (agc8) mRNA, complete cds.
DEFINITION
ACCESSION AF139205
VERSION AF139205.1 GI:7381248

KEYWORDS
SOURCE Abies grandis
ORGANISM Abies grandis

REFERENCE
AUTHORS 1 (bases 1 to 2186)
TITLE Bohlmann, J., Phillips, M., Ramchandiran, V., Katoh, S. and Croteau, R.
CDNA cloning, characterization, and functional expression of four
new monoterpene synthase members of the Trpsd gene family from grand

JOURNAL fir (Abies grandis)
MEDLINE Arch. Biochem. Biophys. 368 (2), 232-243 (1999)
PUBMED 99373092
10441373
REFERENCE 2 (bases 1 to 2186)
AUTHORS Phillips, M.
TITLE Direct Submission
JOURNAL Submitted (30-MAR-1999) Institute of Biological Chemistry,
Washington State University, 289 Clark Hall, Pullman, WA
99164-6340, USA

FEATURES
source location/Qualifiers
1..2186
/organism="Abies grandis"
/mol_type="mRNA"
/db_xref="taxon:46611"
/tissue_type="stem"
/dev_stage="sapling"
1..2186
/gene="agc8"
/note="Trpsd gene family member"
34..1926
/gene="agc8"
/note="monoterpene synthase; includes N-terminal transit
peptide"
/codon_start=1
/product="beta-phenylalanine synthase"
/protein_id="AA061453.1"
/db_xref="GI:7381249"
/translation="MALVSSAPKSCILHKSILRSTHHLKPLRRTIPTLGMCRGKSF
T
P
S
V
M
S
L
T
T
A
V
S
D
D
G
L
Q
R
I
G
D
Y
H
S
N
L
W
D
D
F
I
Q
S
L
S
T
P
Y
G
E
S
Y
R
E
R
A
E
K
L
I
G
E
V
K
I
M
S
M
P
S
E
D
E
S
M
S
P
L
N
D
L
I
E
R
L
M
V
D
S
V
E
R
L
G
I
D
R
H
F
K
E
I
K
S
A
L
D
Y
V
S
Y
N
M
E
K
I
G
C
G
R
D
S
V
F
P
D
V
N
S
T
A
S
G
F
R
T
L
R
L
H
G
Y
S
V
S
E
V
L
F
Q
D
N
Q
P
A
F
S
P
T
K
E
R
D
I
R
T
V
L
N
L
Y
R
A
S
F
I
A
F
P
G
E
K
Y
M
E
A
E
I
F
S
S
R
Y
L
K
E
A
V
Q
K
I
P
V
S
S
L
S
Q
E
I
D
Y
T
L
E
Y
G
M
H
M
P
R
L
E
T
R
N
Y
L
D
V
F
G
H
P
T
S
P
W
L
K
K
R
T
Q
Y
L
D
S
E
K
L
E
L
A
L
E
F
N
I
F
H
S
L
Q
O
K
E
L
Q
Y
S
R
W
I
H
S
G
L
P
E
L
T
F
G
R
H
R
H
V
E
Y
T
L
S
S
C
I
A
T
E
P
K
H
S
A
F
R
L
G
F
A
K
T
C
H
L
I
T
V
L
D
I
Y
D
T
P
G
T
M
D
E
I
E
L
E
N
E
A
V
R
R
W
N
P
S
E
K
E
R
L
P
E
Y
M
K
E
I
Y
M
A
L
Y
E
A
L
T
D
M
A
R
E
A
E
K
T
O
G
R
D
T
L
N
Y
A
R
K
A
E
V
Y
L
D
S
Y
T
Q
E
A
K
W
I
A
S
G
Y
L
P
T
F
E
E
Y
L
E
N
A
K
V
S
S
G
H
R
A
A
L
T
P
L
L
T
D
V
P
L
P
D
D
V
L
K
G
I
D
F
P
S
R
F
N
D
L
A
S
S
F
L
R
L
G
D
T
R
C
Y
K
A
D
R
D
R
G
E
B
A
S
I
S
C
Y
M
K
D
N
P
G
L
T
E
D
A
L
N
H
I
N
A
M
I
N
D
I
K
E
L
N
W
E
L
L
K
P
D
S
N
I
P
M
T
A
R
K
H
A
Y
E
I
T
R
A
F
H
Q
L
Y
K
Y
R
D
G
F
S
V
A
T
Q
E
T
K
S
L
V
R
R
T
V
L
E
P
V
P
L"

ORIGIN
Alignment Scores:
Pred. No.: 6.65e-175 Length: 2186
Score: 2264.00 Matches: 435
Percent Similarity: 80.53% Conservative: 78
Best local Similarity: 68.29% Mismatches: 98
Query Match: 69.64% Indels: 26
DB: 8 Gaps: 9

US-10-025-145A-65 (1-618) x AF139205 (1-2186)

Qy 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysleu----- 15
Db 34 ATGGCTCTGTTCTTCCGACCC-----AAATCCTGCTGCACAAATCGTTGATC 84
Qy 16 --SerSerSerHisGluIlelyAlaLeuArgArgThrIleProThrleuglyIleCys 34
Db 85 AGGTCTACTCATCATGAGCTCAAGCCTCTGCGAGAACCATCCCAACTCTTGAATGTGT 144
Qy 35 ArgProGlyLySerValAlaHisSerIleAsnMetCysleuThrSerValAlaSerThr 54
Db 145 AGGCGAGGAAATCTTACACCTTCTGTGAGCATGAGTTGACACCGCTGTATCTGAT 204
Qy 55 AspSerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIle 74
Db 205 GATGCTCTACAAAGACGATAGGCTATCATTCATTCATCTCTGGGACGACGATTTTCA 264
Qy 75 GlnSerleuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgleu 94
Db 265 CAGTCTCTA--TCAACGCCCTTATGGGAGCCCTTCTTACCGAGAACGTGCTGAGAACTG 321
Qy 95 IleglyGluVallyAspIleMetPheAsnPhelysSerleuGluAspGlyly----- 112


```
Db 322 ATGGGGAGTGAAGGAG--ATGTTCAATTCAATGCCATCGGAAGATGGAGATCAATG 378
Qy 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGlnArgLeuGly 129
Db 379 AGTCCCCCTCAATGATCTTATTGAACGACTTTGGATGGATAGCGTGAACGTTGGGG 438
Qy 130 IleAspArgHisPheLeuYsGlnIleLeuThrAlaLeuAspTyrValAsnSerTyrTrp 149
Db 439 ATTGATAGACATTTCAAAAAAGAGATAAAATCAGCCCTTGATTATGTTTACAGTTATTGG 498
Qy 150 AsnGlnYsGlyIleGlyCysGlyArgGlnSerValValThrAspLeuAsnSerThrAla 169
Db 499 AACGAAAAAGGTATTGGATGCGGTAGAGATAGTGTCTTCTGATGTCACTCGACTGCC 558
Qy 170 LeuGlnYsLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnVal 189
Db 559 TCGGGGTTTCGAACCTCTCGCCTACACGAGATACAGTGTCTCTCAGAGGTTTGAAGTA 618
Qy 190 PheLeuAspYsAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGlnGlyIle 209
Db 619 TTTCAGAGACCAAAATGGGAGTTTGCATTCCTCTCCTAGTACAAA--GAGAGAGACATC 675
Qy 210 ArgGlnValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlnGlnYsValMet 229
Db 676 AGAACCGTCTGATTTATATCGGCTTCCTTCATTCCTTCCCTGGGAGAAAGTTATG 735
Qy 230 AspGlnAlaGlnThrPheSerThrLeuArgGlnAlaLeuGlnIleProAla 249
Db 736 GAAGAGCGTGAATTTCTCTCAAGATATTGAAGAAGCCGTCGAAAGATTCGGGTC 795
Qy 250 SerSerIleLeuSerLeuGlnIleArgAspValLeuGlnTyrGlyTyrHisThrAsnLeu 269
Db 796 TCCAGT--CTTTCACAGAATAAGACTACACTTTGGAATATGTTGGCACACAAATATG 852
Qy 270 ProArgLeuGlnAlaArgAsnTyrMetAspValPheGlyGlnHisThr----- 285
Db 853 CCAAGATTGGAAACAAGGAATTACTTAGATTATTGGACATCCCTACCACTGCATGGCTC 912
Qy 286 LysAsnLysAsnAla-----AlaGlnYsLeuLeuGlnLeuAlaYsLeuGln 301
Db 913 AAGAAGAAAGAGCGCAATATCTGACAGCGAAAGCTTTTAGAATCGCAAAATTTGGAG 972
Qy 302 PheAsnIlePheHisSerLeuGlnGlnArgGlnLeuYsHisValSerArgTyrTrpLys 321
Db 973 TTCAACATCTTCACTCCCTTCAACAGAGAGGTTACAGTATCTCCAGATGGTGATA 1032
Qy 322 AspSerGlySerProGlnMetThrPheCysArgHisArgHisValGlnTyrTyrAlaLeu 341
Db 1033 CATTCGGGTTTGCCTGAACCTGACCTTGGTGGCATCTGTACGCTGGAATACTACACCCTG 1092
Qy 342 AlaSerCysIleAlaPheGlnProGlnHisSerGlyPheArgLeuGlyPheThrLysMet 361
Db 1093 AGCTCTTGCACTGCGACTGAGCCCAACATTTCTGCATTCAGATTGGGCTTTGCCAAAACG 1152
Qy 362 SerHisLeuIleThrValLeuAspAspMetTyrAspValPheGlyThrValAspGlnLeu 381
Db 1153 TGTCACTTTATTCACGGTCTGACGATATCTACGACACTTTCGGAACGATGATAAATC 1212
Qy 382 GlnLeuPheThrAlaThrIleYsArgTyrAspProSerAlaMetGlnCysLeuProGln 401
Db 1213 GAACTCTTCAACGAGCGAGTAGAGATGGAATCCGTCGAGAAAGAACGCCCTCCAGAA 1272
Qy 402 TyrMetLeuGlyValTyrMetMetValTyrHisThrValAsnGlnMetAlaArgValAla 421
Db 1273 TATATGAAGAAATCTACATGCGACTCTAGCAAGCCTTAACGTGACATGGCGGAGAGCA 1332
Qy 422 GlnYsAlaGlnGlnYsArgAspThrLeuAsnTyrAlaArgGlnAlaTyrGlnAlaCysPhe 441
Db 1333 GAGAAAGACAAAGCGCGAGACACGCTCAATTATGCTAGAAAGCGTTGGGAAGTTATCTT 1392
Qy 442 AspSerTyrMetGlnGlnAlaYsTyrIleAlaThrGlyTyrLeuProThrPheGlnGln 461
```

```
Db 1393 GATTCGTATACACAAGAACAAAGTGAATGCCACGCGTTATCTGCCAATTTCCAGAGAG 1452
Qy 462 TyrLeuGlnAsnGlyLysValSerSerAlaHisArgProCysAlaLeuGlnProIleLeu 481
Db 1453 TACTTAGAGAACCGGAAGTTAGCTCTGGTCATCGTGACGCGCATGTGACCCCTCCTG 1512
Qy 482 ThrLeuAspIleProPheProAspHisIleLeuYsGlnValAspPheProSerLysLeu 501
Db 1513 ACATTGAGACGATCCGCTTCTGATGACGCTTGAAGGGAATAGATTTCATCGAGATTT 1572
Qy 502 AsnAspLeuIleCysIleIleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAsp 521
Db 1573 AATGATTGGCATCTCTCTCTTAGACTTAAGAGGTGACACACGATGCTTACAAAGCAGAC 1632
Qy 522 ArgAlaArgGlyGlnGlnAlaSerSerIleSerCysTyrMetLysAspAspProGlnLeu 541
Db 1633 AGGAGCCGAGGAGAAAGACGTCAGCAATATCGTTACATGAAGAAACAATCCCGATTA 1692
Qy 542 ThrGlnGlnAspAlaLeuAsnHisIleAsnPheMetIleArgAspAlaIleArgGlnLeu 561
Db 1693 ACAGAGAGAGATGCTCTCAATCATATGATGCCATGATCAACGACATATCAAGAATTA 1752
Qy 562 AsnTyrGlnLeuLeuYsProAspAsnSerValProIleThrSerLysLysHisAlaPhe 581
Db 1753 AATTGGGAATCTTCAAAACCCGATAGCAATATTCCAATGACTGCACGGAACAATGCTTAT 1812
Qy 582 AspIleSerArgValTyrHisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsn 601
Db 1813 GAGATTAACCAAGCTTTCACCAACTTTACAATATAGAGATGGCTTCAAGCGTTGCCACT 1872
Qy 602 ValGlnThrLysSerLeuValMetArgThrValIleGlnProValProLeu 618
Db 1873 CAGAAACGAAAGTTTGGTGAGAGAACGCTCTTGAACCAAGTGCCTCTT 1923
```

Search completed: July 26, 2004, 19:38:26
Job time : 5701 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 26, 2004, 12:26:29 ; Search time 582 Seconds
(without alignment)
4510.973 Million cell updates/sec

Title: US-10-025-145A-65
3251
Sequence: 1 MALSLTPVSRSCSSSHE.....FANVETKSLVMRTVIEPVPL 618

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues
Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_{p2n}.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10025145/runat_23072004_092622_22880/app_query.fasta_1.775
-DB=N_Geneseq_29Jan04 -QFMT=fastap -SUFFIX=trng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pico -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10025145 @CGN 1 1 708 @runat_23072004_092622_22880 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOC
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|--------------------|
| 1 | 3251 | 100.0 | 2013 | 4 | AAF73411 Grand fir |
| 2 | 2453 | 75.5 | 2018 | 2 | AAX08644 Pinene sy |
| 3 | 2453 | 75.5 | 2018 | 3 | AAA38922 Grand fir |
| 4 | 2453 | 75.5 | 2018 | 4 | AAF73372 Grand fir |
| 5 | 2264 | 69.6 | 2186 | 4 | AAF73412 Grand fir |
| 6 | 2200.5 | 67.7 | 2196 | 2 | AAX08643 Myrcene s |
| 7 | 2200.5 | 67.7 | 2196 | 3 | AAA38927 Grand fir |
| 8 | 2200.5 | 67.7 | 2196 | 4 | AAF73371 Grand fir |

| | | | | | | | |
|----|--------|------|------|---|----------|----------|-----------|
| 9 | 2197.5 | 67.6 | 2205 | 2 | AAX08663 | Aax08663 | Grand fir |
| 10 | 2197.5 | 67.6 | 2205 | 4 | AAF73391 | Aaf73391 | Grand fir |
| 11 | 2137 | 65.7 | 1890 | 4 | AAF73421 | Aaf73421 | Grand fir |
| 12 | 2084.5 | 64.1 | 2429 | 4 | AAF73413 | Aaf73413 | Grand fir |
| 13 | 2031.5 | 62.5 | 2089 | 2 | AAX08645 | Aax08645 | limonene |
| 14 | 2031.5 | 62.5 | 2089 | 3 | AAA38938 | Aaa38938 | Grand fir |
| 15 | 2031.5 | 62.5 | 2089 | 4 | AAF73373 | Aaf73373 | Grand fir |
| 16 | 1617.5 | 49.8 | 1513 | 3 | AAA69551 | Aaa69551 | Pinus rad |
| 17 | 1611.5 | 49.6 | 1634 | 3 | AAA69644 | Aaa69644 | Pinus rad |
| 18 | 1295.5 | 39.8 | 1865 | 3 | AAA38933 | Aaa38933 | Grand fir |
| 19 | 1295.5 | 39.8 | 1885 | 2 | AAX87534 | Aax87534 | Delta-sel |
| 20 | 1295.5 | 39.8 | 1885 | 2 | AAX87533 | Aax87533 | Delta-sel |
| 21 | 1295.5 | 39.8 | 1885 | 2 | AAX87505 | Aax87505 | Grand fir |
| 22 | 1291.5 | 39.7 | 1885 | 2 | AAX87532 | Aax87532 | Delta-sel |
| 23 | 1267.5 | 39.0 | 1173 | 3 | AAA69643 | Aaa69643 | Pinus rad |
| 24 | 1250.5 | 38.5 | 1967 | 2 | AAX87513 | Aax87513 | Grand fir |
| 25 | 1250.5 | 38.5 | 1967 | 2 | AAX08655 | Aax08655 | Grand fir |
| 26 | 1250.5 | 38.5 | 1967 | 4 | AAF73383 | Aaf73383 | Grand fir |
| 27 | 1240.5 | 38.2 | 2700 | 2 | AAT97447 | Aat97447 | Pacific Y |
| 28 | 1240.5 | 38.2 | 2700 | 3 | AAA38931 | Aaa38931 | Yew taxed |
| 29 | 1231 | 37.9 | 1785 | 2 | AAX87535 | Aax87535 | Gamma-hum |
| 30 | 1231 | 37.9 | 1785 | 3 | AAA38934 | Aaa38934 | Grand fir |
| 31 | 1231 | 37.9 | 1977 | 2 | AAX87506 | Aax87506 | Grand fir |
| 32 | 1230 | 37.8 | 1785 | 2 | AAX87536 | Aax87536 | Gamma-hum |
| 33 | 1230 | 37.8 | 1785 | 2 | AAX87537 | Aax87537 | Gamma-hum |
| 34 | 1188.5 | 36.6 | 2528 | 2 | AAX87529 | Aax87529 | Grand fir |
| 35 | 1187 | 36.5 | 2424 | 2 | AAX08654 | Aax08654 | Grand fir |
| 36 | 1187 | 36.5 | 2424 | 3 | AAA38932 | Aaa38932 | Grand fir |
| 37 | 1187 | 36.5 | 2424 | 4 | AAF73382 | Aaf73382 | Grand fir |
| 38 | 1187 | 36.5 | 2525 | 2 | AAX87530 | Aax87530 | E-alpha-b |
| 39 | 1187 | 36.5 | 2528 | 2 | AAX87531 | Aax87531 | E-alpha-b |
| 40 | 1187 | 36.5 | 2571 | 2 | AAX87504 | Aax87504 | Grand fir |
| 41 | 1052.5 | 32.4 | 2861 | 3 | AAA38937 | Aaa38937 | Grand fir |
| 42 | 856 | 26.3 | 695 | 4 | AAF73414 | Aaf73414 | Grand fir |
| 43 | 829.5 | 25.5 | 779 | 3 | AAA69642 | Aaa69642 | Pinus rad |
| 44 | 800 | 24.6 | 1416 | 2 | AAX08656 | Aax08656 | Grand fir |
| 45 | 800 | 24.6 | 1416 | 4 | AAF73384 | Aaf73384 | Grand fir |

ALIGNMENTS

| | | |
|----------|---|--|
| RESULT 1 | AAF73411 | |
| ID | AAF73411 | standard; CDJA; 2013 BP. |
| XX | | |
| AC | AAF73411; | |
| XX | | |
| DT | 30-APR-2001 | (first entry) |
| XX | | |
| DE | Grand fir monoterpene | synthase coding sequence fragment SEQ ID NO: 64. |
| XX | | |
| KW | Monoterpene synthase; | grand fir; cancer; (-)-camphene synthase; |
| KW | myrcene synthase; (-)- | limonene synthase; (-)-pinene synthase; |
| KW | terpinolene synthase; | insect resistance; nutrition; ss. |
| XX | | |
| OS | Abies grandis. | |
| XX | | |
| PN | W0200107565-A2. | |
| XX | | |
| PD | 01-FEB-2001. | |
| XX | | |
| PF | 24-JUL-2000; 2000WO-US020264. | |
| XX | | |
| PR | 26-JUL-1999; 99US-00360545. | |
| XX | | |
| PA | (UNIW) UNIV WASHINGTON STATE RES FOUND. | |
| XX | | |
| PI | Steele CL, Bohlman J, Croteau RB, Phillips MA; | |
| XX | | |
| DR | WPI; 2001-182782/18; | |
| DR | P-PSDB; AAB69390. | |
| XX | | |
| PT | New nucleic acid encoding monoterpene synthases, for increasing terpene | |

PT synthesis in plants, e.g. for increasing resistance to pests or for treatment of cancer.

PS Claim 8; Page 147-149; 175pp; English.

CC The present invention provides the protein and coding sequences of
CC monoterpene synthases from the grand fir. These include (-)-camphene
CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-
CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase
CC and pinene synthase. The sequences can be used to produce transgenic
CC plants expressing high levels of the enzymes, resulting in levels which
CC are useful in protecting against and treating cancers, and to confer
CC insect resistance on plants

SQ Sequence 2013 BP; 591 A; 432 C; 464 G; 526 T; 0 U; 0 Other;

| | |
|------------------------|---------|
| Alignment Scores: | |
| Pred. No. : | 0 |
| Score: | 3251.00 |
| Percent Similarity: | 100.00% |
| Best Local Similarity: | 100.00% |
| Query Match: | 100.00% |
| DB: | 4 |
| Gaps: | |
| Length: | 2013 |
| Matches: | 618 |
| Conservative: | 0 |
| Mismatches: | 0 |
| Indels: | 0 |
| Gaps: | 0 |

US-10-025-145A-65 (1-618) x AAF73411 (1-2013)

| | | | |
|----|-----|---|-----|
| QY | 1 | MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeuSerSerSerHisGlu | 20 |
| Db | 36 | ATGGCTCTTCTTCTATTACTCCGCTGGTTTCCAGGTCGTGCTCAGTCTTCTCATGAG | 95 |
| QY | 21 | IleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArgProGlyLysSerVal | 40 |
| Db | 96 | ATTAAGGCTCTCCGTAGAACAACTCCCACTCTTGAATCTGCAGCGCGGGAATCCGTC | 155 |
| QY | 41 | AlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAspSerValGlnArgArg | 60 |
| Db | 156 | GCGCATTTCCATAACATGTGTGTGACAAAGCTTCGATCTACTGATTCTGTACAGAGACCC | 215 |
| QY | 61 | ValGlyAsnTyrHisSerAsnLeuTyrAspAspAspPheIleGlnSerLeuIleSerThr | 80 |
| Db | 216 | GTGGGCNACTATCATTTCCAACTGTGGAGCATGATTTTCATACAGTCTGTATCTCAACG | 275 |
| QY | 81 | ProTyrGlyAlaProAspTyrArgGlnArgAlaAspArgLeuIleGlyGluValLysAsp | 100 |
| Db | 276 | CCTTATGAGACCACTGATTACCAGCACTGCTGACAGACTTATTGGGAAGTAAAGAT | 335 |
| QY | 101 | IleMetPheAsnPhelysSerLeuGlnAspGlyGlyAsnAspLeuGlnArgLeuLeu | 120 |
| Db | 336 | ATAATGTTCAATTTCAAGTCGCTGGAAGATGAGGCAATGATCTCTTCAACGACTTTTG | 395 |
| QY | 121 | LeuValAspAspValGlnArgLeuGlyIleAspArgHisPhelysLysGluIleLysThr | 140 |
| Db | 396 | CTGGTCGATGACGTTGAACGTTTGGGAATCACAAGCCATTTCAAAAAAGAGATAAAACG | 455 |
| QY | 141 | AlaLeuAspTyrValAlaAsnSerTyrTrpAsnGlnLysGlyIleGlyCysGlyArgGluSer | 160 |
| Db | 456 | GCACTCGATTATGTTAACAGTTATTGAAAGAAAAAGCATTGGATGTGGAGGGAGAGAT | 515 |
| QY | 161 | ValValThrAspLeuAsnSerThrAlaLeuGlyLeuArgThrLeuArgLeuHisGlyTyr | 180 |
| Db | 516 | GTTGTGACTGACCTCAACTCAACCGCTTGGGGCTTCGAACCTCCGACTACACGGAATAC | 575 |
| QY | 181 | ThrValSerSerAspValLeuAsnValPheLysAspLysAsnGlyGlnPheSerSerThr | 200 |
| Db | 576 | ACTGTGCTTCAGATGTTTGAACGTTTAAAGACAAAATGGGCAATTTTCTCCACT | 635 |
| QY | 201 | AlaAsnIleGlnIleGluGlyGluIleArgGlyValLeuAsnLeuPheArgAlaSerLeu | 220 |
| Db | 636 | GCCAATATTCAGATAGAGGAGAGATTAGAGCGCTTCTCAATTATTCAAGGCGCTCCCTC | 695 |
| QY | 221 | ValAlaPheProGlyGlyLysValMetAspGluAlaGluThrPheSerThrLysTyrLeu | 240 |
| Db | 696 | GTCGCCCTTCCCGCGAGAAAGTTATGATGACCTGAACATTTCTTACAAAATATTTTA | 755 |

| | | | |
|----|------|---|------|
| QY | 241 | ArgGluAlaLeuGlnLysIleProAlaSerSerIleLeuSerLeuGluIleArgAspVal | 260 |
| Db | 756 | AGAGAAGCCCTGCMAAAGATTCCGGCATCCAGTAACTTTCACTAGAGATACGGGACGTT | 815 |
| QY | 261 | LeuGluTyrGlyTrpHisThrAsnLeuProArgLeuGluAlaArgAsnTyrMetAspVal | 280 |
| Db | 816 | CTGGATATATGTTGGCACACCAATTGGCCACGGCTTGAAGCAAGGAATTACATGACGTC | 875 |
| QY | 281 | PheGlyGlnHisThrLysAsnLysAsnAlaIleGluLysLeuLeuAlaLysLeu | 300 |
| Db | 876 | TTTGGACAGCACACTAAATAAAGAACGCCGCCGCAAACTTTAGACTTGCATAATTG | 935 |
| QY | 301 | GluPheAsnIlePheHisSerLeuGlnGluArgGluLeuLysHisValSerArgTrpTrp | 320 |
| Db | 936 | GAATTCAATATATTCACTCTTACAAGAGAGAGAGATTAAACATGTTTCCGATGCTGG | 995 |
| QY | 321 | LysAspSerGlySerProGluMetThrPheCysArgHisArgHisValGluTyrTyrAla | 340 |
| Db | 996 | AAAGACTCGGCTTCTCTGAGATGACCTTCTGTGCATCGTCACGTTGAATACTACGCT | 1055 |
| QY | 341 | LeuAlaSerCysIleAlaPheGluProGlnHisSerGlyPheArgLeuGlyPheThrLys | 360 |
| Db | 1056 | TTGGCTTCTGCATTCGCTTCGAGCCTCAACATTCGATTCAGACTCGGCTTACCAAG | 1115 |
| QY | 361 | MetSerHisLeuIleThrValLeuAspAspMetTyrAspValPheGlyThrValAspGlu | 380 |
| Db | 1116 | ATGTCATCTTATCACGCGTTCTTGACGACATGTACGACGTCCTCGGCACAGTAGACGAG | 1175 |
| QY | 381 | LeuGluLeuPheThrAlaThrIleLysArgTrpAspProSerAlaMetGluCysLeuPro | 400 |
| Db | 1176 | CTGGAACCTTCCACAGCGACAATTAAAGATGGATCCGTCGCGATGAATGCCTTCCA | 1235 |
| QY | 401 | GluTyrMetLysGlyValTyrMetMetValTyrHisThrValAsnGluMetAlaArgVal | 420 |
| Db | 1236 | GAATATATGAAGAAGAGTACATGATGTTTATCACACCGTAAATGAATGGCTTCGAGTG | 1295 |
| QY | 421 | AlaGluLysAlaGlnGlyArgAspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCys | 440 |
| Db | 1296 | GCAGAGAAGGCTCAAGGCCGAGACACGCTCAACTATGCAAGACAGCGCTTGGAGCGGT | 1355 |
| QY | 441 | PheAspSerTyrMetGlnGluAlaLysTrpIleAlaThrGlyTyrLeuProThrPheGlu | 460 |
| Db | 1356 | TTTGATTCTGATATGACGAGAAACAAGTGATCGCCACTGCTTATCTGCCACGTTTGAG | 1415 |
| QY | 461 | GluTyrLeuGluAsnGlyLysValSerSerAlaHisArgProCysAlaLeuGlnProIle | 480 |
| Db | 1416 | GAGTACTTGAGAACGGGAAAAGTTAGCTCTGCTCATCGCCATGCGCACTGCAACCATTT | 1475 |
| QY | 481 | LeuThrLeuAspIleProPheProAspHisIleLeuLysGluValAspPheProSerLys | 500 |
| Db | 1476 | CTGACGTTGACATCCCTTCTCTGATCACATCCTCAAGAAAGTTGACTTCCCATCGAAG | 1535 |
| QY | 501 | LeuAsnAspLeuIleCysIleIleLeuArgLeuArgGlyAspThrArgCysTyrLysAla | 520 |
| Db | 1536 | CTCAATGACTTGATATGTATCATCTCTCGATTAAAGAGTGATACACGGTGCTACAGGCA | 1595 |
| QY | 521 | AspArgAlaArgGlyGluGluAlaSerSerIleSerCysTyrMetLysAspAsnProGly | 540 |
| Db | 1596 | GACAGGGCCCGTGAAGAGAAGCTTCGTCTATATCATGTTATATGAAGAACAATCCTGGA | 1655 |
| QY | 541 | LeuThrGluGluAspAlaLeuAsnHisIleAsnPheMetIleArgAspAlaIleArgGlu | 560 |
| Db | 1656 | TTAACGGAAGAAGATGCTCTGAATCATATCACTTCATGATCAGGAGCGCAATCAGAGAA | 1715 |
| QY | 561 | LeuAsnTrpGluLeuLeuLysProAspAsnSerValProIleThrSerLysLysHisAla | 580 |
| Db | 1716 | TTAAATTGGAGCTCTAAAGCCAGACAACAGTGTCCCATCATCTCCAGAAACACGCA | 1775 |
| QY | 581 | PheAspIleSerArgValTrpHisHisGlyTyrArgTyrArgAspGlyTyrSerPheAla | 600 |
| Db | 1776 | TTTGACATTAAGCAGAGTTTGGCATCACGGTTACAGATACCGAGATGGCTACAGCTTTGCC | 1835 |

Qy 601 AsnValGluThrLysSerLeuValMetArgThrValIleGluProValProLeu 618
Db 1836 AACGTGAACAAGAGTTTGGTGTATGAAACCGTCATTTGAACCTGTGCTTTG 1889

RESULT 2

AAx08644

ID AAX08644 standard; cDNA; 2018 BP.

XX AAX08644;

DT 27-SEP-1999 (first entry)

DE pinene synthase gene.

XX Mycrene synthase; limonene synthase; pinene synthase; flavour; aroma;

KW defense; plant seed; oil; meal; ss.

XX Abies grandis.

XX Key Location/Qualifiers

FT CDS 6.1892

FT /*tag= a /product= "pinene synthase"

PN WO9902030-A1.

XX 21-JAN-1999.

XX 10-JUL-1998; 98WO-US014528.

XX 11-JUL-1997; 97US-0052249P.

XX (UNIW) UNIV WASHINGTON STATE RES FOUND.

PI Bohlmann J, Steele CL, Croteau RB;

XX WPI; 1999-120396/10.

DR P-PSDB; AAW85701.

XX New isolated gymnosperm monoterpene synthase DNA - obtained from Grand

PT fir (Abies grandis), used to provide plants with modified production of

PT monoterpenes, e.g. mycrene, limonene or pinene.

XX Claim 10; Page 74-77; 121pp; English.

PS Nucleotide sequences encoding mycrene synthase, limonene synthase and

CC pinene synthase from Grand fir may be incorporated into any organism

CC (e.g. intact plant, animal, microbe), or derived cell culture that

CC produces geranyl diphosphate for the production of the aforementioned

CC enzymes or their products. The sequences when expressed in transfected

CC cells may also be used for the production or modification of flavour and

CC aroma properties, improvement of defense capability, and the alteration

CC of other ecological interactions mediated by mycrene, limonene, pinene,

CC or their derivatives. In particular they can be used for the production

CC of plant seeds for the extraction of oil or meal

XX Sequence 2018 BP; 583 A; 431 C; 479 G; 525 T; 0 U; 0 Other;

SO Alignment Scores: 1.2e-243 Length: 2018

US-10-025-145A-65 (1-618) x AAX08644 (1-2018)

Qy 1 MetAlaLeuSerIleThrProLeuValSerArgSerCysLeu----- 15

Db 6 ATGCTCTAGTTTCTACCGCACCCTGGCTTCCAAATCATGCTGCACAAATCGTTGATC 65

Qy 16 SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGluIleCysArg 35

Db 66 AGTTCTACCATGAGCTTAAGGCTCTCTAGAACAAATTCACGCTTACGAATGAGTAGG 125

Qy 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55

Db 126 CGAGGAAATCTATCACTCCTTCCATCAGCATGAGCTTACACCGTTGTAAACCGATGAT 185

Qy 56 SerValGlnArgValGlyAsnThrHisSerAsnLeuTrpAspAspPheIleGln 75

Db 186 GGTGACGAGACGCGATGGCGATTTCCATTCCAACTCTGGAGCATGATGTCATACAG 245

Qy 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95

Db 246 TCTTTA---CCAACGGCTTATGAGGAAATCGTACCTGAGCGCTGAGAAACTGATC 302

Qy 96 GlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly----- 112

Db 303 GGGGAGTAAGAAC--ATGTTCAATTGATGTCATTAGAGATGAGAGTTAATGAGT 359

Qy 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130

Db 360 CCGCTCAATGATCTCATTCACCGCCTTTGGATTGTCGACAGCCTTGAACTTTGGGATC 419

Qy 131 AspArgHisPheLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150

Db 420 CATAGACATTTCAAAGATGAGATAAATCGCGCTTGATTATGTTACAGTTATTGGGCG 479

Qy 151 GluLysGlyIleGlyCysGlyArgGluSerValThrAspLeuAsnSerThrAlaLeu 170

Db 480 GAAATGGCATCGGATGCGGAGGAGAGTGTGTACTGATCTGAACCTCAACTCGCTTG 539

Qy 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190

Db 540 GGGCTTCGAACTTCAGACTACAGGATACCCGCTGCTTCAGATGTTTCAAGCTTTC 599

Qy 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGluIleArg 210

Db 600 AAGGCCAAATGCGCAGTTTCTGCTCTGAAATATTTCAGACAGATGAAGAGATCAGA 659

Qy 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230

Db 660 GCGCTCTGAATTATTCCGGCCTCTCATTTGCCCTTCCAGGGGGAATAATTAGAT 719

Qy 231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250

Db 720 GAGGCTGAATCTTCTTACCAATATTAAAGAAGCCCTGCAAAGATTCGCGTCTCC 779

Qy 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTrpHisThrAsnLeuPro 270

Db 780 AGT---CTTTCGCGAGAGATCGGGGACGTTTGGATATGTTGGCACACATATTGGCCG 836

Qy 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsnLysAsnAla 290

Db 837 CGATTGGAAGCAAGAAATTACATCCAGTCTTTGGACAGGACACTGAGAACACGAAGTCA 896

Qy 291 -----AlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307

Db 897 TATGTGAGAGCAAAAACTTTAGAACTCGCAAAATTGGAGTTCAACATCTTCAATCC 956

Qy 308 LeuGlnGluArgGluLeuLysHisValSerArgTrpTrpLysAspSerGlySerProGlu 327

Db 957 TTACAAGAAGAGGAGTTAGAAAGTCTGTCAGATGTTGAAAGAAATCGGGTTTCTCTAG 1016

Qy 328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347

Db 1017 ATGACCTTCTGCCGACATCGTACGCGAATACTACACTTTGGCTTCTGCAATGCGTTC 1076

Qy 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367

Db 1077 GAGCCTCACTTCTGATTCACTCGGCTTGGCCACAGACGTGTCACTTATCACGGTT 1136

Qy 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluPheThrAlaThr 387

Db 1137 CTTGACGATATGTACGACACCTTCGGCAGACGTAGACGAGCTTGAACTCTTCACAGCGACA 1196
 QY 388 IleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407
 Db 1197 ATGAAGAGATGGGATCCGTCCTCGATGAGATTGCTTCAGAAATATATGAAAGGAGTGTAC 1256
 QY 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg 427
 Db 1257 ATAGCGGTTTACGACACCGCTAAATGAAATGGCTCGAGAGGACGAGGAGCTCAAGGCCGA 1316
 QY 428 AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu 447
 Db 1317 GATACGCTCACATATGTCTCGGAAAGCTTGGAGGCTTATATGTATGATATGCAAGAA 1376
 QY 448 AlalysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467
 Db 1377 GCAAGGTGATCGCCACTGGTTACTGCTCCCTCTTGATGAGTACTACGAGAATGGGAAA 1436
 QY 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
 Db 1437 GTTAGCTGTGTCATCGCATATCCGCAATTGCAACCCATTCTGACAAATGGACATCCCTTTT 1496
 QY 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507
 Db 1497 CCTGATCATATCTCTCAAGGAAGTTGACTTCCCATCAAAAGCTTAAAGACTTGCGCATGTGCC 1556
 QY 508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu 527
 Db 1557 ATCCTTCGATTACGAGGTGATACGGGGCTTACAAGCGAGCAGGGGCTCGTGAGAAGAA 1616
 QY 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547
 Db 1617 GCTTCTCTATATCATGTTATATGAAGACAATCCTGAGATATCAAGGAAGATGCTCTC 1676
 QY 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLeuLys 567
 Db 1677 GATCATATCAACGCCCATGATCAGTACGTAATCAAAAGATTAAATTGGGAACTTCTCAA 1736
 QY 568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp 587
 Db 1737 CCAGACATCAATGTTCCCATCTCGGCGAAGAAACATGCTTTGACATCGCCAGAGCTTTC 1796
 QY 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607
 Db 1797 CATACGGCTACAAATATCCGAGACGGCTTACAGCGTTGCCAACGTTGAAACGAAGAGTTTG 1856
 QY 608 ValMetArgThrValIleGluProValProLeu 618
 Db 1857 GTACAGAGAACCTCCTTGAATCTGTGCTTTG 1889
 RESULT 3
 AAA38922
 ID AAA38922 standard; DNA; 2018 BP.
 XX
 AC AAA38922;
 XX
 DT 25-AUG-2000 (first entry)
 XX
 DE Grand fir pinene synthase DNA sequence SEQ ID NO:19.
 XX
 KW Synthase; protein co-ordinate data; active site; modification; terpenoid;
 KW 3-dimensional coordinate; alpha carbon atom; plant; terpene synthase;
 KW isoprenoid; breeding programme; fragrance; flavour; pheromone;
 KW defensive agent; pigment; antitumour; steroid hormone;
 KW signal transduction pathway; bile acid; affinity purification;
 KW photoreceptor; enzymatic synthesis; nutrient supplement;
 KW immunological reagent; ds.
 XX
 OS Abies grandis.
 XX
 PN WO200017327-A2.
 XX
 PD 30-MAR-2000.

XX 17-SEP-1999; 99WO-US021419.
 PF
 XX 18-SEP-1998; 98US-010093P.
 XX
 PR 22-APR-1999; 99US-0130628P.
 PR
 PR 23-AUG-1999; 99US-0150262P.
 XX
 PA (KENT) UNIV KENTUCKY RES DEPT.
 PA (SALK) SALK INST BIOLOGICAL STUDIES.
 XX
 PI Chappell J, Manna KR, Noel JP, Starks CM;
 XX
 DR WPI; 2000-292839/25.
 DR
 DR P-PSDB; AAY90837.
 XX
 XX
 PT Novel terpene synthase enzymes, useful for producing terpene
 PT hydrocarbons, e.g. fragrances or antitumor agents, are derived from known
 PT enzymes by specific amino acid alterations.
 XX
 PS Disclosure; Page 363-366; 450pp; English.
 XX
 CC The present invention describes an isolated terpene synthase (I)
 CC comprising a region with at least 20% identity to region 265-535 of a 548
 CC amino acid (aa) sequence (Ia), given in AAY90831. (I) contains nine alpha
 CC -carbon atoms (alphaC) that have interatomic distances, between each
 CC other, within tabulated ranges, have a centre point (within a sphere of
 CC radius 2.3 Angstrom) within tabulated ranges, and have an ordered
 CC arrangement of R groups (defining aa side chains), excluding specific
 CC tabulated arrangements (tables given in the specification). (I), and
 CC related enzymes, are used to produce a wide range of terpenoids (e.g.
 CC cyclic, acyclic, optionally hydroxylated), useful e.g. as fragrances,
 CC flavours, pheromones, defensive agents, pigments, antitumour agents,
 CC components of signal transduction pathways, precursors of steroid
 CC hormones and bile acids, as photoreceptors and as co-factor side chains.
 CC Some synthases with little or no catalytic activity (and nucleic acids
 CC encoding them) are used as controls in the analysis of products formed by
 CC enzymatic synthesis; as nutrient supplements; for affinity purification
 CC of isoprenoids; or to develop immunological reagents or nucleic acids for
 CC monitoring expression of terpene synthase or inheritance of the gene in
 CC plant breeding programs. The new synthases may produce novel terpene
 CC products. AAA38910 to AAA38938 and AAY90831 to AAY90859 represent
 CC sequences used in the exemplification of the present invention
 XX
 SQ Sequence 2018 BP; 583 A; 431 C; 479 G; 525 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.2e-243 Length: 2018
 Score: 2453.00 Matches: 475
 Percent Similarity: 84.63% Conservative: 59
 Best Local Similarity: 75.28% Mismatches: 81
 Query Match: 75.45% Indels: 16
 DB: 3 Gaps: 6
 US-10-025-145A-65 (1-618) x AAA38922 (1-2018)
 QY 1 MetaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
 Db 6 ATGGCTTAGTTTCTACCGCACCGTTGGCTTCCAAATCATAGCTGCACAAATCGTTGATC 65
 QY 16 SerSerSerHisGluIleLysAlaLeuValArgGlyThrIleProThrLeuGlyIleCysArg 35
 Db 66 AGTTCTTACCATGAGCTTAAGGCTCTCTAGAACAAATTCAGCTTAGAATGAGTAGG 125
 QY 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
 Db 126 CGAGGGAATCTATCACTCCTTCCATCAGCATGAGCTCTACCAACCGTTGTAACGATGAT 185
 QY 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTyrAspAspAspPheIleGln 75
 Db 186 GGTGTACGAAGACGATGGGCGATTTCATTCCAACCTCTGGGACGATGATCATACAG 245
 QY 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95

Db 246 TCTTTA---CCAACGGCTTATGAGAAATAATCGTACTGAGCGTGTGAGAAACTGATC 302
Qy 96 GYGLVALLYSAPLLEMETPHEASNPHELYSERLEUGLUSPGLYGLY----- 112
Db 303 GGGGAGTAAGAAC---ATGTTCAATTCGATGTCATTAGAGATGAGAGATTATGAGT 359
Qy 113 -----ASNAPLEULEUGLNARGLEULEULEUVALASPRVALGLUARGLEUGLYLE 130
Db 360 CCGCTCAATGATCTCATTCACACGCCCTTGGATTGTCAGACGCCCTTGAACTTGGGATC 419
Qy 131 ASPARGHISPHELYSGLULILEYTHRALALEUASPTYRVALASNSEPTYRTPASN 150
Db 420 CATAGACATTTCAAAAGATGAGATMAAATCGCGCTGATTATGTTACAGTTATTGGGCG 479
Qy 151 GLUYEGLYILEGLCYSGLYARGGLUSERVALTHRASPLEUASNSETHRALALEU 170
Db 480 GAAATAGCATCGGATCGGAGGAGAGTGTGTTACTGATCTGAACCTCAACTGCGTTCG 539
Qy 171 GLYLEARGTHRLAUARGLEUHNISGLYTYRTHRALSERSEASPRVALLEUASNVALPHE 190
Db 540 GGGCTTCGAACCTACGACTACACGGATACCCGGTGTCTTCAGATGTTTCAAACTTTC 599
Qy 191 LYSAPRYSARGGLYGLNPHESERSETHRALASNILEGLNILEGLUGLUILEARG 210
Db 600 AAAGGCCAAATGGGCAGTTTCCCTGCTGAAAATATTTCAGACAGATGAGAAGATCAGA 659
Qy 211 GLYVALLEUASNLEUPHEARGALASERLEUVALALAPHEPROGLYGLUYVALMETASP 230
Db 660 GCGCTTCGAATTTATTCGCGGCTCCCTCATGCTTCCAGGGGAGAAATTATGAGT 719
Qy 231 GLUALAGLUTHRPHESERTHRLYSTYRLEUARGGLUALALEUGLNLYSILEPROLASER 250
Db 720 GAGGTGAATCTTCTTACCMAATATTTAAGAAGCCCTGCAAAAGATTCCGCTCTCC 779
Qy 251 SERILEUSERLEUGLUILEARGSPRVALLEUGLUITYRGLYTRPHISTHRAASNLEUPRO 270
Db 780 AGT---CTTCGCGAGAGATCGGGGACGTTTGGAAATATGTTGGCACACATATTGGCG 836
Qy 271 ARGLEUGLUALARGASNTRYMETASPRVALPHEGLYGLNHIISTHRLYASNLYSASNALA 290
Db 837 CGATTGGAAGCAAGGAATTACATCCAAAGTCTTTGGACAGGACACTGAGAACAGAACTCA 896
Qy 291 -----ALAGLULYSLEULEUGLULEUALALYSLEUGLUPHEASNLEPHEHISER 307
Db 897 TATGTGAAGACAAATACTTTTGAACCTCCCAAAATTGAGTTCAACATCTTTCAATCC 956
Qy 308 LEUGLNLUARGGLULEULYSHISVALISERARGTRTPRLYSAPRSEGLYSEPROGLU 327
Db 957 TTACAAAAGAGGAGTAGAAGTCTGTGTCAGATGCTGAAAGAAATCGGCTTTCTCTGAG 1016
Qy 328 METTHRPHESYARGHISARGHISVALIGLUITYRGLYALALEUASERCYSILEALAPHE 347
Db 1017 ATGACCTTCGCGGACATCGTCACGTGAAATACTACACTTGGCTTCGCAATTGCGTTC 1076
Qy 348 GLUPROGLNHIISERGLYPHEARGLEUGLYPHETHRLYSMETSERHISLEULETHRVAL 367
Db 1077 GAGCCTCAACATCTTGATTCAGACTCGGCTTGGCCAAGACGTGTCACTTATCAGCGTT 1136
Qy 368 LEUASPRMETTYRASPVALPHEGLYTHRALASPRGLULEUGLULEUPHETHRVALATHR 387
Db 1137 CTTGACGATATGTAAGACACCTTCGACAGTAGACGAGCTGGAACCTTTCACACAGCACA 1196
Qy 388 ILELYSARGTRPASRPROSERALAMETGLUCYBLEUPROGLUYTMETLYSGLYVALTYR 407
Db 1197 ATGAAGAGATGGGATCCGCTCTCGATAGATTGCTTCAGAAATATATGAAGAAGTGATAC 1256
Qy 408 METMETVALTYRHISTHRAVALASNGLULEUALARGVALALAGLUYSALAGLNGLYARG 427
Db 1257 ATAGCGGTTTACGACACCGTAATGAATGCTCGAGAGGACAGAGGCTCAAGGCCGA 1316
Qy 428 ASPTHRLEUASNTRYALARGGLNALATPRGLUALACYSPHEASPRSEPTYRMETGLNGLU 447
Db 1317 GATACGCTCAATATGCTCGGAAAGCTTGGAGGCTTATATTGATTCTGATATGCAAGAA 1376

Qy 448 ALALYSTRPILLEALATHRGLYTYRLEUPROTHRPHLEGUGLUITYRLEUGLUASNGLYLYS 467
Db 1377 GCAAGGTGATCGCCNCTGTTACTGCTCCCTTTGATGAGTACTACGAAATGGGAAA 1436
Qy 468 VALSERSERALAHISARGPROCYSALEUGLNPROILEUETHRLEUASNLEPHE 487
Db 1437 GTTAGCTGTGTCATCGCATATCCGCAATGCAACCATTCGTGACAAATGACATCCCTTT 1496
Qy 488 PROASPRHISILEULYSGLUVALASPRPHEPROSERLYSLEUASNAPLEULECYSI 507
Db 1497 CCTGATCATATCTCAAGGAAGTTGACTTCCCATCAAGCTTAACGACTTGGCATGTGCC 1556
Qy 508 ILELEUARGLEUARGGLYASPTHRARGCYSTRLYSALAASPRARGALARGGLUGLU 527
Db 1557 ATCCTTCGATTACGAGGTGATACCGGTCCTACAAAGCGGACAGGCTCGTGAAGAAGA 1616
Qy 528 ALASERSERIESECYSTRMETLYASPRASNPROGLYLEUTHRGLUGLUASPRALALEU 547
Db 1617 GCTTCCTTATATCATGTTATATGAAGACAAATCCTGAGTATCAGAGAAAGATGCTTC 1676
Qy 548 ASNHISILEASNPHEMETILEARGSPRALALEARGGLULEUASNTRPGLULEULELYS 567
Db 1677 GATCATATCAACGCCATGATCAGTACGTAAATCAAAAGATTAAATTGGAACTTCTCAA 1736
Qy 568 PROASPRASNSEVALPROILETHRSERLYSLYSHISALAPHEASPRILESERARGVALTRP 587
Db 1737 CCAGACATGATGTCCCATCTCGGCGAAGAAACATGCTTTTGACATCGCCAGACTTTC 1796
Qy 588 HISHISGLYTRARGTYRARGASPRGLYTRSERPHEALASNVALGLUTHRLYSERLEU 607
Db 1797 CATTACGGCTTACAATAACCGAGACGGCTACAGCGTTGCCAACGTTGAACGAAGAAGTTTG 1856
Qy 608 VALMETARGTHRVALILEGLUPROVALPROLEU 618
Db 1857 GTCAAGAACCCCTCTGTAATCTGTGCTTTG 1889

RESULT 4
AAF73372
ID AAF73372 standard; cDNA; 2018 BP.
XX
AC AAF73372;
XX
DT 30-APR-2001 (first entry)
XX
DE Grand fir (-)-pinene synthase coding sequence SEQ ID NO: 3.
XX
KW Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;
KW myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;
KW terpinolene synthase; insect resistance; nutrition; ss.
XX
OS Abies grandis.
XX
PN W0200107565-A2.
XX
PD 01-FEB-2001.
XX
PF 24-JUL-2000; 2000WO-05020264.
XX
PR 26-JUL-1999; 99US-90360545.
XX
PA (UNIW) UNIV WASHINGTON STATE RES FOUND.
XX
PI Steele CL, Bohlman J, Croten RB, Phillips MA;
XX
DR WPI; 2001-182782/18.
XX
DR P-PSDB; AAB69371.
XX
PT New nucleic acid encoding monoterpene synthases, for increasing terpene
PT synthesis in plants e.g. for increasing resistance to pests or for
XX
PS Claim 38; Page 108-110; 175pp; English.

QY 608 ValMetArgThrValIleGluProValProLeu 618
||| ||||| : : : ||| |||||
Db 1857 GTCACGAGAACCTCCTGATCTGTGCTTG 1889

RESULT 5
AAF73412
ID AAF73412 standard; cDNA; 2186 BP.
XX
AC AAF73412;
XX
DT 30-APR-2001 (first entry)
XX
DE Grand fir monoterpene synthase coding sequence fragment SEQ ID NO: 66.
XX
KW Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;
KW myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;
KW terpinolene synthase; insect resistance; nutrition; ss.
XX
OS Abies grandis.
XX
PN WO200107565-A2.
XX
PD 01-FEB-2001.
XX
PF 24-JUL-2000; 2000WO-US020264.
XX
PR 26-JUL-1999; 99US-00360545.
XX
PA (UNIW) UNIV WASHINGTON STATE RES FOUND.
XX
PI Steele CL, Bohlmann J, Croteau RB, Phillips MA;
XX
DR WPI; 2001-182782/18.
DR P-PSDB; AAB69391.
XX
PT New nucleic acid encoding monoterpene synthases, for increasing terpene
PT synthesis in plants, e.g. for increasing resistance to pests or for
PT treatment of cancer.
XX
PS Claim 13; Page 151-154; 175pp; English.

XX The present invention provides the protein and coding sequences of
CC monoterpene synthases from the grand fir. These include (-)-camphene
CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-
CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase
CC and pinene synthase. The sequences can be used to produce transgenic
CC plants expressing high levels of the enzymes, resulting in levels which
CC are useful in protecting against and treating cancers, and to confer
CC insect resistance on plants

XX
SQ Sequence 2186 BP; 722 A; 440 C; 472 G; 552 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 5.24e-224 Length: 2186
Score: 2264.00 Matches: 435
Percent Similarity: 80.53% Conservative: 78
Best Local Similarity: 68.29% Mismatches: 98
Query Match: 69.64% Indels: 26
DB: 4 Gaps: 9

US-10-025-145A-65 (1-618) x AAF73412 (1-2186)

QY 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
||| ||||| : : : ||| |||||
Db 34 ATGGCTCTGGTTCTTCCGCACCC-----AAATCCTGCCTGCACAAATCGTTGATC 84

QY 16 ---SerSerSerHisGluIleValAlaLeuArgThrIleProThrLeuGlyIleCys 34
||| : : : ||| ||||| : : : ||| ||||| : : : ||| ||||| : : : ||| |||||
Db 85 AGGTCTATCATCATGAGCTCAAGCCTCTGCCGACAGACCATCCCACTCTTGAATGTGT 144

QY 35 ArgProGlyLeuSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThr 54
||| ||| ||||| ||| : : : ||| ||||| ||| ||||| : : : ||| |||||
Db 145 AGGCGAGGGAATCTTTCACACCTCTGTGACGATGAGTTGACSCACCGCTGATCTGAT 204

QY 55 AspSerValGlnArgValGlyAsnTyrHisSerAsnLeuTyrAspAspPheIle 74
||| : : : ||||| : : : ||||| : : : ||||| : : : ||||| : : : |||||
Db 205 GATGGTCTACAAAGACGCATAGGTGACTATCATTCCAATCTCTGGAGCAGCATTTTCATA 264

QY 75 GlnSerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeu 94
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 265 CAGTCTCTTA---TCAACGCCTTATGGGAGCCCTTCTTACCAGAACGTGCTGAGAAACTG 321

QY 95 IleGlyValIleAspIleMetPheAsnPhelysSerLeuGluAspGlyGly----- 112
||| ||||| ||||| : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 322 ATTGGGAGAGTGAAGAG---ATGTTCAATTCATGCCATCGAGAGATGAGATCAATG 378

QY 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGly 129
||| ||||| ||||| : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 379 AGTCCCTCAATGATCTTATGACGACTTTGGATGTCGATAGCGTTGAACGTTGGGG 438

QY 130 IleAspArgHisPheLeuValGlyIleValThrAlaLeuAspTyrValAsnSerTyrTrp 149
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 439 ATTGATAGCATTTCAAAAAGAGATAAATCAGCCCTGATTATGTTTACAGTTATTGG 498

QY 150 AsnGluValGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAla 169
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 499 AACGAAAGATATTTGATGCGGTAGATAGATGTTTTCCTGATGTCAACTGCACTGCC 558

QY 170 LeuGlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnVal 189
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 559 TCGGGGTTTGAACCTCTCGCTACAGGATACAGTGTCTCTTCAAGCTTTTGAAGATA 618

QY 190 PheLeuAspLeuValAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyIle 209
||| : : : ||||| ||||| : : : ||||| ||||| ||||| ||||| ||||| |||||
Db 619 TTTCAGACCAAAATGGGACGTTTGCATCTCTCTCTAGTACAAA---GAGAGAGACATC 675

QY 210 ArgGlyValLeuLeuPheArgValSerLeuValAlaPheProGlyGluValMet 229
||| ||||| ||||| : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 676 AGAACCGTTCTGAAATTATATCCGGCTTCTTTCATTGCGCTTCTCGGAGAAAGTTATG 735

QY 230 AspGluAlaGluThrPheSerThrIleTyrLeuArgGluAlaLeuGlnIleProAla 249
: : : ||||| ||||| : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 736 GAAGAGGCTGAATTTCTCTTCAAGATATTGAAAGAACCGTGCAGAAAGATTCCGGTC 795

QY 250 SerSerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrHisThrAsnLeu 269
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 796 TCCAGT---CTTTCACAGAAATGACTACACTTGGATATAGTTGGCACACAATATAG 852

QY 270 ProArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThr----- 285
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 853 CCAAGATTGGAACAAGAAATTACTAGATGTATTGGACATCCATCCAGTCCATGCTC 912

QY 286 LysAsnLysAsnAla-----AlaGluValLeuLeuGluLeuAlaLysLeuGlu 301
||| ||||| ||||| : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 913 AAGAAGAAAGACGCAATATCTGGACAGCGAAAGCTTTTAGAATCGCAAAATTGGAG 972

QY 302 PheAsnIlePheHisSerLeuGlnGluArgGluLeuLysHisValSerArgTyrTrpLys 321
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 973 TTCAACATCTTCACTCCCTTCAACAGAGAGATTACAGATATCTTCCAGATGCTGATA 1032

QY 322 AspSerGlySerProGluMetThrPheCysArgHisArgHisValGluTyrTyrAlaLeu 341
||| ||||| ||||| : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1033 CATTCGGGTTTGCCTGAACCTGACCTTGTGCGCATCGTACGTTGAATACTACACCCTG 1092

QY 342 AlaSerCysIleAlaPheGluProGlnHisSerGlyPheArgLeuGlyPheThrLysMet 361
: : : ||||| ||||| : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1093 AGCTTTCATTTGCGACTGAGCCCAACATTTGCAATTCAGATGGGCTTGGCAAAACG 1152

QY 362 SerHisLeuIleThrValLeuAspAspMetTyrAspValPheGlyThrValAspGluLeu 381
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1153 TGTCAATCTTATCAGCGTTCTGACGATATCTACGACACTTTCGGAACGATGAGTAATC 1212

QY 382 GluLeuPheThrAlaThrIleLysArgTyrAspProSerAlaMetGluCysLeuProGlu 401
||| ||||| ||||| : : : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1213 GAATCTTCAACGAGGAGGATGAGATGATCCGTCGAGAAAGAACGCTCCACAGA 1272

| | | | | | | |
|-----------------------------------|---|------------------------------|--|------|--|--|
| Oy | | 402 | TyrMetLysGlyValTyrMetMetValTyrHisThrValAsnGluMetAlaArgValAla | 421 | | |
| | | | :: :: :: :: :: | | | |
| Db | | 1273 | TATATGAAGAATCTACATGGCACTCAGAAAGCTTTAATGCATATGGCGGAGGCA | 1332 | | |
| Oy | | 422 | GluLysAlaGlnGlyArgAspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPhe | 441 | | |
| | | | :: | | | |
| Db | | 1333 | GAGAAACACAAGGCCGAGACACGCTCAATTATGTGTAAGGCTTGGAAGTTTACTT | 1392 | | |
| Oy | | 442 | AspSerTyrMetGlnGluAlaLysTrpIleAlaThrGlyTyrLeuProThrPheGlu | 461 | | |
| | | | :: :: :: :: | | | |
| Db | | 1393 | GATTCGTATACACAAGAACAAAGTGATCGCCAGCGGTTATCTGCCAACTTTCGAGAG | 1452 | | |
| Oy | | 462 | TyrLeuGluAsnGlyLysValSerSerAlaHisArgProCysAlaLeuGlnProIleLeu | 481 | | |
| | | | | | | |
| Db | | 1453 | TACTTAGAAGACCAGAGTTAGCTCTGTGCATCGTGCACGGCATTGACACCCCTCTG | 1512 | | |
| Oy | | 482 | ThrLeuAspIleProPheProAspHisIleLeuLysGluValAspPheProSerLysLeu | 501 | | |
| | | | :: :: :: :: :: :: | | | |
| Db | | 1513 | ACATTGACGTACCGCTTCCTGTAGTACGCTTGAAGGGAATGATTTTCCATCGAGATT | 1572 | | |
| Oy | | 502 | AsnAspLeuIleCysIleIleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAsp | 521 | | |
| | | | | | | |
| Db | | 1573 | AATGATTTGGCATCTTCCTTCCTTAGACTAAGAGGTGACACAGATGCTACAAAGCGAC | 1632 | | |
| Oy | | 522 | ArgAlaArgGlyGluGluAlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeu | 541 | | |
| | | | | | | |
| Db | | 1633 | AGGGAACCGAGAGAGAGCGTCAAGCATATCGTGTACATGAAGAACAATCCCGATT | 1692 | | |
| Oy | | 542 | ThrGluGluAspAlaLeuAsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeu | 561 | | |
| | | | | | | |
| Db | | 1693 | ACAGAGGAAGATGCTCTCAATCATATCAATGCCATGATCAACGACATAATCAAAGATT | 1752 | | |
| Oy | | 562 | AsnTrpGluLeuLeuLysProAspAsnSerValProIleThrSerLysLysHisAlaPhe | 581 | | |
| | | | :: :: :: :: | | | |
| Db | | 1753 | AATTGGAACTTCTCAAAACCGATAGCAATATTTCCAATGACTGCACGGAACATGCTTAT | 1812 | | |
| Oy | | 582 | AspIleSerArgValTrpHisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsn | 601 | | |
| | | | ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: | | | |
| Db | | 1813 | GAGATTAACACAGAGCTTCCCAACTTTACAAATATAGAGATGAGCTTCAGCGTTGCCACT | 1872 | | |
| Oy | | 602 | ValGluThrLysSerLeuValMetArgThrValIleGluProValProLeu | 618 | | |
| | | | :: | | | |
| Db | | 1873 | CAAGAAACGAAAAAGTTGGTGAGAGAAACGCTCCTTGAACCAAGTGCTCTT | 1923 | | |
| RESULT 6 | | | | | | |
| AAX08643 standard; cDNA; 2196 BP. | | | | | | |
| ID | AAX08643 | | | | | |
| XX | AAX08643; | | | | | |
| AC | | | | | | |
| XX | | | | | | |
| DT | 27-SEP-1999 | (first entry) | | | | |
| XX | | | | | | |
| DE | Myrcene synthase gene. | | | | | |
| XX | | | | | | |
| KW | Myrcene synthase; limonene synthase; pinene synthase; flavour; aroma; | | | | | |
| KW | defense; plant seed; oil; meal; ss. | | | | | |
| XX | | | | | | |
| OS | Abies grandis. | | | | | |
| XX | | | | | | |
| FH | Key | Location/Qualifiers | | | | |
| FT | CDS | 69..1952 | | | | |
| FT | | /tag= a | | | | |
| FT | | /product= "Myrcene synthase" | | | | |
| XX | | | | | | |
| PN | WO9902030-A1. | | | | | |
| XX | | | | | | |
| PD | 21-JAN-1999. | | | | | |
| XX | | | | | | |
| PF | 10-JUL-1998; | 98WO-US014528. | | | | |
| XX | | | | | | |
| PR | 11-JUL-1997; | 97US-0052249P. | | | | |
| PA | (UNIW) UNIV WASHINGTON STATE RES FOUND. | | | | | |

XX PI Bohlmann J, Steele CL, Croteau RB;
 XX DR WPI; 1999-120396/10.
 XX DR P-PSDB; AAW85700.
 XX PT New isolated gymnosperm monoterpene synthase DNA - obtained from Grand
 XX PT fir (*Abies grandis*), used to provide plants with modified production of
 PS monoterpenes, e.g. myrcene, limonene or pinene.
 XX Claim 9; Page 69-72; 121pp; English.
 CC Nucleotide sequences encoding myrcene synthase, limonene synthase and
 CC pinene synthase from Grand fir may be incorporated into any organism
 CC (e.g. intact plant, animal, microbe), or derived cell culture that
 CC produces geranyl diphosphate for the production of the aforementioned
 CC enzymes or their products. The sequences when expressed in transfected
 CC cells may also be used for the production or modification of flavour and
 CC aroma properties, improvement of defense capability, and the alteration
 CC of other ecological interactions mediated by myrcene, limonene, pinene,
 CC or their derivatives. In particular they can be used for the production
 CC of plant seeds for the extraction of oil or meal
 XX
 XX Sequence 2196 BP; 684 A; 416 C; 468 G; 628 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No.: 2.01e-217 Length: 2196
 Score: 2200.50 Matches: 427
 Percent Similarity: 80.38% Conservative: 77
 Best Local Similarity: 68.10% Mismatches: 106
 Query Match: 67.69% Indels: 17
 DB: 2 Gaps: 7
 US-10-025-145A-65 (1-618) x AAX08643 (1-2196)
 QY 1 MetaLaleuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
 Db 69 ATGGCTCTGTTTCTATCTCACCGTTGGCTTCGAAATCTTGCTCGCAAGTCGTTGATC 128
 QY 16 SerSerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArg 35
 Db 129 AGTTCAATTCATGACATAGAGCTCCCTACATAGAACATCCCAATCTTGAATGCGTAGG 188
 QY 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
 Db 189 CGAGGGAATCTGTACCGCTTCCATGAGCATCAGTTGGCCACCGCTGCACCTGATGAT 248
 QY 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTTPAspAspPheIleGln 75
 Db 249 GGTGTACAAGACGCAATAGGTGACTAACCATTCATATCTGGAGCATGATTTCATACAG 308
 QY 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
 Db 309 TCTCTA--TCAACGCTTATGGGGAACCTCTTACCAGGAACGTGCTGAGATTAAATT 365
 QY 96 GlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly----- 112
 Db 366 GTGGAGGTAAGAAGATA--TTCAATTCAATGATACCTGGATGATGAGAGATTATGAGT 422
 QY 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
 Db 423 TCCTTTAATGATCTCATGCAACGCTTGGATGATGATAGCGTTGAACGTTGGGATA 482
 QY 131 AspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTTPAsn 150
 Db 483 GCTAGACATTTCAGAACGAGATTAACATCAGCTCTGATTATGTTTCCGTTACTGGAG 542
 QY 151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170
 Db 543 GAAACGGCATTTGATGTGGGAGACAGATATTGTTACTGATCTCACTCACTGCGTTG 602
 QY 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190

Db 603 GGGTTTGAACCTCTTCGATTACACGGGTACACTGTATCTCCAGAGCTTTTAAAGCTTTT 662
QY 191 LysAspLysAsnGLYGLnPheserSerThrAlaAsnIleGlnIleGluGLuIleArg 210
Db 663 CAAGATCAAAATGACAGATTGTATGCTGCCCGGT--CAGACAGGGGTGAGATCAGA 719
QY 211 GLyValLeuAsnLeuPheArgAlaSerIleValAlaPheProGluGLuLysValMetAsp 230
Db 720 AGCGTTCTTAATTATATCGGGCTTCCTTCATTGCCCTTCCTGGTGAGAAAGTTATGGAA 779
QY 231 GLuAlaGluThrPheSerThrLysTyrIleuArgGLuAlaLeuGlnLysIleProAlaSer 250
Db 780 GAAGCTGAATCTTCTCCACAAGATATTGAAAGAAAGCTTACAAGAAAGATTCCAGTCTCC 839
QY 251 SerIleuSerLeuGluIleArgAspValLeuGluTyrGLuTyrPheThrAsnLeuPro 270
Db 840 GCT--CTTTCACAAGAGATAAAGTTGTATGGAATATGCTGGCACACAATTTGCCA 896
QY 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGLYGLnHisThrLys-----Asn 287
Db 897 AGATTGGAAGCAAGAAATTACATAGACACCTTGAGAAAGACACCAGTCATGGCTCAAT 956
QY 288 LysAsnAlaAlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307
Db 957 AAAAATGCTGGGAAGAAGCTTTAGAACTTGCAGAAATTTGGAAGTTCAATATATTAACTCC 1016
QY 308 LeuGlnGluArgGluLeuLysHisValSerArgTrrPrrLysAspSerGlySerProGlu 327
Db 1017 TTACAACAAGAAAGAAATTACAATATCTTTGAGATGGTGAAAGAGTCGATTTGCCTTAA 1076
QY 328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347
Db 1077 TTGACATTTGCTCGGCATCGTCATGTGAATTTACACTTTGGCCTCTTGTATTGCCATT 1136
QY 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367
Db 1137 GACCCAAACATTTGTCATTGAGCTAGGCTTGCCTTGTGTCATCTTGTACAGATT 1196
QY 368 LeuAspAspMetTyrAspValPheGLYThrValAspGluLeuGluPheThrAlaThr 387
Db 1197 TTGACGATATTTAACGACACTTTTGAACGATTGACGAGCTTGAACCTTTCACATCTGCA 1256
QY 388 IleLysArgTrrAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407
Db 1257 ATTAAGAGATGGAATTTCATCAGAGATAGAACACCTTCCAGAAATATGAAATGTGTAC 1316
QY 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGLuArg 427
Db 1317 ATGGTCGTGTTGAAACTGTAAATGAACGACAGAGAGCGGAGAACTCAAGGAGAGA 1376
QY 428 AspThrLeuAsnTyrAlaArgGlnAlaTrrGluAlaCysPheAspSerTyrMetGlnGLu 447
Db 1377 AACACTCTCAACTATGTTGAAAGGCTGGGAGGCTTATTTTGATTCAATATATGGAAGAA 1436
QY 448 AlaLysTrrIleAlaThrGLuTyrLeuProThrPheGluGLuTyrLeuGluAsnGLuLys 467
Db 1437 GCAAAATGATCTCTAATGTTATCTGCCAATGTTGAAGAGTACCATGAGAATGGGAAA 1496
QY 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
Db 1497 GTGAGCTCTGCATATCGCGTAGCAACATTGCCAACCCTCTCACTTTGAATGCATGGCTT 1556
QY 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507
Db 1557 CCTGATTAATCTTGAAGGGAATTGATTTTCATCCAGGTTCAATGATTTGGCATCGTCC 1616
QY 508 IleLeuArgLeuArgGLuAspThrArgCysTyrLysAlaAspArgAlaArgGLuGLuGLu 527
Db 1617 TTCTTCGCTACGAGGTGACACACGCTGCTACAAAGCCGATAGGATCGTGTGAAGAA 1676
QY 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGluLeuThrGluGluAspAlaLeu 547
Db 1677 GCTTCGTATATCATGTATATGAAAGCAATCCTGATCAACCGAAGAAATGATGCCCTC 1736

QY 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrrGluLeuLys 567
Db 1737 AATCATATCAATGCGCTGTCATGATGACATTAATCAAGAAATTAATTTGGAACTTCTAAGA 1796
QY 568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrr 587
Db 1797 TCCAACGACAAATATTCCAATGCTGGCCCAAGAAACATGCTTTTGACATTAACAAGAGCTCTC 1856
QY 588 HisHisGLuTyrArgTrrArgAspGLuTyrSerPheAlaAsnValGluThrLysSerLeu 607
Db 1857 CACCATCTCTACATATATCGAGATGGCTTTAGTGTGCCAACACAGAAACAAAAATTG 1916
QY 608 ValMetArgThrValIleGlu 614
Db 1917 GTTATGGAACACTCCTTGAA 1937
RESULT 7
AAA38927
ID AAA38927 standard; DNA; 2196 BP.
XX
AC AAA38927;
XX
DT 25-AUG-2000 (first entry)
XX
DE Grand fir myrcene synthase DNA sequence SEQ ID NO:29.
XX
XX Synthase; protein co-ordinate data; active site; modification; terpenoid;
KW 3-dimensional coordinate; alpha carbon atom; plant; terpene synthase;
KW isoprenoid; breeding programme; fragrance; flavour; pheromone;
KW defensive agent; pigment; antitumour; steroid hormone;
KW signal transduction pathway; bile acid; affinity purification;
KW photoreceptor; enzymatic synthesis; nutrient supplement;
KW immunological reagent; ds.
XX
OS Abies grandis.
XX
PN WO200017327-A2.
XX
PD 30-MAR-2000.
XX
PF 17-SEP-1999; 99NO-US021419.
XX
PR 18-SEP-1998; 98US-0100993P.
PR 22-APR-1999; 99US-0130628P.
PR 23-AUG-1999; 99US-0150262P.
XX
PA (KENT) UNIV KENTUCKY RES DEPT.
PA (SALK) SALK INST BIOLOGICAL STUDIES.
XX
PI Chappell J, Manna KR, Noel JP, Starks CM;
XX
XX MPI; 2000-292839/25.
DR P-PSDB; AAY90842.
XX
PT Novel terpene synthase enzymes, useful for producing terpene
PT hydrocarbons, e.g. fragrances or antitumor agents, are derived from known
PT enzymes by specific amino acid alterations.
XX
PS Disclosure; Page 387-390; 450pp; English.
XX
CC The present invention describes an isolated terpene synthase (I)
CC comprising a region with at least 20% identity to region 265-535 of a 548
CC amino acid (aa) sequence (Ia), given in AAY90831. (I) contains nine alpha
CC -carbon atoms (alphaC) that have interatomic distances, between each
CC other, within tabulated ranges, have a centre point (within a sphere of
CC radius 2.3 Angstrom) within tabulated ranges, and have an ordered
CC arrangement of R groups (defining aa side chains), excluding specific
CC tabulated arrangements (tables given in the specification). (I), and
CC related enzymes, are used to produce a wide range of terpenoids (e.g.
CC cyclic, acyclic, optionally hydroxylated), useful e.g. as fragrances,
CC flavours, pheromones, defensive agents, pigments, antitumour agents,
CC components of signal transduction pathways, precursors of steroid

Qy 608 ValMetArgThrValIleGlu 614
Db 1917 GTTATGGAACACTCCTTGAA 1937

RESULT 8

AAF73371
ID AAF73371 standard; cDNA; 2196 BP.

XX AAF73371;

DT 30-APR-2001 (first entry)

DE Grand fir myrcene synthase coding sequence SEQ ID NO: 1.

XX Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;
KW myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;
KW terpinolene synthase; insect resistance; nutrition; ss.

XX Abies grandis.

PN WO200107565-A2.

PD 01-FEB-2001.

PF 24-JUL-2000; 2000WO-US020264.

PR 26-JUL-1999; 99US-00360545.

PA (UNIW) UNIV WASHINGTON STATE RES FOUND.

PI Steele CL, Bohlmann J, Croteau RB, Phillips MA;

DR WPI; 2001-182782/18.

DR P-PSDB; AAB69370.

PT New nucleic acid encoding monoterpene synthases, for increasing terpene
PT synthesis in plants, e.g. for increasing resistance to pests or for
PT treatment of cancer.

PS Claim 28; Page 103-106; 175pp; English.

XX The present invention provides the protein and coding sequences of
CC monoterpene synthases from the grand fir. These include (-)-camphene
CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-
CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase
CC and pinene synthase. The sequences can be used to produce transgenic
CC plants expressing high levels of the enzymes, resulting in levels which
CC are useful in protecting against and treating cancers, and to confer
CC insect resistance on plants

SQ Sequence 2196 BP; 684 A; 416 C; 468 G; 628 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,01e-217 Length: 2196
Score: 2200.50 Matches: 427
Percent Similarity: 80.38% Conservative: 77
Best Local Similarity: 68.10% Mismatches: 106
Query Match: 67.69% Indels: 17
DB: 4 Gaps: 7

US-10-025-145A-65 (1-618) x AAF73371 (1-2196)

Qy 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
Db 69 ATGGCTCTGGTTCTATCTACCCGTTGGCTTCGAAATCTTGCTGGCGCAAGTCGTTGATC 128
Qy 16 SerSerSerHisGluIleLeuValAlaLeuArgThrIleProThrLeuGlyIleCysArg 35
Db 129 AGTTCAATTTCATGAACATTAAGCCTCCCTATAGAACAATCCCAATCTTGGATGCGTAGG 188
Qy 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
Db 189 CGAGGAAATCTGTACGCGCTTCATGACATCAGTTTGCCACCGCTGCACCTGATGAT 248

Qy 56 SerValGlnArgValAlGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75
Db 249 GGTGTACAAAGACCGCATAGGTGACTACCATTCCAATATCTGGGACGATGATTTCATACAG 308
Qy 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluAlaAspArgLeuIle 95
Db 309 TCTCTA--TCAACGGCTTATGGGAACTCTTACACGAGAACGTCGAGAGATTAAAT 365
Qy 96 G1GluValIlyAspIleMetPheAsnPhelySerLeuGluAspG1GlyIle----- 112
Db 366 GTGAGGTAAAGAGATA--TTCATATTCATGTACTGATGATGAGAAATTAAATGAGT 422
Qy 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
Db 423 TCCTTTATGATCTCATGCAACGCCCTTGGATAGTCGATAGCGTTGAACGTTGGGATA 482
Qy 131 AspArgHisPheIlySerGluIleLeuThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
Db 483 GCTAGACATTTCAAGAACGAGATACATCAGCTCTGATTATGTTTCCGTTACTGGAG 542
Qy 151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170
Db 543 GAAACCGCATTTGGTGTGGAGACAGATATTGTTACTGATCTCAACTCAACTGCGTTG 602
Qy 171 G1LeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190
Db 603 GGGTTTGAACCTTCGATTACAGCGGTACACTGTATCTCCAGCGTTTAAAGCTTTT 662
Qy 191 LysAspLysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGluGlyIleArg 210
Db 663 CAAGATCAAAATGACAGATTGTATGCTCCCGCGT--CAGACAGAGGTGAGATCAGA 719
Qy 211 GlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLysValMetAsp 230
Db 720 AGCGTTCTTAATTATATCGGGCTTCCCTCATTGCTCCCTGGTGAGAAAGTTATGGA 779
Qy 231 GluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIleProAlaSer 250
Db 780 GAAGCTGAATCTTCTCCACAGATATTGAAAGAGCTTACAAAGATTCCAGTCTCC 839
Qy 251 SerIleLeuSerLeuGluIleArgAspValLeuGluTyrGlyTyrHisThrAsnLeuPro 270
Db 840 GCT--CTTACACAGAGATTAAGTTGTTATGGAATATGGTCGACACAAATTTGCCA 896
Qy 271 ArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLys-----Asn 287
Db 897 AGATTGGAAGCAAGAAATTACATAGACACACTTGAGAAAGACACCAGTCATGCTCAAT 956
Qy 288 LysAsnAlaAlaGluLysLeuLeuGluLeuAlaLysLeuGluPheAsnIlePheHisSer 307
Db 957 AAAAATGCTGGGAGAAGAGCTTTAGAACTTGCAAAATTGAGTTCAATATATTAACTCC 1016
Qy 308 LeuGlnGluArgGluLeuLysHisValSerArgTyrTrpLysAspSerGlySerProGlu 327
Db 1017 TTACACAAAGAAAGAAATTACATATCTTTGAGATGGTGGAAGAGTCGATTGGCTTAA 1076
Qy 328 MetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCysIleAlaPhe 347
Db 1077 TTGACATTTGCTCGGCATCGTCATGTGAATTCTACACTTGGCCTCTGTATTGCCATT 1136
Qy 348 GluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIleThrVal 367
Db 1137 GACCCAAACATTTCTGACATTCAGCTAGAGCTTCGCCAAATGTGTATCTTGCACAGTT 1196
Qy 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluLeuPheThrAlaThr 387
Db 1197 TTGAGCATATTATAGCACACTTTGGAACGATTGACGAGCTTGAACCTTCACATCTGCA 1256
Qy 388 IleLysArgTrpAspProSerAlaMetGluCysLeuProGluTyrMetLysGlyValTyr 407
Db 1257 ATTAAGATGTAATTCATCAAGATAGAACACCTTCCAGATATATGAATGTGTGTAC 1316

QY 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArg 427
Db 1317 ATGGTCGTGTTGAAACTGTAAATGAATGCACACGAGAGCGGAGAGAACTCAAGGAGAGA 1376
QY 428 AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu 447
Db 1377 AACACTCTCAACTATGTTGGAAGGCTGGAGGCTTATTGATTGATTATATATAGGAAGAA 1436
QY 448 AlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGlyTyrLeuGluAsnGlyLys 467
Db 1437 GCAAAATGCAATCTTAATGTTATCTGCCAATGTTGAAGAGTACCATGAGAATGGGAAA 1496
QY 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
Db 1497 GTGAGCTCTGCATATCGCGTAGCAACATTCGAACCCATCCTCACTTGAATGCATGGCTT 1556
QY 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507
Db 1557 CCTGATTACATCTTGAAGGGAATGATTTTCCATCCAGGTTCAATGATTTGGCATCGTCC 1616
QY 508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGlu 527
Db 1617 TTCTTCGGCTACGAGGTGACACACGCTGCTACAAGGCCGATAGGATCGTGTGAAGAA 1676
QY 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeu 547
Db 1677 GCTTCGTATATCATGTTATATGAAAGACAATCCTGATCAACCGAAGAGATGCCCTC 1736
QY 548 AsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGluLeuLys 567
Db 1737 AATCATATCAATGCATGTCATGATGACATTAATCAAGAATTAAATTGGGAATCTTAAGA 1796
QY 568 ProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArgValTrp 587
Db 1797 TCCAAACGACAATATTCCAATGCTGGCCAGAAGAACATGCTTTTGACATAACAAGAGCTCTC 1856
QY 588 HisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThrLysSerLeu 607
Db 1857 CACCATCTCTACATATATCGAGATGGCTTAACTGTGCCAAACAGGAACAACAAAAATTG 1916
QY 608 ValMetArgThrValIleGlu 614
Db 1917 GTTATGAAACACTCCTTGAA 1937
RESULT 9
AAK08663
ID AAK08663 standard, cDNA; 2205 BP.
XX
AC AAK08663;
XX
DT 27-SEP-1999 (first entry)
XX
DE Grand Fir monoterpene synthase clone AG3.48.
XX
KW Mycrene synthase; limonene synthase; pinene synthase; flavour;
KW monoterpene synthase; aroma; defense; plant seed; oil; meal; primer; PCR;
KW probe; 8s.
XX
OS Abies grandis.
XX
FH Key Location/Qualifiers
FT CDS 57..1940
FT /*tag= a
FT /product= "Monoterpene synthase"
XX
PN WO9902030-A1.
XX
PD 21-JAN-1999.
XX
PF 10-JUL-1998; 98WO-US014528.
XX
PR 11-JUL-1997; 97US-0052249P.
XX

PA (UNIW) UNIV WASHINGTON STATE RES FOUND.
XX
PI Bohlmann J, Steele CL, Croteau RB;
XX
DR WPI; 1999-120396/10.
DR P-PSDB; AAW85710.
XX
PT New isolated gymnosperm monoterpene synthase DNA - obtained from Grand
PT fir (Abies grandis), used to provide plants with modified production of
PT monoterpenes, e.g. mycrene, limonene or pinene.
XX
PS Example 3; Page 104-107; 121pp; English.
XX
CC Nucleotide sequences encoding mycrene synthase, limonene synthase and
CC pinene synthase from Grand fir may be incorporated into any organism
CC (e.g. intact plant, animal, microbe), or derived cell culture that
CC produces geranyl diphosphate for the production of the aforementioned
CC enzymes or their products. The sequences when expressed in transfected
CC cells may also be used for the production or modification of flavour and
CC aroma properties, improvement of defense capability, and the alteration
CC of other ecological interactions mediated by mycrene, limonene, pinene,
CC or their derivatives. In particular they can be used for the production
CC of plant seeds for the extraction of oil or meal
XX
SQ Sequence 2205 BP; 703 A; 412 C; 463 G; 627 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 4.13e-217 Length: 2205
Score: 2197.50 Matches: 427
Percent Similarity: 80.38% Conservative: 77
Best Local Similarity: 68.10% Mismatches: 106
Query Match: 67.59% Indels: 17
DB: 2 Gaps: 7
US-10-025-145A-65 (1-618) x AAK08663 (1-2205)
QY 1 MetAlaLeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
Db 57 ATGGCTCTGTTCTATCTCAACCGTTGGCTTGAATCTTGCTGCGCAAGTCGTGATC 116
QY 16 SerSerHisGluIleLysAlaLeuArgArgThrIleProThrLeuGlyIleCysArg 35
Db 117 AGTCAATTCAATGAAACATAAGCCTCCCTATGAACAATCCAAATCTTGAATGCGTAGG 176
QY 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
Db 177 CGAGGGAATCTGTCAAGCCTTCCATGAGCATGATTGGCCACCGCTGCACCTGATGAT 236
QY 56 SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTrpAspAspPheIleGln 75
Db 237 GGTGTACAAAGACGATAGTGACTACCATTTCCAATATCTGGAGCATGATTTCATACAG 296
QY 76 SerLeuIleSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeuIle 95
Db 297 TCTCTA---TCAACGCATTAATGGGGAACCTCTTACCAGGAACGTGCTGAGAGATTAAAT 353
QY 96 GlyGluValLysAspIleMetPheAsnPhelySerLeuGluAspGlyGly----- 112
Db 354 GTGGAGTAAGAAGATA---TTCAATTCAATGTACCTGATGATGAAGATTAAATGAGT 410
QY 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGlyIle 130
Db 411 TCCTTTAATGATCTCATGCAACGCCCTTGGATAGTCGATAGCGTTGAACGTTGGGAGTA 470
QY 131 AspArgHisPheLysGlyIleLeuThrAlaLeuAspTyrValAsnSerTyrTrpAsn 150
Db 471 GCTAGACATTTCAAGAACGAGATTAAACATCAGCTCGATTATGTTTCCGTTACTGGAG 530
QY 151 GluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAlaLeu 170
Db 531 GAAACGGCATTTGATGTGGAGAGACAGTATTGTACTGATCTCAACTCAACTGCGTTG 590
QY 171 GlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnValPhe 190

XX PN W0200107565-A2.
XX PD 01-FEB-2001.
XX PF 24-JUL-2000; 2000WO-US020264.
XX PR 26-JUL-1999; 99US-00360545.
XX PA (UNIW) UNIV WASHINGTON STATE RES FOUND.
XX PI Steele CL, Bohlmann J, Croteu RB, Phillips MA;
XX DR MPI; 2001-182782/18.
XX DR P-PSDB; AAB69393.
XX PT New nucleic acid encoding monoterpene synthases, for increasing terpene
PT synthesis in plants, e.g. for increasing resistance to pests or for
PT treatment of cancer.
XX PS Claim 18; Page 163-165; 175pp; English.
XX CC The present invention provides the protein and coding sequences of
CC monoterpene synthases from the grand fir. These include (-)-camphene
CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-
CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase
CC and pinene synthase. The sequences can be used to produce transgenic
CC plants expressing high levels of the enzymes, resulting in levels which
CC are useful in protecting against and treating cancers, and to confer
CC insect resistance on plants
XX SQ Sequence 1890 BP; 550 A; 381 C; 441 G; 518 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6,11e-211 Length: 1890
Score: 2137.00 Matches: 427
Percent Similarity: 78.86% Conservative: 73
Best Local Similarity: 67.35% Mismatches: 114
Query Match: 65.73% Indels: 20
DB: 4 Gaps: 9

US-10-025-145A-65 (1-618) x AAF73421 (1-1890)
QY 1 MetAlaLeuSerIleThrProLeuValSerArgSerCysLeuSer----- 16
DB 1 ATGGCTCTGTTCTATCTTGCCTTGTCTTCCAATCGGTCTGCACAAATCGTGATC 60
QY 17 ---SerSerHisGluIleLeuValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 35
DB 61 GTTCTACTTATGACATTAAGGCTATCAGTACAGAAATCCCAATCTTGATTCGGTGG 120
QY 36 ProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAlaSerThrAsp 55
DB 121 CGAGGGAATCTGTGACACATTCCTCGAATGAGTTGAGCACCGCAGTCTTGATGAT 180
QY 56 ---SerValGlnArgArgValGlyAsnTyrHisSerAsnLeuTyrAspAspPheIle 74
DB 181 CATGCTGTAACAAGACGATAGTCGAGTTTCAATTCATCTGTGGACGACGATTTGATA 240
QY 75 GlnSerLeuSerThrProTyrGlyAlaProAspTyrArgGluArgAlaAspArgLeu 94
DB 241 CAATCTCTA---TCAACGCCCTTATGGGACCTTCATACCGTGAACGTGCTGATGACTT 297
QY 95 IleGlyGluValLysAspIleMetPheAsnPheLysSerLeuGluAspGlyGly----- 112
DB 298 ATTGTGAAGTAAGGCTATA--TTCACTTCAATTTCAGCGAAGATGAGAACTAATC 354
QY 113 -----AsnAspLeuLeuGlnArgLeuLeuValAspAspValGluArgLeuGly 129
DB 355 ACTCCCTCAATGATCTCATTCACAGCCTTTTAATGTCGATAACGTTGAACGTTTAGGG 414
QY 130 IleAspArgHisPheLysLysGluIleLysThrAlaLeuAspTyrValAsnSerTyrTyr 149

DB 415 ATTGATAGACATTTCAAAATGAGATAAAGCAGCACTAGACTATGTTTACAGTTATGG 474
QY 150 AsnGluLysGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAla 169
DB 475 AACGAAAAAGGATGGCAGTGGAGAGTATAGTGTGTGCTGATCTCAACTCACTGCC 534
QY 170 LeuGlyLeuArgThrLeuArgLeuHisGlyTyrThrValSerSerAspValLeuAsnVal 189
DB 535 CTGGGGTTTCCAATTCTTCGACTACACCGATACAGTGTTCCTTCAGATGTGTGGAACAC 594
QY 190 PheLysAsp-----LysAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGly 207
DB 595 TTCAAAGAGAGAGAGAGAGAGGCGCAGTTGTATGTTCCGCC--ATCCAAACAGAGGAA 651
QY 208 GluIleArgGlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGluLys 227
DB 652 GAGATAAAAGCGTTCTGAATTATTCGGCCCTCCCTCATGTGCTTCTGGGAGAGAAA 711
QY 228 ValMetAspGluAlaGluThrPheSerThrLysTyrLeuArgGluAlaLeuGlnLysIle 247
DB 712 GTTATGGAAGAGCGTGAATCTTCTCTAAATATATTTAAAGAAAGCCTTACAAAATATT 771
QY 248 ProAlaSerSerIleLeuSerLeuGlnIleArgAspValLeuGluTyrGlyTyrHisThr 267
DB 772 GCTGTCTCCAGT---CTTTCACGAGAGATAGAGTACGTTCTGAGAGATGTTGCCAAACA 828
QY 268 AsnLeuProArgLeuGluAlaArgAsnTyrMetAspValPheGlyGlnHisThrLysAsn 287
DB 829 AATATGCCAAGATTGGAACAAGAACTATCATCATGATGATTGGAGAGAAACGATCGTAT 888
QY 288 LysAsnAla-----AlaGluLysLeuLeuGluValAlaLysLeuGluPheAsnIle 304
DB 889 GAGACGTTATATATGAACATGAGAAATCTTTAGAAATTGCAAAATTCAGTTCAATATT 948
QY 305 PheHisSerLeuGlnGluArgGluLeuLysHisValSerArgTyrTyrLysAspSerGly 324
DB 949 TTTCACCTCTTAACAACAGAGAGCTAAAGACCTCTCCAGATGTTGGAAGAAATTCCGGT 1008
QY 325 SerProGluMetThrPheCysArgHisArgHisValGluTyrTyrAlaLeuAlaSerCys 344
DB 1009 TTCTCTCACCCTGACATTTCTCTCGGCATGTCATGTGAATTCTACGCTCTGGCATCTGC 1068
QY 345 IleAlaPheGluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeu 364
DB 1069 ATTGAACCTGATCGCAACATTCGGATTCAGACTCGGCTTGCCAAATGTGTCTATCTT 1128
QY 365 IleThrValLeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluPhe 384
DB 1129 ATCAGCGTTTGAACGATATATACGACCTTTGGAAACATGAGAGCTGGAACCTCTTC 1188
QY 385 ThrAlaThrIleLysArgTyrAspProSerAlaMetGluCysLeuProGluTyrMetLys 404
DB 1189 ACTGACGACATTTAAGAGATGGATCCGCTGCCACAGATTTGCTTCAGAGTATATGAAA 1248
QY 405 GlyValTyrMetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAla 424
DB 1249 GGGTTGACATGCTGTTTACGAACCGTAATGAATGCTCGAGAGGACAGACAAGTCT 1308
QY 425 GlnGlyArgAspThrLeuAsnTyrAlaArgGlnAlaTyrGluAlaCysPheAspSerTyr 444
DB 1309 CAAGGCCGAGACGCTCAACGATGCTCGACGAGCTTGGAGGCGCTTATCTTGATTCGTAT 1368
QY 445 MetGlnGluAlaLysTyrIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGlu 464
DB 1369 ATGAAGAAGCTGAGTGATCTCCAGTGTATATCTGCCAACGTTTGAAGAGATACATGAG 1428
QY 465 AsnGlyLysValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAsp 484
DB 1429 ACCAGCAAGTTAGTTTGTGATGCGATATTCGCATTGCAACCACTCTCACTATGAT 1488
QY 485 IleProPheProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeu 504
DB 1489 GTTCCCTTACTCACACATCTCGACGAAATAGACTTTCATTGAGGTTTATGACTTA 1548

Oy 296 GluLeuAlaIysLeuGluPheAsnIlePheHisSerLeuGlnGluArgGluLeuLysHis 315
Db 977 AACTTGCAGAAATTGGAGTTAATATCTTCACTCTTTGCACAGAAAGAGTTGCAATAT 1036
Oy 316 ValSerArgTrpTrpLysAspSerGlySerProGluMetThrPheCysArgHisArgHis 335
Db 1037 ATCTCTGATGCTGGAGAAAGATTCTGTTCATCTCATCTGACTTTTACTGACACCGTCAC 1096
Oy 336 ValGluTrpTrpAlaLeuAlaSerCysIleAlaPheGluProGlnHisSerGlyPheArg 355
Db 1097 GTGAATGACTACACAAATGCGCATCTGCAATTCTATGAGCCGAAACACTCCGCTTTCAGA 1156
Oy 356 LeuGlyPheThrLysMetSerHisLeuIleThrValLeuAspAspMetTyrAspValPhe 375
Db 1157 TTGGGGTTTGCAGAAACATGTCATCTTCAACAGTTCTGATGATATGATACACTTTT 1216
Oy 376 GlyThrValAspGluLeuGluLeuPheThrAlaThrIleLysArgTrpAspProSerAla 395
Db 1217 GGAACACTGGACGAACTCCAACTTTTACGACTGCCCTTAAAGAGATGGGATTTGTCAAG 1276
Oy 396 MetGluCysLeuProGluTyrMetLysGlyValTyrMetMetValTyrHisThrValAsn 415
Db 1277 ACAAGTGTCTTCCAGAAATATGAAAGCAGTATGATGACTGTATCAATGTCTTAAT 1336
Oy 416 GluMetAlaArgValAlaGluLysAlaGlnGlyArgAspThrLeuAsnTyrAlaArgGln 435
Db 1337 GAATTGGCGCAAGAGCTGAGAAAGACTCAAGGCGAGATACGCTCACTAATATTCGCAAT 1396
Oy 436 AlaTrpGluAlaCysPheAspSerTyrMetGlnGluAlaLysTrpIleAlaThrGlyTyr 455
Db 1397 GCTTATGAGTCTCATTTTGTATTCGTTATGACGAGCAAAATGATCTCAAGTGTAT 1456
Oy 456 LeuProThrPheGluGluTyrLeuGluAsnGlyLysValSerSerAlaHisArgProCys 475
Db 1457 CTCCCAACGTTTGAAGAGTACTTGAAGATGGGAAAGTTAGTCCGGTTCTCGCACAGCC 1516
Oy 476 AlaLeuGlnProIleLeuThrLeuAspIleProPheProAspHisIleLeuLysGluVal 495
Db 1517 ACTTTACAAACCATACTCACCCTGGATGACCACTTCTAATTACATGTCAGAAAT 1576
Oy 496 AspPheProSerLysLeuAsnAspLeuIleCysIleIleLeuArgLeuArgGlyAspThr 515
Db 1577 GATTATCCATCTAGGTTCAATGACTGCTTCGCCCTCCTCGGCTACGTGTGACACAG 1636
Oy 516 ArgCysTrpLysAlaAspArgAlaArgGlyGluGluAlaSerSerIleSerCysTyrMet 535
Db 1637 CGCTGCTACAGGCGGATAGGCGCTCGTGAGAGAAGACTTCAGCTATATCGTTATATG 1696
Oy 536 LysAspAsnProGlyLeuThrGluGluAspAlaLeuAsnHisIleAsnPheMetIleArg 555
Db 1697 AAAGACCATCTCTGGATCAACAGAGAAAGATGCTCTCAATCATATCAACGTCATGATCAGT 1756
Oy 556 AspAlaIleArgGluLeuAsnTrpGluLeuLeuLysProAspAsnSerValProIleThr 575
Db 1757 GATGCAATCAGAGAAATTAAATTGGAGCTTCTCAGACAGATAGCAAAAGTCCCATCTCT 1816
Oy 576 SerLysLysHisAlaPheAspIleSerArgValTrpHisHisGlyTyrArgTyrArgAsp 595
Db 1817 TCCAGAAACATGCTTTTGACATCAGCAGAGCTTTCATCACCCTGACAAAGTACCGAGAT 1876
Oy 596 GlyTyrSerPheAlaAsnValGluThrLysSerLeuValMetArgThrValIleGluPro 615
Db 1877 GGTACACTGTTGCGAGTAGTGAACAAAGAAATTGGTGAATGAACAGTTCTTGAACCT 1936
Oy 616 ValProLeu 618
Db 1937 GTGGCATTG 1945
RESULT 13
AAK08645
ID AAK08645 standard; cDNA; 2089 BP.
XX

AC AAK08645;
XX 27-SEP-1999 (first entry)
DT
XX Limonene synthase gene.
DE
XX Mycrene synthase; limonene synthase; pinene synthase; flavour; aroma;
KW defense; plant seed, oil; meal; ss.
XX Abies grandis.
OS
XX
XX
FH Key Location/Qualifiers
FT CDS 73..1986
FT /*tag= a
FT /product= "Limonene synthase"
XX
PN WO9902030-A1.
XX
PD 21-JAN-1999.
XX
XX
PF 10-JUL-1998; 98WO-US014528.
XX
PR 11-JUL-1997; 97US-0052249P.
XX
PA (UNIW) UNIV WASHINGTON STATE RES FOUND.
XX
PI Bohlmann J, Steele CL, Croteau RB;
XX
DR WPI; 1999-120396/10.
DR P-PSDB; AAW85702.
DR
XX
PT New isolated gymnosperm monoterpene synthase DNA - obtained from Grand
PT fir (Abies grandis), used to provide plants with modified production of
PT monoterpenes, e.g. mycrene, limonene or pinene.
XX
PS Claim 11; Page 79-82; 121pp; English.
XX
CC Nucleotide sequences encoding mycrene synthase, limonene synthase and
CC pinene synthase from Grand fir may be incorporated into any organism
CC (e.g. intact plant, animal, microbe), or derived cell culture that
CC produces geranyl diphosphate for the production of the aforementioned
CC enzymes or their products. The sequences when expressed in transfected
CC cells may also be used for the production or modification of flavour and
CC aroma properties, improvement of defense capability, and the alteration
CC of other ecological interactions mediated by mycrene, limonene, pinene,
CC or their derivatives. In particular they can be used for the production
CC of plant seeds for the extraction of oil or meal
XX
SQ Sequence 2089 BP, 638 A; 415 C; 450 G; 586 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 6.08e-200 Length: 2089
Score: 2031.50 Matches: 409
Percent Similarity: 76.67% Conservative: 84
Best Local Similarity: 63.61% Mismatches: 119
Query Match: 62.49% Indels: 31
DB: 2 Gaps: 14
US-10-025-145A-65 (1-618) x AAK08645 (1-2089)
Oy 1 MetAlaLeuLeuSerIleThrProLeu---ValSerArgSerCys----- 14
Db 73 ATGGCTCTCTTCTATCGTATCTTTCAGAGTTCCCAAAATCCTCGGCTGAATCGTTG 132
Oy 15 LeuSerSerHisGluIleLysAlaLeu-----ArgArgThrIleProThrLeuGly 32
Db 133 ATCAGTTCAGCAATGTGCAGAGGCTCTCTGTATCTTACAGAGTCCCAACACTCAGA 192
Oy 33 IleCysArgProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAla 52
Db 193 ATGCGTAGGCCACAGAAAGCTGTGTC-----ATCAACATGAATTGACACACTGATCC 246
Oy 53 SerThrAspSer-----ValGlnArgArgValGluAsnTyrHisSerAsn 67

Db 247 CATCGTATGATATATGTTGGTGTGTTACTGCAAGAAGCGCATAGCCGATCATCCCAAC 306
QY 68 LeuTrpAspAspAspPheIleGlnSerIleuIleSerThrProTyrGlyAlaProAspTyr 87
Db 307 CTGTGGGAGATGATTTTCATACATCATTTG--TCCTCACCTTATGGGGGATCTTCGTAC 363
QY 88 ArgGluArgAlaAspArgLeuIleGlyGluValLysAspIleMetPheAsnPhe----- 105
Db 364 AGTGAACGTGCTGAGACAGCTCGTTGAGGAAGTAAAAAGAG--ATGTTCAATTCAATACCA 420
QY 106 -----LysSerLeuGluAspGlyLysAsnAspLeuLeuGlnArgLeuLeuValAsp 123
Db 421 AATAATAGAAATTATTGTTGCCAAATGATCTCCTTACACGCCCTTGGATGGTGAT 480
QY 124 AspValGluArgLeuGlyIleAspArgHisPheLysLysGluIleLysThrAlaLeuAsp 143
Db 481 AGCATGAAAGCTGTGGGATAGATGACATTCCAAATAGATAGATAGAGCCCTCGAT 540
QY 144 TyrValAsnSerTyrTrpAsnGluLys---GlyIleGlyCysGlyArgGluSerValVal 162
Db 541 TATGTTACAGTTATTGGAAAGAAAGGAGCATTTGGGTGTGGCAGAGATTCTACTTTT 600
QY 163 ThrAspLeuAsnSerThrAlaLeuGlyLeuArgThrLeuArgLeuHisGlyTyrThrVal 182
Db 601 CCTGATCTCAACTCGACTGCTTGGCGCTTCGAACCTCTCGACTGCACGGATACAAATGTG 660
QY 183 SerSerAspValLeuAsnValPheLysAspLysAsnGlyGlnPheSerSerThrAlaAsn 202
Db 661 TCTTCAGATGTGCTGGAATACCTTCAAGATGAAAAAGGGGCAATTTGCTGCCCTGCA--- 717
QY 203 ILeGlnIleGluGlyGluIle---ArgGlyValLeuAsnLeuPheArgAlaSerLeuVal 221
Db 718 ATCTTAACCGAGGACAGATCACTAGAGTGTCTAAATTATATCGGGCTTCCCTGTGC 777
QY 222 AlaPheProGlyGluLysValMetAspGluAlaGluThrPheSerThrLysTyrLeuArg 241
Db 778 GCCTTCCCGGGGAGAAAGTATGAAAGGCTGAATCTTCGGGATCTTATTGAAA 837
QY 242 GluAlaLeuGlnLysIleProAlaSerSerIleLeuSerLeuGluIleArgAspValLeu 261
Db 838 AAAGTCTTACAAAGATTCCGGTCTCCAAT--CTTCAAGAGAGATAGAATATGTTTG 894
QY 262 GluTyrGlyTyrPheIleThrAsnLeuProArgLeuGluAlaArgAsnTyrMetAspValPhe 281
Db 895 GAATATGTTGGCACAAGAAATTTGCCGAGATTGGAAGCAAGAAATTATATCGAGGTCTAC 954
QY 282 -----GlyGlnHisThrLysAsnLysAsnAla-----AlaGluLysLeuLeu 295
Db 955 GAGCAGAGCGGCTATGAAAGCTTAAAGAGATGCCATATATGAACATGAAGAAGCTTTTA 1014
QY 296 GluLeuAlaLysLeuGluPheAsnIlePheHisSerLeuGlnGluArgGluLeuLysHis 315
Db 1015 CAACCTTGCAAAATTGGAGTTCATATCTTCACTCTTGGCAACTAGAGAGTTACAATCT 1074
QY 316 ValSerArgTrpTrpLysAspSerGlySerProGluMetThrPheCysArgHisArgHis 335
Db 1075 ATCTCCAGATGTTGGAAGAATCAGGTCGTCTCACTGACTTTTACACGGCATCGTCAAC 1134
QY 336 ValGluTyrTyrAlaLeuAlaSerCysIleAlaPheGluProGlnHisSerGlyPheArg 355
Db 1135 GTGGAATACTACACTATGGCATCTTGCAATTTCTATGTTGCCAAACATTCAGCTTCAGA 1194
QY 356 LeuGlyPheThrLysMetSerHisLeuIleThrValLeuAspAspMetTyrAspValPhe 375
Db 1195 ATGAGTTTGTCAAAAGTGTGTCACTTGTGAACAGTTCTCGATGATATATATGACACTTTT 1254
QY 376 GlyThrValAspGluLeuGluLeuPheThrAlaThrIleLysArgTrpAspProSerAla 395
Db 1255 GGAACATGAACGAACCTCCAACTTTTACGAGATGCAATTAAAGAGATGGGATTTGTCAACG 1314
QY 396 MetGluCysLeuProGluTyrMetLysGlyValTyrMetMetValTyrHisIleThrValAsn 415

Db 1315 ACAAGTGGCTTCCAGAAATATATGAAGAAGAGTGTACATGGACTTGTATCAATGCATTAAT 1374
QY 416 GluMetAlaArgValAlaGluLysAlaGlnGlyArgAspThrLeuAsnTyrAlaArgGln 435
Db 1375 GAAATGCTGGAAGAGCGTGAAGACTCAAGGCCGAGATATGCTCAACTATATTCAAAT 1434
QY 436 AlaTrpGluAlaCysPheAspSerTyrMetGlnGluAlaLysTrpIleAlaThrGlyTyr 455
Db 1435 GCTTGGGAAGCCCTATTTGATACCTTTATGCAAGAAGCAAGTGATCTCCAGCAGTTAT 1494
QY 456 LeuProThrPheGluGluTyrLeuGluAsnGlyLysValSerSerAlaHisArgProCys 475
Db 1495 CTCCCAACGTTTGAGAGTACTTGAAGAATGCAAAAGTTAGTTCTGCTTCGCATAGCC 1554
QY 476 AlaLeuGlnProIleLeuThrLeuAspIleProPheProAspHisIleLeuLysGluVal 495
Db 1555 ACATTACAAACCATTTCTCACTTTGGATGTACCACTTCCTGATTAATCTGCAAGAAATT 1614
QY 496 AspPheProSerLysLeuAsnAspLeuIleCysIleIleLeuArgLeuArgGlyAspThr 515
Db 1615 GATTAATCCATCCAGATTCATAGAGTTAGCTTGTCCATCCTTCGACTACGAGGTGACACG 1674
QY 516 ArgCysTyrLysAlaAspArgAlaArgGlyGluAlaSerSerIleSerCysTyrMet 535
Db 1675 CGCTGTCACAAGCGGATAGGCGCGTGAGAGAAGAGCTTCACTATATCGTTATATG 1734
QY 536 LysAspAsnProGlyLeuThrGluGluAspAlaLeuAsnHisIleAsnPheMetIleArg 555
Db 1735 AAAGACCATCCTGGATCAATAGAGGAAGATGCTCTCAATCATATCAACGCATGATCAGT 1794
QY 556 AspAlaIleArgGluLeuAsnTrpGluLeuLysProAspAsnSerValProIleThr 575
Db 1795 GATGCAATCAGAGATTAATTGGAGCTTCTCAGACCGGATAGCAAAAGTCCCATCTCT 1854
QY 576 SerLysLysHisAlaPheAspIleSerArgValTyrPheIleGlyTyrArgTyrArgAsp 595
Db 1855 TCCAAGAAACATGCTTTTGACATCACAGAGCTTCCATCATGTCTACAAATATCGAGAT 1914
QY 596 GlyTyrSerPheAlaAsnValGluThrLysSerLeuValMetArgThrValIleGluPro 615
Db 1915 GGTTACACTGTTTCCAAACAGCAACAAAGAAATTGGTGATGAACAAACGTTCTTGAACCT 1974
QY 616 ValProLeu 618
Db 1975 CTGCTTTG 1983
RESULT 14
AAA38938
ID AAA38938 standard; DNA; 2089 BP.
XX AC AAA38938;
XX AC
XX AC
DT 25-AUG-2000 (first entry)
XX DE Grand fir limonene synthase DNA sequence SEQ ID NO:57.
XX KW Synthase; protein co-ordinate data; active site; modification; terpenoid;
KW 3-dimensional coordinate; alpha carbon atom; plant; terpene synthase;
KW isoprenoid; breeding programme; fragrance; flavour; pheromone;
KW defensive agent; pigment; antitumour; steroid hormone;
KW signal transduction pathway; bile acid; affinity purification;
KW photoreceptor; enzymatic synthesis; nutrient supplement;
KW immunological reagent; ds.
XX KW
OS Abies grandis.
XX PN WO200017327-A2.
XX PD 30-MAR-2000.
XX PF 17-SEP-1999; 99WO-US021419.
XX PR 18-SEP-1998; 98US-0100993P.

PR 22-APR-1999; 99US-0130628P.
PR 23-AUG-1999; 99US-0150262P.
XX
PA (KENT) UNIV KENTUCKY RES DEPT.
PA (SALK) SALK INST BIOLOGICAL STUDIES.
XX
PI Chappell J, Manna KR, Noel JP, Sparks CM;
XX
DR WPI, 2000-292839/25.
DR P-PSDB; AAY90859.

XX
PT Novel terpene synthase enzymes, useful for producing terpene
PT hydrocarbons, e.g. fragrances or antitumor agents, are derived from known
PT enzymes by specific amino acid alterations.
XX
PS Disclosure; Page 445-448; 450pp; English.

XX
CC The present invention describes an isolated terpene synthase (I)
CC comprising a region with at least 20% identity to region 265-535 of a 548
CC amino acid (aa) sequence (Ia), given in AAY90831. (I) contains nine alpha
CC -carbon atoms (alphaC) that have interatomic distances, between each
CC other, within tabulated ranges, have a centre point (within a sphere of
CC radius 2.3 Angstrom) within tabulated ranges, and have an ordered
CC arrangement of R groups (defining aa side chains), excluding specific
CC tabulated arrangements (tables given in the specification). (I), and
CC related enzymes, are used to produce a wide range of terpenoids (e.g.
CC cyclic, acyclic, optionally hydroxylated), useful e.g. as fragrances,
CC flavours, pheromones, defensive agents, pigments, antitumor agents,
CC components of signal transduction pathways, precursors of steroid
CC hormones and bile acids, as photoreceptors and as co-factor side chains.
CC Some synthases with little or no catalytic activity (and nucleic acids
CC encoding them) are used as controls in the analysis of products formed by
CC enzymatic synthesis; as nutrient supplements; for affinity purification
CC of isoprenoids; or to develop immunological reagents or nucleic acids for
CC monitoring expression of terpene synthase or inheritance of the gene in
CC plant breeding programs. The new synthases may produce novel terpene
CC products. AAA38910 to AAA38938 and AAY90831 to AAY90859 represent
CC sequences used in the exemplification of the present invention

XX
SQ Sequence 2089 BP; 638 A; 415 C; 450 G; 586 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.08e-200 Length: 2089
Score: 2031.50 Matches: 409
Percent Similarity: 76.67% Conservative: 84
Best Local Similarity: 63.61% Mismatches: 119
Query Match: 62.49% Indels: 31
DB: 3 Gaps: 14

US-10-025-145A-65 (1-618) x AAA38938 (1-2089)

QY 1 MetAlaLeuSerIleThrProLeu---ValSerArgSerCys----- 14
DB 73 ATGGCTCTCTTTCTATCGTATCTTTGCAGGTTCCCAATCCTGCGGCTGAATCGTTG 132
QY 15 LeuSerSerSerHisGluIleLysAlaLeu-----ArgArgThrIleProThrLeuGly 32
DB 133 ATCAGTTCACGAATGTGCAGAGGCTCTGTATCTCTACAGCAGTCCCAACTCAGA 192
QY 33 IleCysArgProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAla 52
DB 193 ATGCGTAGCGGACAGAAAGCTGTGC-----ATCAACATGAATTCACCACTGTATCC 246
QY 53 SerThrAspSer-----ValGlnArgArgValGlyAsnTyrHisSerAsn 67
DB 247 CATCGTAGTAAATATAGTGTGTGTACTGCAAGAAGCATAGCCGATCATCATCCCAAC 306
QY 68 LeuTyrAspAspAspPheIleGlnSerIleLeuSerThrProTyrGlyAlaProAspTyr 87
DB 307 CTGTGGGAAGATGATTTCATACATCATTCG---TCCTCACCTTATGGGGATCTTCGTAC 363
QY 88 ArgGluArgAlaAspArgLeuIleGlyGluValLysAspIleMetPheAsnPhe----- 105

DB 364 AGTGAACGTCTGAGACAGTCTGTGAGGAAGTAAAGAG--ATGTTCAATTCAATACCA 420
QY 106 -----LysSerLeuGluAspGlyLysAsnAspLeuGlnArgLeuLeuValAsp 123
DB 421 AATAATAGAGAAATTAATTGGTTCACAAATGATCTCCTTACACGCGCTTGGATGGTGAT 480
QY 124 AspValGluArgLeuGlyIleAspArgHisPheLysLysGluIleLysThrAlaLeuAsp 143
DB 481 AGCATTTGAACGTCTGGGATAGATAGACATTTCCAAATGAGATAGAGTAGAGCCCTCGAT 540
QY 144 TyrValAsnSerTyrTyrAsnGluLys---GlyIleGlyCysGlyArgGluSerValVal 162
DB 541 TATGTTTACAGTTATTGGAAAGGAAGAGGCAATTGGGTGTGGCAGAGATTCTACTTTT 600
QY 163 ThrAspLeuAsnSerThrAlaLeuGlyLeuArgThrLeuArgLeuHisGlyTyrThrVal 182
DB 601 CCTGATCTCACTCGACTGCGCTTGGCGCTTGAACCTCTTCGACTGCAGATACATGTG 660
QY 183 SerSerAspValLeuAsnValPheLysAspLysAsnGlyGlnPheSerSerThrAlaAsn 202
DB 661 TCTTCAGATGTGCTCGAATACTTCAAGATGAAGAGGCGCATTTTCCTGCCCTGCA--- 717
QY 203 IleGlnIleGluGlyGluIle---ArgGlyValLeuAsnLeuPheArgAlaSerLeuVal 221
DB 718 ATCCTAACCGAGGACAGATCAGATCAGATGTTCTTAATTATATCGGCTTCCCTGCTC 777
QY 222 AlaPheProGlyGlyLysValMetAspGluAlaGluThrPheSerThrLysTyrLeuArg 241
DB 778 GCCTTTCCCGGGAGAAAGTTATGGAAGGCGTGAATCTTCCGCACTTATTTGAAA 837
QY 242 GluAlaLeuGlnLysIleProAlaSerSerIleLeuSerLeuGluIleArgAspValLeu 261
DB 838 AAGTCTTACAAAGATTCCGCTTCCCAAT--CTTCAGAGAGATGAATATAGTATTG 894
QY 262 GluTyrGlyTyrHisThrAsnLeuProArgLeuGluAlaArgAsnTyrMetAspValPhe 281
DB 895 GAATATGTTGGCACACGAATTTGCCGAGATTGGAAGCAAGAAATATATACGAGTCTAC 954
QY 282 -----GlyGlnHisThrLysAsnLysAsnAla-----AlaGluLysLeuLeu 295
DB 955 GAGCAGAGCGGCTATGAAGCTTAAACGAGATGCCATATATGACATGAAGAAGCTTTTA 1014
QY 296 GluLeuAlaLysLeuGluPheAsnIlePheHisSerLeuGlnGluArgGluLeuLysHis 315
DB 1015 CAACCTTGCAAAATTTGAGTTCAATATCTTTCACTCTTTCGAACTAAGAGAGTTACAATCT 1074
QY 316 ValSerArgTyrLysAspSerGlySerProGluMetThrPheCysArgHisArgHis 335
DB 1075 ATCTCCAGATGTGGAAAGAAATCAGTTCGTCTCAACTGACTTTTACACGGCATCTGCAC 1134
QY 336 ValGluTyrTyrAlaLeuAlaSerCysIleAlaPheGluProGlnHisSerGlyPheArg 355
DB 1135 GTGAATATCACTATGCGCATCTTGCAATTCTATGTGGCCAAACATTCAGCTTTCAGA 1194
QY 356 LeuGlyPheThrLysMetSerHisIleLeuThrValLeuAspAspMetTyrAspValPhe 375
DB 1195 ATGAGTTGTTCAAAGTGTGTGATCTGTAAACAGTTCTCGATGATATATATGACACTTTT 1254
QY 376 GlyThrValAspGluLeuGluLeuPheThrAlaThrIleLysArgTyrAspProSerAla 395
DB 1255 GGAACAATGAACGAATCCCACTTTTACGGATGCAATTAAGAGATGGGATTTGTCAACG 1314
QY 396 MetGluCysLeuProGluTyrMetLysGlyValTyrMetMetValTyrHisThrValAsn 415
DB 1315 ACAAGGTGGCTTCCAGAAATATATGAAGAGGTGTACATGAGACTGTGTATCAATGCAATTA 1374
QY 416 GluMetAlaArgValAlaGluLysAlaGlnGlyArgAspThrLeuAsnTyrAlaArgGln 435
DB 1375 GAATATGTGGAAGAGGCTGAGAAAGCTCAAGGCCGAGATATGCTCAACTATATTCAAAT 1434
QY 436 AlaTyrGluAlaCysPheAspSerTyrMetGlnGluAlaLysTyrIleAlaThrGlyTyr 455
DB 1435 GCTTGGGAAGCCCTATTATGATACCTTATGCAAGAAAGCAAGTGATCTCCAGCAGTTAT 1494

QY 456 LeuProThrPheGluGluTyrLeuGluAsnGlyLysValSerSerAlaHisArgProCys 475
|||||
Db 1495 CTCCAACGTTTGAGAGTACTGAGAATGCAAAAGTAGTTCTGGTCTCCGATAGCC 1554
QY 476 AlaLeuGlnProIleuThrLeuAspIleProPheProAspHisIleLeuLysGluVal 495
|||||
Db 1555 ACATTACAAACCATTTCTCACTTGGATGTAACCACTTCTGATTACATACTGCAGAAGAAAT 1614
QY 496 AspPheProSerLysLysLeuAsnAspIleLeuCysIleIleLeuArgLeuArgGlyAspThr 515
|||||
Db 1615 GATTATCCATCCAGATCAATGAGTTAGCTTCGTCATCTTCGACTACGAGGTGACACG 1674
QY 516 ArgCysTyrLysAlaAspArgAlaArgGlyGluGluAlaSerSerIleSerCysTyrMet 535
|||||
Db 1675 CGTGCTTCAAGCGCGATAGGCCCCGTGAGAAAGAGCTTCAGCTATATCGTGTATATG 1734
QY 536 LysAspAsnProGlyLeuThrGluGluAspAlaLeuAsnHisIleAsnPhenMetIleArg 555
|||||
Db 1735 AAAGACATCTCTGATCAATAGAGAGATGCTCTCAATCATATCAACGCCATGATCAGT 1794
QY 556 AspAlaIleArgGluLeuAsnTrpGluLeuLeuLysProAspAsnSerValProIleThr 575
|||||
Db 1795 GATGCATCAGAGATTAATTTGGAGCTTCTCAGACCGAGTAGCAAAAGTCCCATCTCT 1854
QY 576 SerLysLysHisAlaPheAspIleSerArgValTrpHisIleGlyTyrArgTyrArgAsp 595
|||||
Db 1855 TCCAAGAAACATGCTTTGACATCACAGAGCTTTCATCATGTCTTACAAATATCGAGAT 1914
QY 596 GlyTyrSerPheAlaAsnValGluThrLysSerLeuValMetArgThrValIleGluPro 615
|||||
Db 1915 GGTTACATGTTTCCCAACAACGAAAGAAATTTGGTGAATGAACCGTTCTTGAACCT 1974
QY 616 ValProLeu 618
::: |||
Db 1975 CTCGCTTG 1983
RESULT 15
AAF73373
ID AAF73373 standard; cDNA; 2089 BP.
XX AAF73373;
AC AAF73373;
XX
DT 30-APR-2001 (first entry)
XX
DE Grand fir (-)-limonene synthase coding sequence SEQ ID NO: 5.
XX
KW Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;
KW myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;
KW terpinolene synthase; insect resistance; nutrition; ss.
XX
OS Abies grandis.
XX
PN WO200107565-A2.
XX
PD 01-FEB-2001.
XX
PF 24-JUL-2000; 2000WO-US020264.
XX
PR 26-JUL-1999; 99US-00360545.
XX
PA (UNIW) UNIV WASHINGTON STATE RES FOUND.
XX
PI Steele CL, Bohlmann J, Croten RB, Phillips MA;
XX
DR WPI; 2001-182782/18.
DR P-PSDB; AAB69372.
XX
XX New nucleic acid encoding monoterpene synthases, for increasing terpene
PT synthesis in plants, e.g. for increasing resistance to pests or for
PT treatment of cancer.
XX
PS Claim 33; Page 112-115; 175pp; English.

XX
CC The present invention provides the protein and coding sequences of
CC monoterpene synthases from the grand fir. These include (-)-camphene
CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-
CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase
CC and pinene synthase. The sequences can be used to produce transgenic
CC plants expressing high levels of the enzymes, resulting in levels which
CC are useful in protecting against and treating cancers, and to confer
CC insect resistance on plants
XX
SQ Sequence 2089 BP; 638 A; 415 C; 450 G; 586 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.08e-200 Length: 2089
Score: 2031.50 Matches: 409
Percent Similarity: 76.67% Conservative: 84
Best Local Similarity: 63.61% Mismatches: 119
Query Match: 62.49% Indels: 31
DB: 4 Gaps: 14

US-10-025-145A-65 (1-618) x AAF73373 (1-2089)
QY 1 MetalaleuLeuSerIleThrProLeu--ValSerArgSerCys----- 14
|||||
Db 73 ATGGCTCTCTTCTATCGTATCTTTGCAGGTTCCCAATCTCGCGGCTGAATCGTTG 132
QY 15 LeuSerSerSerHisGluIleLysAlaLeu-----ArgArgThrIleProThrLeuGly 32
::: |||||
Db 133 ATCAGTTCACGAATGTGCAGAGGCTCTGTATCTGTACAGACAGTCCCAACACTCAGA 192
QY 33 IleCysArgProGlyLysSerValAlaHisSerIleAsnMetCysLeuThrSerValAla 52
::: |||||
Db 193 ATGCCTAGCGCAGACAGAAAGCTCTGTC-----ATCAACATGAATAATGACCACTGTATCC 246
QY 53 SerThrAspSer-----ValGlnArgArgValGlyAsnTyrHisSerAsn 67
|||
Db 247 CATCGTATGATATAATGCTGGTGTGTACTGCAAAAGACGCATAGCCGATCATCCCAAC 306
QY 68 LeuTrpAspAspAspPheIleGlnSerLeuIleSerThrProTyrGlyAlaProAspTyr 87
|||||
Db 307 CTGTGGGAAGATGATTTCATACATCATTTG--TCCTCACCTTATGGGGATCTTCGTAC 363
QY 88 ArgGluArgAlaAspArgLeuIleGlyGluValLysAspIleMetPheAsnPhe----- 105
|||||
Db 364 AGTGAACGTGCTGAGACAGTCTGTGAGGAAGTAAAGAG--ATGTTCAATTCATATACCA 420
QY 106 -----LysSerLeuGluAspGlyGlyAsnAspLeuGlnArgLeuLeuValAsp 123
::: |||||
Db 421 AATAATAGAGAATTATTTGGTCCAAAATGATCTCCTTACACGCCCTTGGATGTGAT 480
QY 124 AspValGluArgLeuGlyIleAspArgHisPheLysLysGluIleIleLysThrAlaLeuAsp 143
::: |||||
Db 481 AGCATTGAACGTCTGGGATAGATAGACATTTCCAAAATGAGATAAGATAGCCCTCGAT 540
QY 144 TyrValAsnSerTyrTrpAsnGlyLys--GlyIleGlyCysGlyArgGluSerValVal 162
|||||
Db 541 TATGTTTACAGTTATTGGAAGGAAAGGAGCATTTGGGTGGCAGAGATTCTACTTTT 600
QY 163 ThrAspLeuAsnSerThrAlaLeuGlyLeuArgThrLeuArgLeuHisGlyTyrThrVal 182
|||||
Db 601 CCTGATCTCAACTCGACTGCTTGCGCCCTTCGAACCTCTTCGACTGCACGGATACAATGTG 660
QY 183 SerSerAspValLeuAsnValPheLysAspLysAsnGlyGlnPheSerSerThrAlaAsn 202
|||||
Db 661 TCTTCAGATGTGCTGAATACTTCAAAAGATGAAAAGGGGCAATTTGCTGCCCTGCA--- 717
QY 203 IleGlnIleGluGlyGluIle--ArgGlyValLeuAsnLeuPheArgAlaSerLeuVal 221
|||||
Db 718 ATCCTAACCGAGGACAGATCACTAGAAGTGTCTAAATTATATCGGGCTTCCCTGTGC 777
QY 222 AlaPheProGlyGlyLysValMetAspGluAlaGluThrPheSerThrLysTyrLeuArg 241
|||||
Db 778 GCCTTCCCGGGGAGAAAGTATTGGAAGAGGCTGAATCTTCTCGGCATCTTATTGAAA 837

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 26, 2004, 16:58:47 ; Search time 3466 Seconds
(without alignments)
5324.532 Million cell updates/sec

Title: US-10-025-145A-65
Perfect score: 3251
Sequence: 1 MALLSITPLVSRSCLSSSH.....FANVETKSLVRRVIEPVPL 618

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delep 6.0 , Delext 7.0

Searched: 27513289 segs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10025145/runat_23072004_092623_22902/app_query.fasta_1.775
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=exc -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10025145 @CGN 1 1 5180 @runat_23072004_092623_22902 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST: *
1: em_estba: *
2: em_esthum: *
3: em_estin: *
4: em_estmu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_htc: *
9: gb_est1: *
10: gb_est2: *
11: gb_htc: *
12: gb_est3: *
13: gb_est4: *
14: gb_est5: *
15: em_estfun: *
16: em_estom: *
17: em_gss_hum: *
18: em_gss_inv: *
19: em_gss_pln: *
20: em_gss_vrt: *
21: em_gss_fun: *
22: em_gss_mam: *
23: em_gss_mus: *
24: em_gss_pro: *
25: em_gss_rod: *
26: em_gss_phg: *
27: em_gss_vrl: *
28: gb_gss1: *

29: gb_gss2: *
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 1066 | 32.8 | 745 | 14 | CF477103 RTW3_5_A |
| 2 | 907 | 27.9 | 700 | 14 | CF474786 RTW2_7_B |
| 3 | 888 | 27.3 | 696 | 14 | CF401916 RTW1_15_ |
| 4 | 872 | 26.8 | 669 | 14 | CF479802 RTW3_12_ |
| 5 | 864 | 26.6 | 697 | 13 | BQ196773 NXLV105_B |
| 6 | 853 | 26.2 | 599 | 13 | BX680641 BX680641 |
| 7 | 802 | 24.7 | 599 | 12 | BG526917 NXPV_057 |
| 8 | 795 | 24.5 | 804 | 14 | CF666338 RTCNT1_22 |
| 9 | 786 | 24.2 | 616 | 14 | CF663845 RTCNT1_5_ |
| 10 | 764 | 23.5 | 637 | 14 | CF476978 RTW3_5_A |
| 11 | 733 | 22.5 | 481 | 9 | AL750951 AL750951 |
| 12 | 723 | 22.2 | 740 | 14 | CF477562 RTW3_8_G |
| 13 | 717 | 22.1 | 516 | 13 | BQ698077 NXPV_064_ |
| 14 | 713 | 21.9 | 517 | 13 | BX677624 BX677624 |
| 15 | 698 | 21.5 | 539 | 10 | AM287756 EST0004_S |
| 16 | 681 | 20.9 | 569 | 10 | AM287754 EST0002_S |
| 17 | 680 | 20.9 | 557 | 14 | CF666483 RTCNT1_23 |
| 18 | 658 | 20.2 | 651 | 14 | CF479884 RTW3_12_ |
| 19 | 657.5 | 20.2 | 534 | 10 | AM287755 EST0003_S |
| 20 | 656 | 20.2 | 682 | 14 | CF663768 RTCNT1_5_ |
| 21 | 607 | 18.7 | 430 | 13 | BQ702557 NXSI_129_ |
| 22 | 587.5 | 18.1 | 591 | 14 | CA305371 haep004xK |
| 23 | 579.5 | 17.8 | 2029 | 11 | AY107369 Zea mays |
| 24 | 559 | 17.2 | 618 | 9 | AL750955 AL750955 |
| 25 | 550 | 16.9 | 541 | 14 | CF672979 RTCNT1_75 |
| 26 | 526.5 | 16.2 | 725 | 14 | CF397293 RTDS3_2_A |
| 27 | 525 | 16.1 | 547 | 10 | BG039521 NXSI_099_ |
| 28 | 517.5 | 15.9 | 1983 | 11 | AY105371 Zea mays |
| 29 | 515.5 | 15.9 | 725 | 14 | CF470471 RTDS1_17_ |
| 30 | 507.5 | 15.6 | 629 | 9 | AU299287 AU299287 |
| 31 | 496.5 | 15.3 | 843 | 14 | CF208265 CAB20003_ |
| 32 | 489 | 15.0 | 574 | 14 | CF474640 RTW2_7_B |
| 33 | 489 | 15.0 | 733 | 14 | CF666270 RTCNT1_22 |
| 34 | 488 | 15.0 | 2028 | 11 | AY110842 Zea mays |
| 35 | 481 | 14.8 | 730 | 13 | BX682869 BX682869 |
| 36 | 477.5 | 14.7 | 896 | 29 | CG847800 ZMMBB031 |
| 37 | 476 | 14.6 | 634 | 14 | CF397946 RTDS3_23_ |
| 38 | 475 | 14.6 | 597 | 14 | CF666416 RTCNT1_23 |
| 39 | 465.5 | 14.3 | 585 | 12 | BG318038 NXPV_008_ |
| 40 | 453 | 13.9 | 574 | 9 | AW065088 ST39E04_P |
| 41 | 446.5 | 13.7 | 766 | 13 | BU814724 N032C12_P |
| 42 | 439.5 | 13.5 | 552 | 13 | BQ696096 NXPV_036_ |
| 43 | 429.5 | 13.2 | 530 | 9 | AU298829 AU298829 |
| 44 | 427 | 13.1 | 750 | 12 | BG351484 111F08 Ma |
| 45 | 418.5 | 12.9 | 824 | 14 | CD852160 DH0ALL252 |

ALIGNMENTS

RESULT 1
CF477103 745 bp mRNA linear EST 08-SEP-2003
LOCUS RTW3_5_A06.gi_A022 well watered loblolly pine roots W3 Pinus
DEFINITION taeda_cDNA clone RTW3_5_A06_A022 5', mRNA sequence.
ACCESSION CF477103
VERSION CF477103.1 GI:34505972
KEYWORDS EST.
SOURCE Pinus taeda (loblolly pine)
ORGANISM Pinus taeda
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
REFERENCE 1 (bases 1 to 745)

AUTHORS
Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W., Dean, J.,
Gebremedhin, M., Dervinis, C., Martin, T., White, T., Davis, J. and
Neale, D.
TITLE
An EST database from well-watered loblolly pine (Pinus taeda) roots
JOURNAL
Unpublished (2003)
COMMENT
Other ESTs: RTMW3_5_A06_b1_A022
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu

RNA prepared and library constructed by W. Walter Lorenz, School of
Forestry, University of Georgia; plant material prepared at the
University of Florida; sequencing done in the Laboratory for
Genomics and Bioinformatics, University of Georgia. Sequence ends
have been trimmed to exclude vector and regions below Phred quality
16. Three-prime sequences are presented as their reverse complement
and have been trimmed to exclude polyA.
Seq primer: JENREV (CAGGAACAGCTATGACC).

FEATURES
source
location/Qualifiers
1..745

/organism="Pinus taeda"
/mol_type="mRNA"
/strain="CCCLONES"
/db_xref="taxon:3352"
/clone="RTMW3_5_A06_A022"
/lab_host="DH10B-T1 phage-resistant E. coli"
/note="lib="Well-watered loblolly pine roots WM3"
/note="Vector: pSL1180; Site 1: EcoRI; Site 2: XhoI; The
library was prepared from polyA+ RNA from loblolly pine
(Pinus taeda) roots watered to pot capacity every other
day. Pre-dawn water potential remained -0.3 MPa +/-0.1.
Roots were harvested for RNA isolation. Double-stranded
cDNA was cloned unidirectionally into pSL1180. Inserts
excised with EcoRI (5' end) and XhoI (3' end)."

ORIGIN

Alignment Scores:
Pred. No.: 4.36e-112 Length: 745
Score: 1066.00 Matches: 195
Percent Similarity: 87.90% Conservative: 23
Best Local Similarity: 78.63% Mismatches: 30
Query Match: 32.79% Indels: 0
DB: 14 Gaps: 0

US-10-025-145A-65 (1-618) x CF477103 (1-745)

Oy 356 LeuGlyPheThrLyMetSerHisLeuIleThrValLeuAspArgMetTyrAspValPhe 375
Db 2 CTCGGCTTTGCCAAATCCTGTCAATATCAACCGTCTTGATGATATGTACGACACCTTC 61
Oy 376 GlyThrValAspGluLeuGluPheThrAlaThrIleLysArgTTrpAspProSerAla 395
Db 62 GGAACACTCGACGAGCTCGAACTCTTCACAGCTGCAATTAAAGATGGAGATCCGTCGGCG 121
Oy 396 MetGluCysLeuProGluTyrMetLysGlyValTyrMetMetValTyrHisThrValAsn 415
Db 122 ACAGAGTGCTTCCAGAAATATGAAAGAGATTACATGATAGATTACAAACACTGTAAT 181
Oy 416 GluMetAlaArgValAlaGluLysAlaGlnLysArgAspThrLeuAsnTyrAlaArgGln 435
Db 182 GAAATGTCTCAGGAGGACAGACAGCGCTCAAGGCCGAGACACGCTCACTATTGTCGACAG 241
Oy 436 AlaTrpGluAlaCysPheAspSerTyrMetGlnGluAlaLysTrpIleAlaThrGlyTyr 455
Db 242 GCTTGGGAGGAATATATTGATTTCGTATATGCAAGAAGCAAGTGATGCCAGTGGTGAG 301
Oy 456 LeuProThrPheGluGluTyrLeuGluAsnGlyLysValSerSerAlaHisArgProCys 475
Db 302 GTGCCAATTTGAGAGTACTACGAAACGGGAAATTAAGCTTGCTGATCGCGTATCG 361

Oy 476 AlaLeuGlnProIleLeuThrLeuAspIleProPheProAspHisIleLeuLysGluVal 495
Db 362 GCATTGCAACCCATTCTGACGACCGACATCCCTTTCTTGACGACAGCTCCTCAAGAGAGCT 421
Oy 496 AspPheProSerLysLeuAsnAspLeuIleCysIleIleLeuArgLeuArgGlyAspThr 515
Db 422 GACATTCATCGAAGCTCAATGACTTGGCATCTGCCATTCTTCGATTACGAGAGATACG 481
Oy 516 ArgCysTyrLysAlaAspArgAlaArgGlyGluGluAlaSerSerIleSerCysTyrMet 535
Db 482 CGCTGCTACGAGCGGACAGGCGCTGGAGAGAAGAGCTTCGTATATCTGTATTATG 541
Oy 536 LysAspAsnProGlyLeuThrGluGluAspAlaLeuAsnHisIleAsnPhemeticLeuArg 555
Db 542 AAAGACAATCCTGAGCAACGGAAGAAGATGCTCTCAATCATATCAACGCCATGATCAGT 601
Oy 556 AspAlaIleArgGluLeuAsnTrpGluLeuLysProAspAsnSerValProIleThr 575
Db 602 GATGTAATTAAAGATTTAATTGGAGCTTCTCAACCAACACAGACGCTTCCCATATCT 661
Oy 576 SerLysLysHisAlaPheAspIleSerArgValTTrpHisHisGlyTyrArgTyrArgAsp 595
Db 662 GCCAATAAACATGCTTTTGACATTAGCAGAGCTTTCATTTATGCGCTACAAATATCGAGAT 721

RESULT 2
CF474786 700 bp mRNA linear EST 05-SEP-2003
LOCUS RTMW2_7_B11_g1_A021 Well-watered loblolly pine roots WM2 Pinus
DEFINITION taeda cDNA clone RTMW2_7_B11_A021 5', mRNA sequence.
ACCESSION CF474786
VERSION CF474786.1 GI:34492158
KEYWORDS EST.
SOURCE Pinus taeda (loblolly pine)
ORGANISM Pinus taeda

REFERENCE
AUTHORS
Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W., Dean, J.,
Gebremedhin, M., Dervinis, C., Martin, T., White, T., Davis, J. and
Neale, D.
TITLE
An EST database from well-watered loblolly pine (Pinus taeda) roots
JOURNAL
Unpublished (2003)
COMMENT
Other ESTs: RTMW2_7_B11_b1_A021
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu

RNA prepared and library constructed by W. Walter Lorenz, School of
Forestry, University of Georgia; plant material prepared at the
University of Florida; sequencing done in the Laboratory for
Genomics and Bioinformatics, University of Georgia. Sequence ends
have been trimmed to exclude vector and regions below Phred quality
16. Three-prime sequences are presented as their reverse complement
and have been trimmed to exclude polyA.
Seq primer: JENREV (CAGGAACAGCTATGACC).

FEATURES
source
location/Qualifiers
1..700

/organism="Pinus taeda"
/mol_type="mRNA"
/strain="CCCLONES"
/db_xref="taxon:3352"
/clone="RTMW2_7_B11_A021"
/lab_host="DH10B-T1 phage-resistant E. coli"
/note="lib="Well-watered loblolly pine roots WM2"
/note="Vector: pSL1180; Site 1: EcoRI; Site 2: XhoI; The
library was prepared from polyA+ RNA from loblolly pine

Qy 444 TyrMetGlnGluAlaIalysTrpIleAlaThrGlyTyrLeuProThrPheGlnGluTyrLeu 463
Db 301 TATATACAGAAGCAAGCTGATTCACGTGTTATCTTCCACGTTCCAGAGTACCTC 360
Qy 464 GluAsnGlyLysValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeu 483
Db 361 GAGAAATGGGAAGGTGAGCTTCGGCTCTGCATTAACCAACGCTGAAACCATGCTGACTTTG 420
Qy 484 AspIleProPheProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAsp 503
Db 421 GGGTTTCTCTCTCCGCCCTCGAATCCTGACAGAAATTGACTTTCCATTCGAAATTCAATGAT 480
Qy 504 LeuIleCysIleIleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAla 523
Db 481 TTGATATGTGCCATCTTCGACTGAAAGGTGACACTCAATGCTACAGAGCTGACAGGGCG 540
Qy 524 ArgGlyGlnGluAlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGlu 543
Db 541 CGTGAGAGAAGAGCTTCGCCGCTATCGTTATATGAAGACCATCTCGAATAACAGAG 600
Qy 544 GluAspAlaLeuAsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrp 563
Db 601 GAAGATGCTGTCAATCAATCAATGCTATGTGTCGATACTTAACCAAGGAATGATTGG 660
Qy 564 GluLeuLeuLysProAspAsnSerValProIleThr 575
Db 661 GAGTTACTTAGACCCGACAGCGGTGTCCCATCTCT 696

RESULT 4
CF479802/c 669 bp mRNA linear EST 08-SBP-2003
LOCUS RTMW3_12_D02_b1_A022 Well-watered loblolly pine roots WM3 Pinus
DEFINITION taeda cDNA clone RTMW3_12_D02_A022 3', mRNA sequence.
ACCESSION CF479802
VERSION CF479802.1 GI:34508671
KEYWORDS EST.
SOURCE Pinus taeda (loblolly pine)
ORGANISM Pinus taeda

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
1 (bases 1 to 669)
Pratt,L., Cordonnier-Pratt,M.-M., Lorenz,W.W., Dean,J.,
Gebremedhin,M., Dervinis,C., Martin,T., White,T., Davis,J.,
Cannon,R., Owen,A. and Neale,D.
EST database from well-watered loblolly pine (Pinus taeda) roots
Unpublished (2003)
Other ESTs: RTMW3_12_D02_g1_A022
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu

RNA prepared and library constructed by W. Walter Lorenz, School of
Forestry, University of Georgia; plant material prepared at the
University of Florida; sequencing done in the laboratory for
Genomics and Bioinformatics, University of Georgia. Sequence ends
have been trimmed to exclude vector and regions below Phred quality
16. Three-prime sequences are presented as their reverse complement
and have been trimmed to exclude polyA.
Seq primer: M13-21 (TGTAACAACGACGCCAGT)
POLYA=NO.

FEATURES
source location/Qualifiers
1..669

/organism="Pinus taeda"
/mol_type="mRNA"
/strain="CCLONES"
/db_xref="taxon:3352"
/db_xref="RTMW3_12_D02_A022"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_1ib="Well-watered loblolly pine roots WM3"
/note="Vector: pSL180; Site_1: EcoRI; Site_2: XhoI; The

library was prepared from polyA+ RNA from loblolly pine
(Pinus taeda) roots watered to pot capacity every other
day. Pre-dawn water potential remained -0.3 MPa +/-0.1.
Roots were harvested for RNA isolation. Double-stranded
cDNA was cloned unidirectionally into pSL180. Inserts
excised with EcoRI (5' end) and XhoI (3' end)."

ORIGIN
Alignment Scores:
Pred. No.: 1.01e-89 Length: 669
Score: 872.00 Matches: 154
Percent Similarity: 85.14% Conservative: 35
Best Local Similarity: 69.37% Mismatches: 33
Query Match: 26.82% Indels: 0
DB: 14 Gaps: 0

US-10-025-145A-65 (1-618) x CF479802 (1-669)

Qy 321 LysAspSerGlySerProGlnMetThrPheCysArgHisArgHisValGluTyrTyrAla 340
Db 667 AAAGATTATGGATTCCCTGAATAACATTCTCACGGCATCGTACGTAATACTACTACT 608
Qy 341 LeuAlaSerCysIleAlaPheGlnProGlnHisSerGlyPheArgLeuGlyPheThrLys 360
Db 607 TTAGCAGCTTGCAATGCAATGATTCCTAAACATTCTGCGTTTCGACTAGGATTGGTAA 548
Qy 361 MetSerHisLeuIleThrValLeuAspAspMetTyrAspValPheGlyThrValAspGlu 380
Db 547 ATAACTATATGATCAGATCAGATTCGACGATATCTACGACACTTCGAAACATGAGAG 488
Qy 381 LeuGlnLeuPheThrAlaThrIleLysArgTrpAspProSerAlaMetGluCysLeuPro 400
Db 487 CTCAACTCTTAACCGCAGCGTTTAAAGATGGATCCGTTTCGATAGAGTGTCTTCCA 428
Qy 401 GluTyrMetLysGlyValTyrMetMetValTyrHisThrValAsnGluMetAlaArgVal 420
Db 427 GATTATATGAAGAAGAGTGTACATGCGGTTTACGACACACATCAACGAATGGACAGAG 368
Qy 421 AlaGluLysAlaGlnGlyArgAspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCys 440
Db 367 GCCAGAAATTCAGAGCTGGGATACAGTCAGCTATGCTCGAAATCTTGGAGGCTTTT 308
Qy 441 PheAspSerTyrMetGlnGluAlaIalysTrpIleAlaThrGlyTyrLeuProThrPheGln 460
Db 307 ATGGTCTTATATACAGAAGCCAAAGTGAATTCAGTGTGTTATCTTCCACAGTTGAC 248
Qy 461 GluTyrLeuGluAsnGlyLysValSerSerAlaHisArgProCysAlaLeuGlnProIle 480
Db 247 GAGTACCTCGAAGATGGGAAGGTGAGCTTCGGCTTCGCAATACCAACGCTGAACCATG 188
Qy 481 LeuThrLeuAspIleProPheProAspHisIleLeuLysGluValAspPheProSerLys 500
Db 187 CTGACTTTGGGGTTTCTCTTCGCCCTCGAATCTGCAGAAATGACTTTCATCGAA 128
Qy 501 LeuAsnAspLeuIleCysIleIleLeuArgLeuArgGlyAspThrArgCysTyrLysAla 520
Db 127 TTCAATGATTGATATGTGCCATCTTCGACTGAAGGTGACACTCAATGCTACAGGCT 68
Qy 521 AspArgAlaArgGlyGluGluAlaSerSerIleSerCysTyrMetLysAspAsnProGly 540
Db 67 GACAGGCGCGGTGAGGAAGAGCTTCGGCCGTATCGTGTATATGAAGAACCATCTTGA 8
Qy 541 LeuThr 542
Db 7 ATAAACA 2

RESULT 5
BQ196773 697 bp mRNA linear EST 07-MAY-2003
LOCUS NXLV105_B02_F NXLV (NsF xylem Late wood Vertical) Pinus taeda cDNA
DEFINITION clone NXLV105_B02 5' similar to Arabidopsis thaliana sequence
At4g16730 limonene cyclase like protein see
http://mips.gsf.de/proj/ehal/db/index.html, mRNA sequence.

ACCESSION BQ196773
VERSION BQ196773.1 GI:20379276
KEYWORDS EST.
SOURCE Pinus taeda (loblolly pine)
ORGANISM Pinus taeda
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. Sederoff, R. 1 (bases 1 to 697)
AUTHORS Sederoff, R.
TITLE Molecular Basis of Wood Formation in the Pine Megagenome
JOURNAL Unpublished (2000)
COMMENT Contact: Sederoff, Ron
Forest Biotechnology
North Carolina State University
840 Main Campus Drive, Centennial Campus, Campus Box 7247, Raleigh, NC 27695, USA
Tel: 919 515 7800
Fax: 919 515 7801
Email: ron_sederoff@ncsu.edu, jerri_johnson@ncsu.edu
Please see http://web.ahc.umn.edu/biodata/nsfpine/ for further information.
Seq primer: T3.
Location/Qualifiers
1..697
/organism="Pinus taeda"
/mol_type="mRNA"
/strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
/clone="NXLV105_B02"
/tissue_type="primary xylem"
/dev_stage="late wood"
/lab_host="XL1-Blue"
/clone_lib="NXLV (Nsf Xylem Late wood Vertical)"
/note="Vector: pTriplex; Site 1: EcorI; The library is from late (summer-August) wood, taken from below the crown of a 20 year old tree. The harvested xylem tissue was on the cusp between transitional and mature wood. NOTE: The sequences contain a 'cDNA adapter' between the EcorI site and the start of the EST. The adapter sequence is 'AATCGGCATTATGGCC'."

ORIGIN
Alignment Scores:
Pred. No.: 9.21e-89 Length: 697
Score: 864.00 Matches: 162
Percent Similarity: 85.45% Conservative: 20
Best Local Similarity: 76.06% Mismatches: 31
Query Match: 26.58% Indels: 0
DB: 13 Gaps: 0
US-10-025-145A-65 (1-618) x BQ196773 (1-697)

Qy 406 VALTYRmeNctVALTYRHISTHrvalaNGluMeCaLaargvalaAGluYsAlaGln 425
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 23 GTTACATGATAGTTTACACACTGTAAATGAATGTCTCAGAGGAGCAACAAGGCTCAA 82
426 GLYARgAspThrleuAsnTYRAlaargGlnaLaTrpGluAlaCysPheAspSerTYrMet 445
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 83 GGCCGAGACACGCTCACTATTGTGCAGAGGCTTGGAGGAATATATTGATGCGTATATG 142
446 GlnGluAlaLysTrpIleAlaThrGlyTYRleuProThrPheGluGluTYRleuGluAsn 465
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 143 CAAGAAGCAAGTGATCGCCCGTGTGAGGTGCCAACATTGTGAGGAGTACTATGAGAAC 202
466 GLYLysValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIle 485
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 203 GGGAAGTTAGCTGTGTCATCGCGATCGCATTTGCAACCATTGTGACGACGACATC 262
486 ProPheProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIle 505
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 263 CCTTTCCTGAGCAGCTCTCAAGGAAGTTGACATTCCATCGAAGCTCAATGACTTGACA 322
506 CysIleIleLeuArgLeuArgGlyAspThrArgCysTYRlySAlaAspArgAlaArgGly 525

Db 323 TCTGCCATTCTTCGATTACGAGGGGATACGGCTGCTACCAGCGGACAGGCCCGCTGA 382
Qy 526 GLUGluAlaSerSerIleSerCysTYRmetLysAspAsnProGlyLeuThrGluLysAsp 545
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 383 GAGAAGCTTCGTGTATATCTGTATTATGAAGAACAATCCTGGAACAACAGAGGAAGAT 442
Qy 546 AlaleuAsnHisIleAsnPhemeIleArgAspAlaIleArgGluLeuAsnTrpGluLeu 565
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 443 GCTCTCAATCATCTCAACGCCCATGATCATGTAATTAAAGATTAAATTGGAGCTT 502
Qy 566 LeuLysProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSerArg 585
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 503 CTCAATCAACACAGCAGCGTCTCCCATATCTGCCAAACATGCTTTGACATTAGCAGA 562
Qy 586 VALTrpHisIleGlyTYRArgTYRArgAspGlyTYRSerPheAlaAsnValGluThrLys 605
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 563 GCTTCCATTGTGCTACAAATATCGAGATGGCTACAGCGTTGCCAACATTGAACNNNN 622
Qy 606 SerLeuValMetArgThrValIleGluProValProLeu 618
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 623 NGTTGGTGANNNNNIACCGTCATTGATCTGTCACTTTA 661

RESULT 6
BX680641 599 bp mRNA linear EST 28-OCT-2003
LOCUS BX680641 RS Pinus pinaster cDNA clone RS46D06, mRNA sequence.
DEFINITION BX680641
ACCESSION BX680641
VERSION BX680641.1 GI:38015099
KEYWORDS EST.
SOURCE Pinus pinaster
ORGANISM Pinus pinaster
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. Frigerio, J. and Plomion, C.
REFERENCE 1 (bases 1 to 599)
AUTHORS Identification of water-deficit responsive genes in Maritime pine (Pinus pinaster Ait.) using an EST approach
TITLE Unpublished (2002)
JOURNAL Contact: Frigerio JM
COMMENT Genetic et Amelioration 69
INRA
route d'Arcachon 33612 Cestas CEDEX France
Email: Frigerio@pierroton.inra.fr
Email: Frigerio@pierroton.inra.fr
Seq primer: T3.
Location/Qualifiers
1..599
/organism="Pinus pinaster"
/mol_type="mRNA"
/db_xref="taxon:71647"
/clone="RS46D06"
/tissue_type="root"
/dev_stage="6 weeks old seedling"
/lab_host="SOLR"
/clone_lib="RS"
/note="Vector: Uni-ZAP XR; ecotype: Landes; The library was made from the roots of 6 weeks old seedlings grown in hydroponic conditions. A three weeks drought stress treatment was applied by lowering the osmotic potential of the nutrient solution to -0.45 MPa using 170 g/l of polyethylene glycol as an osmoticum. A mixture of genotypes were used. Oligo-dT primed cDNA was directionally cloned into the EcorI-XhoI lambda-ZAP vector arms and mass-excised to form a pBluescript phagemid"

ORIGIN
Alignment Scores:
Pred. No.: 1.31e-87 Length: 599
Score: 853.00 Matches: 161
Percent Similarity: 87.94% Conservative: 14
Best Local Similarity: 80.90% Mismatches: 24
Query Match: 26.24% Indels: 1

DB: 13 Gaps: 0

US-10-025-145A-65 (1-618) x BX680641 (1-599)

Qy 399 LeuProGluTyrMetLysGlyValTyrMetMetValTyrHisThrValAsnGluMetAla 418
|||||:::|||||
Db 3 CTTCCACAATATATGAAAGGAAT-TACATGATGGTTTACACACCCGTTAAATGAATGTCT 61

Qy 419 ArgValAlaGluLysAlaGlnGlyArgAspThrLeuAsnTyrAlaArgGlnAlaTyrGlu 438
|||:::|||||
Db 62 GCGAGGACAGAAAGGCTCAAGGCCGAGACACTCTCAACTATGCTGACAGAGCTTGGAG 121

Qy 439 AlaCysPheAspSerTyrMetGlnGluAlaLysTrpIleAlaThrGlyTyrLeuProThr 458
|||||
Db 122 GATTATCTTGATTGCTATATGCAAGACAAAGTGATAGCCACGGGTTATCTGCCAACG 181

Qy 459 PheGluGluTyrLeuGluAsnGlyLysValSerSerAlaHisArgProCysAlaLeuGln 478
|||||
Db 182 TTCGAGGATACTTGGAGAACGGGAAAGTTAGCTCTGGGCATCGCGTTCGGCGTGCAG 241

Qy 479 ProIleLeuThrLeuAspIleProPheProAspHisIleLeuLysGluValAspPhePro 498
|||:::|||||
Db 242 CCCATGCTGACGATGACATCCCTCTTCTCTCACATCCTCAAGGAAGTTGACTTCCCA 301

Qy 499 SerLysLeuAsnAspLeuIleCysIleIleLeuArgLeuArgGlyAspThrArgCysTyr 518
|||||
Db 302 TCCAACCTCAATGACTTGGCATGTGCCATCTTGATTACGAGGTGATACCCGATGTAT 361

Qy 519 LysAlaAspArgAlaArgGlyGluGluAlaSerSerIleSerCysTyrMetLysAspAsn 538
:::|||||
Db 362 CAGAGGACAGGGCTCGTGAGAGAAACCTCGGTATATCTTGTATATGAAGAACAAAC 421

Qy 539 ProGlyLeuThrGluGluAspAlaLeuAsnHisIleAsnPheMetIleArgAspAlaIle 558
|||||
Db 422 CCTGAGCAACAGAGAGATGCTCTTAATCATCTCAATGTCATGTCAGTGGCGTAATT 481

Qy 559 ArgGluLeuAsnTrpGluLeuLeuLysProAspAsnSerValProIleThrSerLysLys 578
:::|||||
Db 482 AAAGAAATTAATTTGGAGCTTCTCAAAACCCGACACAGTGTGCCATTTCTTCCAGAAA 541

Qy 579 HisAlaPheAspIleSerArgValTrpHisGlyTyrArgTyrArgAspGlyTyr 597
|||||
Db 542 ATTACTTTTGACATTACCAGAGCTTTCATTACGGTTACAAATACGAGATGGCTAC 598

RESULT 7
BG526917 599 bp mRNA linear EST 07-MAY-2003

LOCUS NXPV_057 D04 F NXPV (NsF Xylem Planings wood Vertical) Pinus taeda
DEFINITION cDNA clone NXPV_057 D04 5' similar to Arabidopsis thaliana sequence
At4g16730 limonene cyclase like protein see
http://mips.gsf.de/proj/thal/db/index.html, mRNA sequence.

ACCESSION BG526917
VERSION BG526917.1 GI:13536796
KEYWORDS EST.
SOURCE pinus taeda (loblolly pine)
ORGANISM pinus taeda

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
JOURNAL 1 (bases 1 to 599)
COMMENT Molecular Basis of Wood Formation in the Pine Megagenome
Unpublished (2000)
Contact: Sederoff, Ron
Forest Biotechnology
North Carolina State University
840 Main Campus Drive, Centennial Campus, Campus Box 7247, Raleigh,
NC 27695, USA
Tel: 919 515 7800
Fax: 919 515 7801
Email: ron.sederoff@ncsu.edu, jerri.johnson@ncsu.edu
Please see http://web.ahc.umn.edu/biodata/nsfpine/ for further
information.
Seq primer: T3.

FEATURES

source location/Qualifiers

1..599
/organism="pinus taeda"
/mol_type="mRNA"
/strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
/clone="NXPV_057 D04"
/issue_type="Xylem"
/cell_type="Planings (secondary)"
/dev_stage="Transitional"
/lab_host="XLI-Blue"
/clone_lib="NXPV (NsF Xylem Planings wood Vertical)"
/note="Vector: Bluescript SK; Site 1: Eco RI; Site 2:
XhoI; The library is from early (spring) secondary wood,
taken from a ten year old tree in the transitional phase.
The tree is a kind gift of the Westvaco Corporation.
Secondary xylem was harvested from the tree by peeling
back the bark and primary xylem and then removing the
underlying tissue with a block plane. NOTE: The sequences
contain a 'cDNA adapter' between the EcoRI site and the
start of the EST. The adapter sequence is
'AATCGGACAGAG'."

ORIGIN

Alignment Scores:

Pred. No.: 1.04e-81 Length: 599
Score: 802.00 Matches: 150
Percent Similarity: 83.92% Conservative: 17
Best Local Similarity: 75.38% Mismatches: 32
Query Match: 24.67% Indels: 0
DB: 12 Gaps: 0

US-10-025-145A-65 (1-618) x BG526917 (1-599)

Qy 395 AlaMetGluCysLeuProGluTyrMetLysGlyValTyrMetMetValTyrHisThrVal 414
|||||
Db 3 GCGACAGAGTGCCCTCCAGAAATATGAAAGAGTTTACATGATGTTACACACTGTA 62

Qy 415 AsnGluMetAlaArgValAlaGluLysAlaGlnGlyArgAspThrLeuAsnTyrAlaArg 434
|||||
Db 63 AATGAATGTCTCAGAGGACAGCAAGGCTCAAGGCCGAGACAGCTCAACTATTGTGCA 122

Qy 435 GlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGluAlaLysTrpIleAlaThrGly 454
|||||
Db 123 CAGGCTTGGAGGAAATATATGATGCTATATGCAAGAACAAAGTGATCGCCAGTGT 182

Qy 455 TyrLeuProThrPheGluGluTyrLeuGluAsnGlyLysValSerSerAlaHisArgPro 474
|||:::|||||
Db 183 GAGGTGCCAACATTTGAGAGTACTATGAGAACGGAAAGTTAGCTTGTGTCATCGCTA 242

Qy 475 CysAlaLeuGlnProIleLeuThrLeuAspIleProPheProAspHisIleLeuLysGlu 494
|||||
Db 243 TCGGCAATTGCAACCCATTTTGACGACCGACATCCCTTCTCGAGACAGTCTCAAGGAA 302

Qy 495 ValAspPheProSerLysLeuAsnAspLeuIleCysIleIleLeuArgLeuArgGlyAsp 514
|||||
Db 303 GTTGACATTCCATTCGACGCTCAATGACTTGGCATCTGCCATTCTTGATTACGAGGGGAT 362

Qy 515 ThrArgCysTyrLysAlaAspArgAlaArgGlyGluGluAlaSerSerIleSerCysTyr 534
|||||
Db 363 ACGCGCTGCTACCNMGCGACAGGGCCGTGAGAGAAAGCTTCGTATATCTTGTTAT 422

Qy 535 MetLysAspAsnProGlyLeuThrGluGluAspAlaLeuAsnHisIleAsnPheMetIle 554
|||||
Db 423 ATGAAGACAAATCTNNAACAAGAGAGATGCTCTCAATCATCTCAACGCCATGATC 482

Qy 555 ArgAspAlaIleArgGluLeuAsnTrpGluLeuLeuLysProAspAsnSerValProIle 574
|||
Db 483 AGTGATGTTATTANANNNTTAATTTGGAGCTTCTCAACCAACAAGCGTTCACATA 542

Qy 575 ThrSerLysLysHisAlaPheAspIleSerArgValTrpHisGlyTyrArgTyr 593
:::|||||
Db 543 TCTGCCAANNNCATGCTTTGACATTANCNNNNNNNTCCNNVTGTGGCTACAATAT 599

RESULT 8
LOCUS CF666338 804 bp mRNA linear EST 07-OCT-2003
DEFINITION RTCNT1_22_C05_g1_A029 Root control Pinus taeda cDNA clone
RTCNT1_22_C05_A029 5', mRNA sequence.
ACCESSION CF666338
VERSION CF666338.1 GI:37563605
KEYWORDS EST.
SOURCE Pinus taeda (loblolly pine)
ORGANISM Pinus taeda
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 804)
AUTHORS Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W., Zimmermann, C. and Dean, J.F.D.
TITLE An EST database from untreated loblolly pine (Pinus taeda) roots
JOURNAL Unpublished (2003)
COMMENT Other ESTs: RTCNT1_22_C05_b1_A029
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
RNA prepared and library constructed by W. Walter Lorenz (School of Forest Resources, University of Georgia); plant material prepared by Craig Zimmermann (School of Forest Resources, University of Georgia) using rooted cuttings provided by the Forest Biology Research Cooperative (FBRC) and the CCLONES project a the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.
Seq primer: JENREV (CAGGAACAGCTATGACC).
FEATURES
source
1..804
Location/Qualifiers
/organism="Pinus taeda"
/mol_type="mRNA"
/strain="3 CCLONES"
/db_xref="taxon:3352"
/clone="RTCNT1_22_C05_A029"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="Root control"
/note="Organ: root; Vector: pSL180; Site 1: EcoRI; Site 2: XhoI; The library was prepared from polyA+ RNA from the roots of 1-year-old loblolly pine (Pinus taeda) cuttings that were rooted and then planted in washed sand. Just before harvesting roots for RNA isolation, the rooted cuttings were maintained for 27 days (April 2003) under ambient conditions in a local greenhouse. They were kept on a weekly regimen of 0.5x nutrient-complete Hoagland's solution and supplemented with additional water sufficient to maintain a 15% soil moisture content. Double-stranded cDNA was cloned unidirectionally into pSL180. Inserts can be excised with EcoRI (5' end) and XhoI (3' end)."
ORIGIN
Alignment Scores:
Pred. No.: 1.16e-80 Length: 804
Score: 795.00 Matches: 169
Percent Similarity: 76.81% Conservative: 33
Best Local Similarity: 64.26% Mismatches: 47
Query Match: 24.45% Indels: 14
DB: 14 Gaps: 6
US-10-025-145A-65 (1-618) x CF666338 (1-804)
QY 1 MecAlaIeuLeuSerIleThrProLeuValSerArgSerCysLeu----- 15
Db 20 ATGGCTCTGTTTCTGTCTGCCGTTGAATCCAAACTGTGTCTGCGCAGAACGTTGTTTC 79

QY 16 SerSerSerHisGluIleLeuValAlaLeuArgGThrIleProThrLeuGlyIleCysArg 35
Db 80 GGTTTAGTCAATGAGCTGAAAGCTATCCATAGTACAGTCCCAAATCTTGGAATGTGCAGG 139
QY 36 ProGlyLeuSerValAlaHisSerIleAsnMet--CysLeuThrSerValAlaSerThr 54
Db 140 GGAGGGAATCCATAGCACCTTCTATGACATGAGTTGCAGCACCTCCGTTTCTAATGAG 199
QY 55 AspSerValGlnArgArgValGlyAsnTyrrHisSerAsnLeuTrpAspAspPheIle 74
Db 200 GATGGGTACCAAGACGATAGCTGTGCATCATCCAACTTTGGAGCATGATCCATA 259
QY 75 GlnSerLeuIleSerThrProTyrrGlyAlaProAspTyrrArgGluArgAlaAspArgLeu 94
Db 260 GCCTCTCTC---TCCACTCTCATGAGGACCTTCTTACCCTAAGCGCGCTGATAACTT 316
QY 95 IleGlyGluValIleHisAspIleMetPheAsnPhelySerLeuGluAspGlyIle----- 112
Db 317 ATAGGGGAAGTAAATAATATC--TTGATTTAATGTCAGTGAGAGATGAGATTTCACC 373
QY 113 -----AsnAspLeuLeuGlnArgLeuLeuValAlaAspAspValGluArgLeuGly 129
Db 374 AGTCCCTCAGTGAACCTCCATCACCGCTCTGATGTCGATAGCTTGAACGGTTGGGA 433
QY 130 IleAspArgHisPheLeuIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThr 149
Db 434 ATGATAGGATTTCAAGACGAGATAATTCTGCTCTGATCATGTTTACAGTTATTGG 493
QY 150 AsnGlyLeuGlyIleGlyCysGlyArgGluSerValValThrAspLeuAsnSerThrAla 169
Db 494 ACCGAAAAGGCATTGGACGTGGCAGAAAGTGTGACTGATCTCAACTCACTGCC 553
QY 170 LeuGlyLeuArgThrLeuArgLeuHisGlyTyrrThrValSerSerAspValLeuAsnVal 189
Db 554 TTGGGCTTCGAAGCTCTCCGACTACACGATACACAGTGTCTTACATGTTCTGATCAC 613
QY 190 PheLeuAspIleAsnGlyGlnPheSerSerThrAlaAsnIleGlnIleGlyGluIle 209
Db 614 TTCAAAAACGAGAGAGGGGAGTTTACTTGCTCTGCC--ATTCAACAGAAAGAGAGATA 670
QY 210 ArgGlyValLeuAsnLeuPheArgAlaSerLeuValAlaPheProGlyGlyValMet 229
Db 671 AGAGATGCTCTCAATTATTTCGGGCACTCTCATTCGCTTCCGCGAATAAATTATG 730
QY 230 AspGluAlaGluThrPheSerThrTyrrLeuArgGluAlaLeuGlnIleProAla 249
Db 731 GAGCGCGCTGAATCTTCTCTACATGATTTAAAGATGCCCTCAAAAAGATTCCGCC 790
QY 250 SerSerIle 252
Db 791 TCCGCTCTT 799
RESULT 9
LOCUS CF663845 616 bp mRNA linear EST 07-OCT-2003
DEFINITION RTCNT1_5_B08_g1_A029 Root control Pinus taeda cDNA clone
RTCNT1_5_B08_A029 5', mRNA sequence.
ACCESSION CF663845
VERSION CF663845.1 GI:37561088
KEYWORDS EST.
SOURCE Pinus taeda (loblolly pine)
ORGANISM Pinus taeda
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 616)
AUTHORS Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W., Zimmermann, C. and Dean, J.F.D.
TITLE An EST database from untreated loblolly pine (Pinus taeda) roots
JOURNAL Unpublished (2003)
COMMENT Other ESTs: RTCNT1_5_B08_b1_A029
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210

Email: mmprratt@uga.edu
RNA prepared and library constructed by W. Walter Lorenz (School of Forest Resources, University of Georgia); plant material prepared by Craig Zimmermann (School of Forest Resources, University of Georgia) using rooted cuttings provided by the Forest Biology Research Cooperative (FBRC) and the CCLONES project a the University of Florida; sequencing done in the laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.
Seq primer: JENREV (CAGGAACAGCTATGACC).

FEATURES
source
location/Qualifiers
1..616
/organism="Pinus taeda"
/mol_type="mRNA"
/strain="3 CCLONES"
/db_xref="taxon:3352"
/clone="RTCNT1_5_B08_A029"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="Root control"
/note="Organ: root; Vector: pSL1180; Site_1: EcoRI; Site_2: XhoI; The library was prepared from polyA+ RNA from the roots of 1-year-old loblolly pine (Pinus taeda) cuttings that were rooted and then planted in washed sand. Just before harvesting roots for RNA isolation, the rooted cuttings were maintained for 27 days (April 2003) under ambient conditions in a local greenhouse. They were kept on a weekly regimen of 0.5x nutrient-complete Hoagland's solution and supplemented with additional water sufficient to maintain a 15% soil moisture content. Double-stranded cDNA was cloned unidirectionally into pSL1180. Inserts can be excised with EcoRI (5' end) and XhoI (3' end)."

Alignment Scores:
Pred. No.: 7.81e-80 Length: 616
Score: 786.00 Matches: 143
Percent Similarity: 83.08% Conservative: 24
Best Local Similarity: 71.14% Mismatches: 34
Query Match: 24.18% Indels: 0
DB: 14 Gaps: 0

ORIGIN
US-10-025-145A-65 (1-618) x CF663845 (1-616)
QY 286 LysAnlYsASmAlaIaGlYsLeuLeuGlYleuAlaLysLeuGlYpHeAsnIlePhe 305
Db 12 AAGACGACGACCAAGACCAGGAAGCTTTAGAACTTGCAAAATTGGAGTTCAATATCTTT 71
QY 306 HisSerLeuGIngluArgGluLeuLysHisValSerArgTrpTrpLysAspSerGlySer 325
Db 72 CACTCCTTAACAGCAAAAGAGTTAAACAGCTGCCAGATGGTGAAAGATTGGGTTTC 131
QY 326 ProGluMetThrPheCysArgHisArgHisValGluTyrTrpAlaLeuAlaSerCysIle 345
Db 132 TCTCACTGACATTCACCTCGGCATGTCACGTCGAATTCACACTTTGGCCTCGCATT 191
QY 346 AlaPheGluProGlnHisSerGlyPheArgLeuGlyPheThrLysMetSerHisLeuIle 365
Db 192 GCCACTGAGCCCCAACAATTCAGCATTTGGGCTTGGCCAAAACGTATTATCTTGA 251
QY 366 ThrValLeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluLeuPheThr 385
Db 252 ATAGTTCTGGACGACATCATGACACTTTCGGAACAATGAGAGCTCGAACTCTTACA 311
QY 386 AlaThrIleLysArgTrpAspTrpSerAlaMetGluCysLeuProGluTyrMetLysGly 405
Db 312 GCCGCAATTAAAGATGGATCCGTCGCCAGGAGTTCTCTCCAGAAATATGAAAGGC 371

QY 406 ValTyrMetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluLysAlaGln 425
Db 372 ATATATATGTTGTTTACGATTGCCGTTAATCAAAATGGCTTCAGAGCGGAGAGAGTCAA 431
QY 426 GlyArgAspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMet 445
Db 432 GGCGAGACACGCTCACCCTACCTCGAAATACGTGGAGAGCCGTAATTGATCGCTTCTG 491
QY 446 GIngluAlaLysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsn 465
Db 492 GAAGAACCAAGTGTGATGTCACGCGTTATATACCACCGTTGAGAGATTGGAGAAC 551
QY 466 GlyLysValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIle 485
Db 552 GGGAAGGTGAGTTTGGGTATCGACAGCACCACTGCACACCCATCTCAGCTTGATATT 611
QY 486 Pro 486
Db 612 CCC 614

RESULT 10
CF476978 637 bp mRNA linear EST 08-SEP-2003
LOCUS CF476978
DEFINITION RTMW3_5_A06.b1_A022 well-watered loblolly pine roots WM3 Pinus taeda cDNA clone RTMW3_5_A06_A022 3', mRNA sequence.
ACCESSION CF476978 GI:34505847
VERSION CF476978.1
KEYWORDS EST.
SOURCE Pinus taeda (loblolly pine)
ORGANISM Pinus taeda

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 637)
Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W., Dean, J., Gebremedhin, M., Dervinis, C., Martin, T., White, T., Davis, J. and Neale, D.

TITLE An EST database from well-watered loblolly pine (Pinus taeda) roots
JOURNAL Unpublished (2003)
COMMENT Other ESTs: RTMW3_5_A06.g1_A022
Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmprratt@uga.edu
RNA prepared and library constructed by W. Walter Lorenz, School of Forestry, University of Georgia; plant material prepared at the University of Florida; sequencing done in the laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.
Seq primer: M13-21 (TGTAACAACGACGGCCAGT)
POLYA=Yes.

FEATURES
source
location/Qualifiers
1..637
/organism="Pinus taeda"
/mol_type="mRNA"
/strain="CCLONES"
/db_xref="taxon:3352"
/clone="RTMW3_5_A06_A022"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="well-watered loblolly pine roots WM3"
/note="Vector: pSL1180; Site_1: EcoRI; Site_2: XhoI; The library was prepared from polyA+ RNA from loblolly pine (Pinus taeda) roots watered to pot capacity every other day. Pre-dawn water potential remained -0.3 MPa +/-0.1. Roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL1180. Inserts excised with EcoRI (5' end) and XhoI (3' end)."

ORIGIN

Alignment Scores:

Pred. No.: 2.92e-77 Length: 637
Score: 764.00 Matches: 142
Percent Similarity: 86.41% Conservative: 17
Best Local Similarity: 77.17% Mismatches: 25
Query Match: 23.50% Indels: 0
DB: 14 Gaps: 0

US-10-025-145A-65 (1-618) x CF476978 (1-637)

QY 435 GlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGluAlaLysTrpIleAlaThrGly 454
DB 3 CAGGCTTGGAGGAATATATTGATTCGTATATGCAAGAGCAAGTGGATCGCCAGTGT 62
QY 455 TyrLeuProThrPheGluGluTyrLeuGluAsnGlyLysValSerSerAlaHisArgPro 474
DB 63 GAGGTGCCAATTTGAGAGTACTACGAAACGGAAATTAAGTCTGTCGTCATCGCGTA 122
QY 475 CysAlaLeuGlnProIleLeuThrLeuAspIleProPheProAspHisIleLeuLysGlu 494
DB 123 TCGGCATGCAACCCATCTTGACGACGACATCCCTTCTCGACGACGTCCTCAAGAA 182
QY 495 ValAspPheProSerLysLeuAsnAspIleLeuArgLeuArgGlyAsp 514
DB 183 GCTGACATTCATCGAAGCTCATGATGCTGATTCGCCATTCCTCGATTAAGAGAGAT 242
QY 515 ThrArgCysTyrLysAlaAspArgAlaArgGlyGluAlaSerSerIleSerCysTyr 534
DB 243 ACGCGCTGCTACCAAGCGGACAGGCGCCGTCGAGAGAAAGCTTCGTATATCTTGTAT 302
QY 535 MetLysAspAsnProGlyLeuThrGluAspAlaLeuAsnHisIleAsnPheMetIle 554
DB 303 ATGAAGACAAATCTGAGCAACGGAAGATGCTCTCAATCATATCAACGCCATGATC 362
QY 555 ArgAspAlaIleArgGluLeuAsnTrpGluLeuLysProAspAsnSerValProIle 574
DB 363 AGTGAATGTAATTAAGATTAATTTGGAGCTTCTCAACCAACAGCAGCGTCCCAT 422
QY 575 ThrSerLysLysHisAlaPheAspIleSerArgValTrpHisHisGlyTyrArgTyrArg 594
DB 423 TCTGCCAAAAACATGCTTTTGACATTAAGAGAGCTTCCATTAATGCTACAATATCGA 482
QY 595 AspGlyTyrSerPheAlaAsnValGluThrLysSerLeuValMetArgThrValIleGlu 614
DB 483 GATGGCTACAGCGTTGCCAGCATTAACAAGAGTTGGTGAAGCGAACCGTCATTGAT 542
QY 615 ProValProLeu 618
DB 543 GCTGTGACTTTA 554

RESULT 11
AL750951 481 bp mRNA linear EST 20-JUN-2002
LOCUS AL750951 RS pinus pinaster cDNA clone RS02D01 similar to PINENE
DEFINITION SYNTHASE, mRNA sequence.
ACCESSION AL750951
VERSION AL750951.1 GI:21492198
KEYWORDS EST.
SOURCE pinus pinaster
ORGANISM pinus pinaster
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
1 (bases 1 to 481)
AUTHORS Frigerio, J. and Plomion, C.
TITLE Identification of water-deficit responsive genes in Maritime pine
(Pinus pinaster Ait.) using an EST approach
JOURNAL Unpublished (2002)
COMMENT Contact: Frigerio JM
Genetique et Amelioration 69
INRA
route d'Arcachon 33612 Cestas CEDEX France
Email: Frigerio@pierroton.inra.fr
Seq primer: T3.

FEATURES

source

location/Qualifiers

1..481
/organism="Pinus pinaster"
/mol_type="mRNA"
/db_xref="taxon:71647"
/clone="RS02D01"
/cissue_type="root"
/dev_stage="6 weeks old seedling"
/lab_host="SOLR"
/clone_lib="RS"

/note="Vector: Uni-ZAP XR; ecotype: Landes; The library was made from the roots of 6 weeks old seedlings grown in hydroponic conditions. A three weeks drought stress treatment was applied by lowering the osmotic potential of the nutrient solution to -0.45 MPa using 170 g/l of polyethylene glycol as an osmoticum. A mixture of genotypes were used. Oligo-dT primed cDNA was directionally cloned into the EcoRI-XhoI lambda-ZAP vector arms and mass-excised to form a pBluescript phagemid"

ORIGIN

Alignment Scores:

Pred. No.: 6.76e-74 Length: 481
Score: 733.00 Matches: 134
Percent Similarity: 90.62% Conservative: 11
Best Local Similarity: 83.75% Mismatches: 15
Query Match: 22.55% Indels: 0
DB: 9 Gaps: 0

US-10-025-145A-65 (1-618) x AL750951 (1-481)

QY 335 HisValGluTyrTyrAlaLeuAlaSerCysIleAlaPheGluProGlnHisSerGlyPhe 354
DB 2 CACGTGAGTACTACACTTTGGCTTCCTGCATCGCGTTGAGCCCAACATTCGATTC 61
QY 355 ArgLeuGlyPheThrLysMetSerHisLeuIleThrValLeuAspAspMetTyrAspVal 374
DB 62 AGACTCGGCTTTGCCAAAGCGTGTCTATATACACTGTTCTCGACGATATGACACCTC 121
QY 375 PheGlyThrValAspGluLeuGluPheThrAlaThrIleLysArgTyrAspProSer 394
DB 122 TTGGGAACGTTGATGAGCTCAACTGTTCAAGCCGCAATTAAGATGGATCCGTCC 181
QY 395 AlaMetGluCysLeuProGluTyrMetLysGlyValTyrMetMetValTyrHisThrVal 414
DB 182 GCCACAGATTGCCCTCCACAAATATGAAGAATTACATGATGTTTACAACACCGTA 241
QY 415 AsnGluMetAlaArgValAlaGluLysAlaGlnGlyArgAspThrLeuAsnTyrAlaArg 434
DB 242 AATGAATGTCTGCGGAGCACAGAGGCTCAAGCCGAGACACTCTCAACTATGCTCGA 301
QY 435 GlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGluAlaLysTrpIleAlaThrGly 454
DB 302 CAGGCTTGGAGGATTAATCTTGATTCGTATATGCAAGAGCAAGTGAATGACCGGT 361
QY 455 TyrLeuProThrPheGluGluTyrLeuGluAsnGlyLysValSerSerAlaHisArgPro 474
DB 362 TATCTGCCAAGCTTCGAGGAATACTTGAGAAACGGAAAGTTAGCTTGGGCATCGCGTG 421
QY 475 CysAlaLeuGlnProIleLeuThrLeuAspIleProPheProAspHisIleLeuLysGlu 494
DB 422 TCGGCGTTGCAACCATGCTGACGATGACATCCCTTCTCTCATCATCTCAAGAA 481

RESULT 12

CF477562/c 740 bp mRNA linear EST 08-SEP-2003
LOCUS RTMW3_8_G10_g1_A022 Well-watered loblolly pine roots W3 Pinus
DEFINITION taeda cDNA clone RTMW3_8_G10_A022 5', mRNA sequence.
ACCESSION CF477562
VERSION CF477562.1 GI:34506431
KEYWORDS EST.
SOURCE Pinus taeda (loblolly pine)
ORGANISM Pinus taeda

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 740)
Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W. W., Dean, J., Gebremedhin, M., Dervinis, C., Martin, T., White, T., Davis, J. and Neale, D.
An EST database from well-watered loblolly pine (Pinus taeda) roots Unpublished (2003)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmp Pratt@uga.edu
RNA prepared and library constructed by W. Walter Lorenz, School of Forestry, University of Georgia; plant material prepared at the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.
Seq primer: JENREV (CAGGAACAGCTATGACC).

FEATURES
source
1..740
/organism="Pinus taeda"
/mol_type="mRNA"
/strain="CCLONES"
/db_xref="taxon:3352"
/clone="RTW3_8_G10_A022"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="Well-watered loblolly pine roots WM3"
/note="Vector: pSL180; Site 1: EcoRI; Site 2: XhoI; The library was prepared from polyA+ RNA from loblolly pine (Pinus taeda) roots watered to pot capacity every other day. Pre-dawn water potential remained -0.3 MPa +/-0.1. Roots were harvested for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL180. Inserts excised with EcoRI (5' end) and XhoI (3' end)."

ORIGIN

Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:

2.14e-72
723.00
84.54%
66.49%
22.24%
14

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

740
129
35
30
0
0

US-10-025-145A-65 (1-618) x CF477562 (1-740)

Qy 425 GlnGlyArgAspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyr 444
Db 739 CAAGGCTGGGATACAGTCAGCTATGCTCGAAATCTTGGAGGCTTTTATTGTGCTTAT 680
Qy 445 MetGlnGluAlaLysTrpIleAlaThrGlyTyrLeuProThrPheGlnGluTyrLeuGlu 464
Db 679 ATACAAGAGCCCAAGTGGATTTCAGTGGTTATCTTCCACGTTCCAGCAGTACCTCGAG 620
Qy 465 AsnGlyValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAsp 484
Db 619 AATGGGAAGTCACTTCGGCTCTCGCATACACGCTCGAACCCATGCTGACTTTGGGG 560
Qy 485 IleProPheProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeu 504
Db 559 TTTCTCTTCCTCCGCTCGAATCCTGCAGGAATGACTTTCATCCGAATTCATGATTGG 500
Qy 505 IleCysIleIleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArg 524
Db 499 ATATGTGCATCTTCGACTGAAAGGTGACACTCAATGCTACCAAGGCTGACAGGCGCGT 440
Qy 525 GlyGlnGluAlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGlnGlu 544

Db 439 GGAGAAGAAGCTTCGGCCCGTATCGTTATATGAAAGCAATCCTGGAATAACAGAGAA 380
Qy 545 AspAlaLeuAsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeuAsnTrpGlu 564
Db 379 GATGCTGTCAATCAAGTCAATGCTATGTGTCGATAACTTAACCAAGAACTGAATTGGAG 320
Qy 565 LeuLeuLysProAspAsnSerValProIleThrSerLysLysHisAlaPheAspIleSer 584
Db 319 TTAATTAGACCCGACAGCGGTGTTCATCTCTTACAGAAGGTTGCTTTGACATTGGC 260
Qy 585 ArgValTrpHisHisGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsnValGluThr 604
Db 259 AGAGTTTTCATTACGTTACAAATAACAGAGATGGCTTCAGTGTGCCAGTATGAAATA 200
Qy 605 LysSerLeuValMetArgThrValIleGluProValProLeu 618
Db 199 AAGATTGTGTACACAAGAACCGTGTGAACACTGTGCTTTG 158

RESULT 13
BQ698077
LOCUS
DEFINITION

BQ698077 516 bp mRNA linear EST 07-MAY-2003
NXPV_064_C05_F NXPV (Nsf Xylem Planings wood Vertical) Pinus taeda
cDNA clone NXPV_064_C05 5' similar to Arabidopsis thaliana sequence
Atlg61680 hypothetical protein see
http://mips.gsf.de/proj/thal/db/index.html, mRNA sequence.

BQ698077
BQ698077.1 GI:21823393
EST.
Pinus taeda (loblolly pine)

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 516)
Sederoff, R.
Molecular Basis of Wood Formation in the Pine Megagenome
Unpublished (2000)
Contact: Sederoff, Ron
Forest Biotechnology
North Carolina State University
840 Main Campus Drive, Centennial Campus, Campus Box 7247, Raleigh, NC 27695, USA
Tel: 919 515 7800
Fax: 919 515 7801
Email: ron.sederoff@ncsu.edu, jerri.johnson@ncsu.edu
Please see http://web.ahc.umn.edu/biodata/nsfpine/ for further information.
Seq primer: T3.

FEATURES
source
1..516
/organism="Pinus taeda"
/mol_type="mRNA"
/strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
/clone="NXPV_064_C05"
/tissue_type="Xylem"
/cell_type="Planings (secondary)"
/dev_stage="Transitional"
/lab_host="XLI-Blue"
/clone_lib="NXPV (Nsf Xylem Planings wood Vertical)"
/note="Vector: Bluescript SK; Site 1: Eco RI; Site 2: XhoI; The library is from early (spring) secondary wood, taken from a ten year old tree in the transitional phase. The tree is a kind gift of the Westvaco Corporation. Secondary xylem was harvested from the tree by peeling back the bark and primary xylem and then removing the underlying tissue with a block plane. NOTE: The sequences contain a 'cDNA adapter' between the EcoRI site and the start of the EST. The adapter sequence is 'AATTCGACAGAG'."

ORIGIN

Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:

5.46e-72
516

Score: 717.00 Matches: 133
Percent Similarity: 88.17% Conservative: 16
Best Local Similarity: 78.70% Mismatches: 20
Query Match: 22.05% Indels: 0
DB: 13 Gaps: 0

US-10-025-145A-65 (1-618) x BQ698077 (1-516)

QY 442 ApsSerTyrMetGlnGluAlaIleTyrPheAlaThrGlyTyrLeuProThrPheGluGlu 461
|||:::|||||
DB 8 GATGCCGTATATCCAGAAGCAAGTGATGCCAGTGGTGAGGTGCCAATTTGAGAG 67
QY 462 TyrLeuGluAaNGlyLysValSerSerAlaHisArgProCysAlaLeuGlnProIleLeu 481
|||:::|||||
DB 68 TACTATGAGAACGGAAAGTTAGCTGTGTCATCGCGTATCGGCATTTGCAACCATTTTG 127
QY 482 ThrLeuAspIleProPheProAspHisIleLeuLysGluValAspPheProSerLysLeu 501
|||:::|||||
DB 128 ACGACCGACATCCCTTCTTCCAGACGCTCTCAAGAGAGTTGACATTCCATCGCAGCTC 187
QY 502 AsnAspLeuIleCysIleIleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAsp 521
|||:::|||||
DB 188 AATGACTTGCGCATCTGCCATTCTCGATTACGAGGGGATACGGCTGCTACCAAGCGGAC 247
QY 522 ArgAlaArgGlyGluGluAlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeu 541
|||:::|||||
DB 248 AGGGCCCGTGAGAGAGAGCTTCGTATATCTTGTATATGAAGACAATCCTGGAACA 307
QY 542 ThrGluGluAspAlaLeuAsnHisIleAsnPheMetIleArgAspAlaIleArgGluLeu 561
|||:::|||||
DB 308 ACAGAGGAGAGATGCTCTCAATCATCTCAACGCCATGATCAGTGTATTAAAGGATTA 367
QY 562 AsnTrpGluLeuLeuLysProAspAsnSerValProIleThrSerLysLysHisAlaPhe 581
|||:::|||||
DB 368 AATTGGAGCTTCTCAAAACCAACGACGCTTCCCATATCTGCCAAAACATGCTTTT 427
QY 582 AspIleSerArgValTrpHisIleGlyTyrArgTyrArgAspGlyTyrSerPheAlaAsn 601
|||:::|||||
DB 428 GACATTAGCAGAGCTTTCATTTGCTGCTACAAATATCGAGATGGCTACAGCGTTGCCAAC 487
QY 602 ValGluThrLysSerLeuValMetArg 610
:::|||||
DB 488 ATTGAACAAGAGTTGGTGAAGAGA 514

RESULT 14

BX677624 517 bp mRNA linear EST 28-OCT-2003
LOCUS BX677624 RN Pinus pinaster cDNA clone RN42B08, mRNA sequence.
DEFINITION BX677624
ACCESSION BX677624
VERSION BX677624.1 GI:38011576

KEYWORDS EST.
SOURCE Pinus pinaster
ORGANISM Pinus pinaster

REFERENCE 1 (bases 1 to 517)
AUTHORS Frigerio,J. and Plomion,C.
TITLE Identification of water-deficit responsive genes in Maritime pine
(Pinus pinaster Ait.) using an EST approach
JOURNAL Unpublished (2002)
COMMENT Contact: Frigerio JM
Genetique et Amelioration 69

JOURNAL COMMENT

route d'Arcachon 33612 Cestas CEDEX France
Email: Frigerio@pierroton.inra.fr
Email: Frigerio@pierroton.inra.fr
Seq primer: T3.

FEATURES

source 1..517
location/Qualifiers
/organism="Pinus pinaster"
/mol_type="mRNA"
/db_xref="taxon:71647"
/clone="RN42B08"

/cissue_type="root"
/dev_stage="6 weeks old seedling"
/lab_host="SOLR"
/clone_lib="RN"
/note="Vector: Uni-ZAP XR; ecotype: Landes; The library
was made from the roots of 6 weeks old seedlings grown in
hydroponic conditions. A mixture of genotypes were used.
Oligo-dT primed cDNA was directionally cloned into the
EcoRI-XhoI lambda-ZAP vector arms and mass-excised to form
a pBluescript phagemid"

ORIGIN

Alignment Scores:
Pred. No.: 1.59e-71 Length: 517
Score: 713.00 Matches: 136
Percent Similarity: 86.63% Conservative: 13
Best Local Similarity: 79.07% Mismatches: 23
Query Match: 21.93% Indels: 1
DB: 13 Gaps: 0

US-10-025-145A-65 (1-618) x BX677624 (1-517)

QY 394 SerAlaMetGluCysLeuProGluTyrMetLysGlyValTyrMetMetValTyrHisThr 413
|||:::|||||
DB 1 TCGGCGACAGAGTGCCCTTCCAGATATATGAAAGAGT-TACATGATAGTTTACACACT 59
QY 414 ValAsnGluMetAlaArgValAlaGluLysAlaGlnGlyArgAspThrLeuAsnTyrAla 433
|||:::|||||
DB 60 ATAAATGAATGTCTCAAGAGGCGACAGACAGCTCAAGCCGACGCTCACTATTGT 119
QY 434 ArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGluAlaIleTyrPheAlaThr 453
|||:::|||||
DB 120 CGACAGGCTTGGAGAGATATATTGATGCGTATATGCAAGAGCAAGTGATCGCCAGT 179
QY 454 GlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLysValSerSerAlaHisArg 473
|||:::|||||
DB 180 GGTGAGTGCCAAACATTTGAGGAGTATATGAGAACGGAAAGTTAGCTTGGTCACTGC 239
QY 474 ProCysAlaLeuGlnProIleLeuThrLeuAspIleProPheProAspHisIleLeuLys 493
|||:::|||||
DB 240 GTATCGGCATTGCAACCCATCTGACGACGACATCCCTTCTTCCAGACAGCTCTCAAG 299
QY 494 GluValAspPheProSerLysLeuAsnAspLeuIleCysIleIleLeuArgLeuArgGly 513
|||:::|||||
DB 300 GAAGTGACATTCCTCATGAGCTCATGACTTGCGCATCTGCCATTCTTGATTACGAGGG 359
QY 514 AspThrArgCysTyrLysAlaAspArgAlaArgGlyGluGluAlaSerSerIleSerCys 533
|||:::|||||
DB 360 GACACTCGCTCTACCAAGCGGACAGCGCCCTGGAGAGAGAGCTTCGGGTATATCTTGT 419
QY 534 TyrMetLysAspAsnProGlyLeuThrGluGluAspAlaLeuAsnHisIleAsnPheMet 553
|||:::|||||
DB 420 TATATGAAGACAATCTGTGAACACAGAGAGATGCTCTCAATCATATCAACGCCATG 479
QY 554 IleArgAspAlaIleArgGluLeuAsnTrpGluLeu 565
|||:::|||||
DB 480 ATCAGTGATGTATTAAAGATTAAATTGGAGCTT 515

RESULT 15

AW287756 539 bp mRNA linear EST 07-JAN-2000
LOCUS AW287756
DEFINITION EST0004 Sitka spruce drill-wounded bark Picea sitchensis cDNA clone
25-1-3-5' similar to mono-terpene synthase, mRNA sequence.
ACCESSION AW287756
VERSION AW287756.1 GI:6681768

KEYWORDS EST.
SOURCE Picea sitchensis (Sitka spruce)
ORGANISM Picea sitchensis

REFERENCE 1 (bases 1 to 539)
AUTHORS Wang,S.X., Hunter,W. and Plant,A.L.
TITLE Isolation of terpene synthase gene-specific probes from Sitka

JOURNAL
COMMENT

spruce and induction of gene expression by simulated white pine
weevil damage
Unpublished (2000)
Contact: Wang SX
Department of Biological Sciences
Simon Fraser University
8888 University Drive, Burnaby, BC V5A1S6, Canada
Tel: 604 584 8870
Fax: 604 584 8873
Email: sxwang@bigfoot.com
Clone sequence of a RT-PCR product from the mRNA of drill-wounded
Bark tissue
PCR primers
FORWARD: Mult-F10
BACKWARD: Mult-R18
Insert length: 539 Std Error: 0.00
Seq primer: M13 Reverse and M13 Forward.
High quality sequence stop: 539.
Location/Qualifiers

FEATURES
source

1..539
/organism="Picea sitchensis"
/mol_type="mRNA"
/db_xref="taxon:3332"
/clone="25-1-3"
/issue_type="bark"
/clone_lib="Sitka spruce drill-wounded bark"
/note="mRNA isolated from drill-wounded bark tissues;
RT-PCR product"

ORIGIN

Alignment Scores:
Pred. No.: 9.35e-70 Length: 539
Score: 698.00 Matches: 126
Percent Similarity: 84.09% Conservative: 22
Best Local Similarity: 71.59% Mismatches: 28
Query Match: 21.47% Indels: 0
DB: 10 Gaps: 0

US-10-025-145A-65 (1-618) x AW287756 (1-539)

QY 368 LeuAspAspMetTyrAspValPheGlyThrValAspGluLeuGluPheThrAlaThr 387
Db 3 CTCGACGACCTGTACGACACATTCGAAACAATGACGAAATCGAATCTTCACAGAAGCA 62
QY 388 IleYsArgTrpAspProSerAlaMetGluCysLeuProGluTyrMetIysGlyValTyr 407
Db 63 GTCAGAGATGGGATCCGTCGAGACAGAGACCTTCAGACTATATGAAAGAGGTGAC 122
QY 408 MetMetValTyrHisThrValAsnGluMetAlaArgValAlaGluIysAlaGlnGlyArg 427
Db 123 ATGGTACTCTACGAAGCCCTAACTGAAATGGCTCAAGAGCGGAGAAACACAGGCCGA 182
QY 428 AspThrLeuAsnTyrAlaArgGlnAlaTrpGluAlaCysPheAspSerTyrMetGlnGlu 447
Db 183 GACACGCTCAACTATGTCTGAAAGGCTTGGAGATTATCTGATTCGTATATTCAAGAA 242
QY 448 AlaIysTrpIleAlaThrGlyTyrLeuProThrPheGluGluTyrLeuGluAsnGlyLys 467
Db 243 GCAAGTGGATCGCCAGTGTATCTGCCAACATTTCAGAGTACTTTGAGAACGGGAAA 302
QY 468 ValSerSerAlaHisArgProCysAlaLeuGlnProIleLeuThrLeuAspIleProPhe 487
Db 303 ATTAGCTTGCTTATCGCGACGGGCAATTGACACCCATCCTCACAATTGGACGTACCGCTT 362
QY 488 ProAspHisIleLeuLysGluValAspPheProSerLysLeuAsnAspLeuIleCysIle 507
Db 363 CCTGAATACATCTTGAAGGAATGATTTCCATCGAGATTCAATGATTTGGCATCTTCC 422
QY 508 IleLeuArgLeuArgGlyAspThrArgCysTyrLysAlaAspArgAlaArgGlyGlu 527
Db 423 TTCCTTCGACTAAGAGGTGACACACGCTGCTACAAAGCGGATAGGCGCCGTGGAAGAA 482
QY 528 AlaSerSerIleSerCysTyrMetLysAspAsnProGlyLeuThrGlu 543

Db 483 GCTTCGTGCATATCTTGCTACATGAAGACCACTGCTACATGAA 530

Search completed: July 26, 2004, 20:35:39
Job time : 3477 secs